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(54) Title: NOVEL PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

(57) Abstract: The present invention provides polynucleotides and secreted proteins encoded by the polynucleotides. The proteins include a variety of fusion proteins, including fusions comprising a signal peptide selected from the group consisting of signal peptides shown in SEQ ID NO:M, wherein M is an even integer from 2 to 422, operably linked to a second polypeptide. The invention further provides therapeutic and diagnostic methods utilizing the polynucleotides, polypeptides, and antagonists of the polypeptides.

Description

5 NOVEL PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

BACKGROUND OF THE INVENTION

Within the field of genetic engineering, polynucleotides encoding proteins of interest have been identified and cloned by methods that require a detailed
10 knowledge of the structure and/or function of the polynucleotide or the encoded protein. These methods include hybridization screening, polymerase chain reaction (PCR), and expression cloning.

With the more recent advent of large DNA sequence databases and the accompanying data analysis tools, identification of genes of interest is possible through
15 the analysis of raw sequence data. Databases can be "mined" to locate sequences that resemble (are "homologous to") sequences of known function. Alignment of similar sequences can be used to place novel sequences within families of structurally similar sequences. These analytical tools can be combined with structural information obtained from, for example, X-ray crystallography to predict the higher order structure
20 of a novel polypeptide. These analyses also facilitate prediction of polypeptide function. These recent technological advances have greatly increased the pace of gene discovery.

Genetic engineering has made available a number of genes and proteins of pharmaceutical or other economic importance. Such proteins include, for example,
25 tissue plasminogen activator (t-PA) (U.S. Patent No. 4,766,075), coagulation factor VII (U.S. Patent No. 4,784,950), erythropoietin (U.S. Patent No. 4,703,008), platelet derived growth factor (U.S. Patent No. 4,889,919), and various industrial enzymes (e.g., U.S. Patents Nos. 5,965,384; 5,942,431; and 5,922,586).

Although estimates vary as to the amount of the human genome that has
30 been identified to date, there remains a need in the art for further characterization of the human genome and the proteins encoded thereby. Previously unknown genes and proteins will be useful in the treatment and/or prevention of many human diseases, included diseases that have heretofore been refractory to treatment.

35 SUMMARY OF THE INVENTION

Within one aspect of the invention there is provided an isolated polypeptide comprising fifteen contiguous amino acid residues of a polypeptide as

shown in SEQ ID NO:M, wherein M is an even integer from 2 to 422. Within one embodiment, the isolated polypeptide is from 15 to 2235 amino acid residues in length. Within another embodiment, the at least fifteen contiguous amino acid residues of SEQ ID NO:M are operably linked via a peptide bond or polypeptide linker to a second polypeptide selected from the group consisting of maltose binding protein, an immunoglobulin constant region, a polyhistidine tag, and a peptide as shown in SEQ ID NO:423. Within another embodiment, the polypeptide comprises at least 30 contiguous residues of SEQ ID NO:M. Within a further embodiment, the polypeptide comprises at least 47 contiguous residues of SEQ ID NO:M. Within additional embodiments, the polypeptide is selected from the group consisting of polypeptides of SEQ ID NOS: 4, 6, 8, 10, 12, 16, 18, 24, 28, 42, 48, 54, 62, 66, 68, 70, 72, 82, 90, 92, 94, 96, 98, 102, 106, 108, 110, 112, 122, 124, 130, 134, 136, 138, 140, 156, 158, 162, 164, 166, 168, 174, 178, 180, 186, 202, 204, 206, 208, 210, 224, 230, 232, 234, 236, 240, 242, 250, 252, 254, 258, 262, 270, 272, 284, 286, 288, 294, 300, 302, 306, 310, 312, 314, 316, 322, 324, 328, 326, 336, 338, 342, 344, 348, 350, 366, 368, 374, 378, 386, 388, 396, 398, 402, 406, 408, 412, 416, and 420; the group consisting of polypeptides of SEQ ID NOS: 4, 6, 8, 12, 16, 18, 24, 28, 42, 48, 54, 62, 66, 68, 70, 72, 90, 92, 94, 96, 98, 102, 106, 108, 110, 112, 122, 124, 130, 134, 138, 140, 156, 158, 162, 164, 166, 168, 174, 178, 180, 202, 204, 206, 210, 224, 230, 234, 236, 240, 242, 252, 254, 258, 262, 270, 272, 284, 286, 288, 294, 300, 302, 306, 312, 314, 322, 324, 326, 336, 338, 342, 344, 348, 350, 366, 368, 374, 378, 386, 388, 396, 398, 402, 406, 408, 412, 416, and 420; the group consisting of polypeptides of SEQ ID NOS: 4, 6, 8, 12, 16, 18, 24, 28, 42, 48, 54, 66, 68, 70, 72, 90, 92, 94, 96, 98, 102, 106, 108, 110, 112, 122, 124, 130, 134, 138, 140, 156, 158, 162, 164, 166, 168, 174, 178, 180, 202, 204, 206, 210, 224, 230, 234, 236, 240, 242, 252, 254, 258, 262, 270, 272, 284, 286, 288, 294, 300, 302, 306, 312, 314, 322, 324, 326, 338, 342, 344, 348, 350, 366, 368, 374, 378, 386, 388, 396, 398, 402, 406, 408, 412, and 416; or the group consisting of polypeptides of SEQ ID NOS: 6, 8, 12, 18, 24, 42, 48, 54, 66, 68, 70, 72, 90, 92, 96, 98, 102, 106, 110, 122, 134, 138, 140, 156, 158, 162, 164, 168, 174, 178, 180, 204, 206, 210, 224, 230, 234, 236, 240, 242, 252, 254, 258, 270, 272, 284, 286, 288, 294, 300, 302, 306, 312, 314, 324, 326, 338, 342, 344, 348, 350, 366, 368, 374, 378, 386, 388, 396, 398, 402, 408, 412, and 416.

Within a second aspect of the invention there is provided an isolated, mature protein encoded by a polynucleotide sequence selected from the group consisting of SEQ ID NO:N, wherein N is an odd integer from 1 to 421. Within certain embodiments, N is 3, 5, 7, 9, 11, 15, 17, 23, 27, 41, 47, 53, 61, 65, 67, 69, 71, 81, 89, 91, 93, 95, 97, 101, 105, 107, 109, 111, 121, 123, 129, 133, 135, 137, 139, 155,

157, 161, 163, 165, 167, 173, 177, 179, 185, 201, 203, 205, 207, 209, 223, 229, 231, 233, 235, 239, 241, 249, 251, 253, 257, 261, 269, 271, 283, 285, 287, 293, 299, 301, 305, 309, 311, 313, 315, 321, 323, 327, 325, 335, 337, 341, 343, 347, 349, 365, 367, 373, 377, 385, 387, 395, 397, 401, 405, 407, 411, 415, or 419; N is 3, 5, 7, 11, 15, 17, 23, 27, 41, 47, 53, 61, 65, 67, 69, 71, 89, 91, 93, 95, 97, 101, 105, 107, 109, 111, 121, 123, 129, 133, 137, 139, 155, 157, 161, 163, 165, 167, 173, 177, 179, 201, 203, 205, 209, 223, 229, 233, 235, 239, 241, 251, 253, 257, 261, 269, 271, 283, 285, 287, 293, 299, 301, 305, 311, 313, 321, 323, 325, 335, 337, 341, 343, 347, 349, 365, 367, 373, 377, 385, 387, 395, 397, 401, 405, 407, 411, 415, or 419; N is 3, 5, 7, 11, 15, 17, 23, 27, 41, 47, 53, 65, 67, 69, 71, 89, 91, 93, 95, 97, 101, 105, 107, 109, 111, 121, 123, 129, 133, 137, 139, 155, 157, 161, 163, 165, 167, 173, 177, 179, 201, 203, 205, 209, 223, 229, 233, 235, 239, 241, 251, 253, 257, 261, 269, 271, 283, 285, 287, 293, 299, 301, 305, 311, 313, 321, 323, 325, 337, 341, 343, 347, 349, 365, 367, 373, 377, 385, 387, 395, 397, 401, 405, 407, 411, or 415; or N is 5, 7, 11, 17, 23, 41, 47, 53, 65, 67, 69, 71, 89, 91, 95, 97, 101, 105, 109, 121, 133, 137, 139, 155, 157, 161, 163, 167, 173, 177, 179, 203, 205, 209, 223, 229, 233, 235, 239, 241, 251, 253, 257, 269, 271, 283, 285, 287, 293, 299, 301, 305, 311, 313, 323, 325, 337, 341, 343, 347, 349, 365, 367, 373, 377, 385, 387, 395, 397, 401, 407, 411, or 415.

A third aspect of the invention provides isolated polynucleotides encoding the polypeptides disclosed above. Within certain embodiments of the invention the polynucleotides comprise a sequence of nucleotides as shown in SEQ ID NO:N, wherein N is an odd integer as defined above

Within a fourth aspect of the invention there is provided an expression vector comprising the following operably linked elements: a transcription promoter; a DNA segment encoding a polypeptide as shown in SEQ ID NO:M, wherein M is an even integer from 2 to 422; and a transcription terminator. Within certain embodiments, M is 4, 6, 8, 10, 12, 16, 18, 24, 28, 42, 48, 54, 62, 66, 68, 70, 72, 82, 90, 92, 94, 96, 98, 102, 106, 108, 110, 112, 122, 124, 130, 134, 136, 138, 140, 156, 158, 162, 164, 166, 168, 174, 178, 180, 186, 202, 204, 206, 208, 210, 224, 230, 232, 234, 236, 240, 242, 250, 252, 254, 258, 262, 270, 272, 284, 286, 288, 294, 300, 302, 306, 310, 312, 314, 316, 322, 324, 328, 326, 336, 338, 342, 344, 348, 350, 366, 368, 374, 378, 386, 388, 396, 398, 402, 406, 408, 412, 416, or 420; M is 4, 6, 8, 12, 16, 18, 24, 28, 42, 48, 54, 62, 66, 68, 70, 72, 90, 92, 94, 96, 98, 102, 106, 108, 110, 112, 122, 124, 130, 134, 138, 140, 156, 158, 162, 164, 166, 168, 174, 178, 180, 202, 204, 206, 210, 224, 230, 234, 236, 240, 242, 252, 254, 258, 262, 270, 272, 284, 286, 288, 294, 300, 302, 306, 312, 314, 322, 324, 326, 336, 338, 342, 344, 348, 350, 366, 368, 374, 378, 386, 388, 396, 398, 402, 406, 408, 412, 416, or 420; M is 4, 6, 8, 12, 16, 18, 24, 28, 42,

48, 54, 66, 68, 70, 72, 90, 92, 94, 96, 98, 102, 106, 108, 110, 112, 122, 124, 130, 134, 138, 140, 156, 158, 162, 164, 166, 168, 174, 178, 180, 202, 204, 206, 210, 224, 230, 234, 236, 240, 242, 252, 254, 258, 262, 270, 272, 284, 286, 288, 294, 300, 302, 306, 312, 314, 322, 324, 326, 338, 342, 344, 348, 350, 366, 368, 374, 378, 386, 388, 396, 398, 402, 406, 408, 412, or 416; or M is 6, 8, 12, 18, 24, 42, 48, 54, 66, 68, 70, 72, 90, 92, 96, 98, 102, 106, 110, 122, 134, 138, 140, 156, 158, 162, 164, 168, 174, 178, 180, 204, 206, 210, 224, 230, 234, 236, 240, 242, 252, 254, 258, 270, 272, 284, 286, 288, 294, 300, 302, 306, 312, 314, 324, 326, 338, 342, 344, 348, 350, 366, 368, 374, 378, 386, 388, 396, 398, 402, 408, 412, or 416.

10 A fifth aspect of the invention provides a cultured cell comprising the expression vector disclosed above. The cultured cell can be used, *inter alia*, within a method of producing a polypeptide, the method comprising (a) culturing the cell under conditions whereby the sequence of nucleotides is expressed, and (b) recovering the polypeptide. The invention also provides a polypeptide produced by this method.

15 Within a sixth aspect of the invention there is provided an isolated polynucleotide encoding a fusion protein, wherein the fusion protein comprises a secretory peptide selected from the group consisting of secretory peptides shown in SEQ ID NO:M, wherein M is an even integer as defined above, operably linked to a second polypeptide.

20 Within a seventh aspect of the invention there is provided an expression vector comprising the following operably linked elements: a transcription promoter; a DNA segment encoding a fusion protein as disclosed above; and a transcription terminator. The invention further provides a cultured cell comprising this expression vector, wherein the cell expresses the DNA segment and produces the encoded fusion protein. Also provided is a method of producing a protein comprising culturing the cell under conditions whereby the DNA segment is expressed, and recovering the second polypeptide. Within one embodiment the recovered second polypeptide is joined to a portion of a protein of SEQ ID NO: M, wherein M is an even integer as defined above.

25 Within a further aspect of the invention there is provided a computer-readable medium encoded with a data structure comprising SEQ ID NO:X, wherein X is an integer from 1 to 422.

30 Within an additional aspect of the invention there is provided an antibody that specifically binds to a protein selected from of the group consisting of SEQ ID NO:M, wherein M is an even integer as defined above.

35 These and other aspects of the invention will become evident upon reference to the following detailed description of the invention.

DETAILED DESCRIPTION OF THE INVENTION

Prior to setting forth the invention in detail, it may be helpful to the understanding thereof to define the following terms:

The term "affinity tag" is used herein to denote a polypeptide segment that can be attached to a second polypeptide to provide for purification of the second polypeptide or provide sites for attachment of the second polypeptide to a substrate. In principal, any peptide or protein for which an antibody or other specific binding agent is available can be used as an affinity tag. Affinity tags include a poly-histidine tract, protein A (Nilsson et al., *EMBO J.* 4:1075, 1985; Nilsson et al., *Methods Enzymol.* 198:3, 1991), glutathione S transferase (Smith and Johnson, *Gene* 67:31, 1988), Glu-Glu affinity tag (Grussenmeyer et al., *Proc. Natl. Acad. Sci. USA* 82:7952-7954, 1985; see SEQ ID NO:423), substance P, Flag™ peptide (Hopp et al., *Biotechnology* 6:1204-1210, 1988), maltose binding protein (Kellerman and Ferenci, *Methods Enzymol.* 90:459-463, 1982; Guan et al., *Gene* 67:21-30, 1987), streptavidin binding peptide, thioredoxin, ubiquitin, cellulose binding protein, T7 polymerase, immunoglobulin constant domain, or other antigenic epitope or binding domain. See, in general, Ford et al., *Protein Expression and Purification* 2: 95-107, 1991. Affinity tags can be used individually or in combination. DNAs encoding affinity tags and otehr reagents are available from commercial suppliers (e.g., Pharmacia Biotech, Piscataway, NJ; Eastman Kodak, New Haven, CT; New England Biolabs, Beverly, MA).

The term "allelic variant" is used herein to denote any of two or more alternative forms of a gene occupying the same chromosomal locus. Allelic variation arises naturally through mutation, and may result in phenotypic polymorphism within populations. Gene mutations can be silent (no change in the encoded polypeptide) or may encode polypeptides having altered amino acid sequence. The term allelic variant is also used herein to denote a protein encoded by an allelic variant of a gene.

The terms "amino-terminal" and "carboxyl-terminal" are used herein to denote positions within polypeptides. Where the context allows, these terms are used with reference to a particular sequence or portion of a polypeptide to denote proximity or relative position. For example, a certain sequence positioned carboxyl-terminal to a reference sequence within a polypeptide is located proximal to the carboxyl terminus of the reference sequence, but is not necessarily at the carboxyl terminus of the complete polypeptide.

A "complement" of a polynucleotide molecule is a polynucleotide molecule having a complementary base sequence and reverse orientation as compared to a reference sequence. For example, the sequence 5' ATGCACGGG 3' is complementary to 5' CCCGTGCAT 3'.

"Corresponding to", when used in reference to a nucleotide or amino acid sequence, indicates the position in a second sequence that aligns with the reference position when two sequences are optimally aligned.

The term "degenerate nucleotide sequence" denotes a sequence of
5 nucleotides that includes one or more degenerate codons (as compared to a reference polynucleotide molecule that encodes a polypeptide). Degenerate codons encompass different triplets of nucleotides, but encode the same amino acid residue (i.e., GAU and GAC triplets each encode Asp).

The term "expression vector" is used to denote a DNA molecule, linear
10 or circular, that comprises a segment encoding a polypeptide of interest operably linked to additional segments that provide for its transcription, wherein said segments are arranged in a way that does not exist naturally. Such additional segments include promoter and terminator sequences, and may also include one or more origins of replication, one or more selectable markers, an enhancer, a polyadenylation signal, etc.
15 Expression vectors are generally derived from plasmid or viral DNA, or may contain elements of both.

The term "isolated", when applied to a polynucleotide, denotes that the polynucleotide has been removed from its natural genetic milieu and is thus free of other extraneous or unwanted coding sequences, and is in a form suitable for use within
20 genetically engineered protein production systems. Such isolated molecules are those that are separated from their natural environment and include cDNA and genomic clones. Isolated DNA molecules of the present invention are free of other genes with which they are ordinarily associated, but may include naturally occurring 5' and 3' untranslated regions such as promoters and terminators. The identification of
25 associated regions will be evident to one of ordinary skill in the art (see for example, Dynan and Tijan, *Nature* 316:774-78, 1985).

An "isolated" polypeptide or protein is a polypeptide or protein that is found in a condition other than its native environment, such as apart from blood and animal tissue. In a preferred form, the isolated polypeptide or protein is substantially
30 free of other polypeptides or proteins, particularly other polypeptides or proteins of animal origin. It is preferred to provide the polypeptides or proteins in a highly purified form, i.e. greater than 95% pure, more preferably greater than 99% pure. When used in this context, the term "isolated" does not exclude the presence of the same polypeptide or protein in alternative physical forms, such as dimers or alternatively glycosylated or
35 derivatized forms.

A "mature protein" is a protein that is produced by cellular processing of a primary translation product of a DNA sequence. Such processing may include

removal of a secretory signal peptide, sometimes in combination with a propeptide. Mature sequences can be predicted from full-length sequences using methods known in the art for predicting cleavage sites. See, for example, von Heijne (*Nuc. Acids Res.* 14:4683, 1986). The sequence of a mature protein can be determined experimentally
5 by expressing a DNA sequence of interest in a eukaryotic host cell and determining the amino acid sequence of the final product. For proteins lacking secretory peptides, the primary translation product will be the mature protein.

"Operably linked", when referring to DNA segments, indicates that the segments are arranged so that they function in concert for their intended purposes, e.g.,
10 transcription initiates in the promoter and proceeds through the coding segment to the terminator. When referring to polypeptides, "operably linked" includes both covalently (e.g., by disulfide bonding) and non-covalently (e.g., by hydrogen bonding, hydrophobic interactions, or salt-bridge interactions) linked sequences, wherein the desired function(s) of the sequences are retained.

15 The term "ortholog" denotes a polypeptide or protein obtained from one species that is the functional counterpart of a polypeptide or protein from a different species. Sequence differences among orthologs are the result of speciation.

"Paralogs" are distinct but structurally related proteins made by an organism. Paralogs are believed to arise through gene duplication. For example, α -
20 globin, β -globin, and myoglobin are paralogs of each other.

A "polynucleotide" is a single- or double-stranded polymer of deoxyribonucleotide or ribonucleotide bases read from the 5' to the 3' end. Polynucleotides include RNA and DNA, and may be isolated from natural sources, synthesized *in vitro*, or prepared from a combination of natural and synthetic
25 molecules. Sizes of polynucleotides are expressed as base pairs (abbreviated "bp"), nucleotides ("nt"), or kilobases ("kb"). Where the context allows, the latter two terms may describe polynucleotides that are single-stranded or double-stranded. When the term is applied to double-stranded molecules it is used to denote overall length and will be understood to be equivalent to the term "base pairs". It will be recognized by those
30 skilled in the art that the two strands of a double-stranded polynucleotide may differ slightly in length and that the ends thereof may be staggered as a result of enzymatic cleavage; thus all nucleotides within a double-stranded polynucleotide molecule may not be paired. Such unpaired ends will in general not exceed 20 nt in length.

A "polypeptide" is a polymer of amino acid residues joined by peptide
35 bonds, whether produced naturally or synthetically. Polypeptides of less than about 10 amino acid residues are commonly referred to as "peptides".

The term "promoter" is used herein for its art-recognized meaning to denote a portion of a gene containing DNA sequences that provide for the binding of RNA polymerase and initiation of transcription. Promoter sequences are commonly, but not always, found in the 5' non-coding regions of genes.

- 5 A "protein" is a macromolecule comprising one or more polypeptide chains. A protein may also comprise non-peptidic components, such as carbohydrate groups. Carbohydrates and other non-peptidic substituents may be added to a protein by the cell in which the protein is produced, and will vary with the type of cell. Proteins are defined herein in terms of their amino acid backbone structures;
- 10 substituents such as carbohydrate groups are generally not specified, but may be present nonetheless.

- A "secretory signal sequence" is a DNA sequence that encodes a polypeptide (a "secretory peptide") that, as a component of a larger polypeptide, directs the larger polypeptide through a secretory pathway of a cell in which it is synthesized.
- 15 The larger polypeptide is commonly cleaved to remove the secretory peptide during transit through the secretory pathway.

- The present invention is based in part upon the discovery of a group of novel, protein-encoding DNA molecules. These DNA molecules and the amino acid sequences that they encode are shown in SEQ ID NO:1 through SEQ ID NO:436.
- 20 Sequence analysis predicts that each of the encoded proteins includes an amino-terminal secretory peptide. These secretory peptides are shown below in Table 1, wherein residue numbers are in reference to the indicated SEQ ID NO. As will be understood by those skilled in the art, the cleavage sites predicted by conventional models of secretory peptide cleavage (e.g., von Heijne, *Nuc. Acids Res.* 14:4683, 1986)
- 25 are not always exact and may vary by as much as ± 5 residues. In addition, cleavage may occur at multiple sites within 5 residues of the indicated position. The mature form of any given protein may thus consist of a plurality of species differing at their amino termini.

Table 1

| <u>Protein</u> | <u>SEQ ID NO:</u> | <u>Residues 1-</u> |
|----------------|-------------------|--------------------|
| AFP210015 | 2 | 14 |
| AFP170681 | 4 | 26 |
| AFP413680 | 6 | 28 |
| AFP483037 | 8 | 14 |
| AFP230872 | 10 | 27 |
| AFP178828 | 12 | 14 |
| AFP200134 | 14 | 23 |
| AFP195796 | 16 | 22 |
| AFP477303 | 18 | 18 |
| AFP354334 | 20 | 25 |
| AFP250287 | 22 | 17 |
| AFP177000 | 24 | 26 |
| AFP278176 | 26 | 21 |
| AFP202885 | 28 | 18 |
| AFP221312 | 30 | 23 |
| AFP239757 | 32 | 22 |
| AFP226311 | 34 | 20 |
| AFP305901 | 36 | 20 |
| AFP325549 | 38 | 20 |
| AFP81988 | 40 | 14 |
| AFP199200 | 42 | 20 |
| AFP290395 | 44 | 23 |
| AFP212675 | 46 | 20 |
| AFP326051 | 48 | 17 |
| AFP512441 | 50 | 18 |
| AFP55098 | 52 | 15 |
| AFP169796 | 54 | 21 |
| AFP280706 | 56 | 25 |
| AFP383165 | 58 | 23 |
| AFP195467 | 60 | 26 |
| AFP134225 | 62 | 22 |
| AFP261193 | 64 | 28 |
| AFP324422 | 66 | 28 |
| AFP374312 | 68 | 28 |
| AFP258118 | 70 | 24 |
| AFP74517 | 72 | 25 |
| AFP254653 | 74 | 18 |
| AFP108666 | 76 | 21 |
| AFP8766 | 78 | 15 |
| AFP397185 | 80 | 20 |
| AFP195042 | 82 | 21 |
| AFP310695 | 84 | 26 |
| AFP70022 | 86 | 19 |
| AFP121670 | 88 | 22 |
| AFP345861 | 90 | 15 |

| | | |
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| AFP395942 | 92 | 16 |
| AFP170291 | 94 | 21 |
| AFP297548 | 96 | 22 |
| AFP188135 | 98 | 28 |
| AFP302388 | 100 | 19 |
| AFP263430 | 102 | 17 |
| AFP201273 | 104 | 18 |
| AFP98983 | 106 | 25 |
| AFP581958 | 108 | 20 |
| AFP404202 | 110 | 19 |
| AFP207203 | 112 | 15 |
| AFP220790 | 114 | 19 |
| AFP536326 | 116 | 23 |
| AFP257473 | 118 | 22 |
| AFP248380 | 120 | 16 |
| AFP276202 | 122 | 20 |
| AFP227568 | 124 | 23 |
| AFP229039 | 126 | 20 |
| AFP176297 | 128 | 17 |
| AFP356885 | 130 | 17 |
| AFP226938 | 132 | 16 |
| AFP138504 | 134 | 29 |
| AFP359196 | 136 | 24 |
| AFP501809 | 138 | 27 |
| AFP152733 | 140 | 15 |
| AFP541394 | 142 | 23 |
| AFP243183 | 144 | 20 |
| AFP80739 | 146 | 18 |
| AFP361806 | 148 | 26 |
| AFP483930 | 150 | 21 |
| AFP257336 | 152 | 25 |
| AFP195800 | 154 | 23 |
| AFP179530 | 156 | 19 |
| AFP279267 | 158 | 14 |
| AFP299766 | 160 | 29 |
| AFP244615 | 162 | 16 |
| AFP325761 | 164 | 22 |
| AFP226024 | 166 | 22 |
| AFP257094 | 168 | 27 |
| AFP197103 | 170 | 27 |
| AFP271855 | 172 | 17 |
| AFP324816 | 174 | 29 |
| AFP407963 | 176 | 25 |
| AFP369635 | 178 | 17 |
| AFP93743 | 180 | 28 |
| AFP243230 | 182 | 15 |
| AFP169316 | 184 | 21 |
| AFP130852 | 186 | 15 |

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| AFP194191 | 188 | 22 |
| AFP213472 | 190 | 21 |
| AFP360430 | 192 | 22 |
| AFP491309 | 194 | 21 |
| AFP193428 | 196 | 23 |
| AFP366534 | 198 | 22 |
| AFP22706 | 200 | 27 |
| AFP389012 | 202 | 14 |
| AFP137186 | 204 | 24 |
| AFP127023 | 206 | 21 |
| AFP389687 | 208 | 16 |
| AFP293220 | 210 | 25 |
| AFP425535 | 212 | 25 |
| AFP301494 | 214 | 25 |
| AFP345421 | 216 | 19 |
| AFP216667 | 218 | 26 |
| AFP247951 | 220 | 29 |
| AFP4464 | 222 | 22 |
| AFP561930 | 224 | 28 |
| AFP192851 | 226 | 22 |
| AFP252759 | 228 | 20 |
| AFP199044 | 230 | 20 |
| AFP357958 | 232 | 28 |
| AFP117501 | 234 | 15 |
| AFP194554 | 236 | 23 |
| AFP371069 | 238 | 23 |
| AFP313600 | 240 | 19 |
| AFP262739 | 242 | 18 |
| AFP180730 | 244 | 27 |
| AFP287227 | 246 | 28 |
| AFP75785 | 248 | 26 |
| AFP174843 | 250 | 15 |
| AFP250422 | 252 | 15 |
| AFP198645 | 254 | 17 |
| AFP238111 | 256 | 16 |
| AFP460626 | 258 | 24 |
| AFP271081 | 260 | 14 |
| AFP277752 | 262 | 16 |
| AFP291338 | 264 | 15 |
| AFP551038 | 266 | 22 |
| AFP301579 | 268 | 20 |
| AFP266188 | 270 | 16 |
| AFP275580 | 272 | 28 |
| AFP298054 | 274 | 21 |
| AFP348226 | 276 | 23 |
| AFP349106 | 278 | 23 |
| AFP288248 | 280 | 15 |
| AFP436476 | 282 | 19 |

| | | |
|-----------|-----|----|
| AFP352125 | 284 | 14 |
| AFP62060 | 286 | 25 |
| AFP236718 | 288 | 21 |
| AFP75775 | 290 | 25 |
| AFP407487 | 292 | 23 |
| AFP280451 | 294 | 27 |
| AFP11675 | 296 | 29 |
| AFP348656 | 298 | 16 |
| AFP277451 | 300 | 19 |
| AFP287436 | 302 | 14 |
| AFP116043 | 304 | 28 |
| AFP138740 | 306 | 26 |
| AFP15192 | 308 | 17 |
| AFP169968 | 310 | 27 |
| AFP173341 | 312 | 23 |
| AFP17588 | 314 | 23 |
| AFP176427 | 316 | 20 |
| AFP192633 | 318 | 14 |
| AFP193013 | 320 | 15 |
| AFP193881 | 322 | 16 |
| AFP195562 | 324 | 16 |
| AFP199922 | 326 | 18 |
| AFP204736 | 328 | 17 |
| AFP206179 | 330 | 27 |
| AFP221877 | 332 | 23 |
| AFP222758 | 334 | 26 |
| AFP227032 | 336 | 24 |
| AFP229269 | 338 | 27 |
| AFP232213 | 340 | 25 |
| AFP237679 | 342 | 21 |
| AFP249599 | 344 | 28 |
| AFP275215 | 346 | 21 |
| AFP290397 | 348 | 26 |
| AFP306591 | 350 | 18 |
| AFP310297 | 352 | 20 |
| AFP314720 | 354 | 19 |
| AFP318671 | 356 | 29 |
| AFP323575 | 358 | 21 |
| AFP327160 | 360 | 20 |
| AFP329002 | 362 | 29 |
| AFP345415 | 364 | 24 |
| AFP347179 | 366 | 24 |
| AFP359138 | 368 | 23 |
| AFP365372 | 370 | 17 |
| AFP367284 | 372 | 23 |
| AFP372822 | 374 | 26 |
| AFP374595 | 376 | 29 |
| AFP375952 | 378 | 25 |

| | | |
|-----------|-----|----|
| AFP382913 | 380 | 17 |
| AFP389184 | 382 | 23 |
| AFP404208 | 384 | 20 |
| AFP404279 | 386 | 29 |
| AFP409112 | 388 | 26 |
| AFP413111 | 390 | 19 |
| AFP415635 | 392 | 15 |
| AFP421092 | 394 | 17 |
| AFP436666 | 396 | 25 |
| AFP448623 | 398 | 19 |
| AFP454192 | 400 | 20 |
| AFP49026 | 402 | 28 |
| AFP51688 | 404 | 28 |
| AFP525341 | 406 | 16 |
| AFP545268 | 408 | 15 |
| AFP592620 | 410 | 22 |
| AFP62197 | 412 | 23 |
| AFP68229 | 414 | 25 |
| AFP71288 | 416 | 15 |
| AFP77851 | 418 | 27 |
| AFP81957 | 420 | 15 |
| AFP85168 | 422 | 27 |

A secretory peptide of a protein of the present invention can be used to direct the secretion of other proteins of interest from a host cell. Thus, the present invention provides, *inter alia*, fusions comprising such a secretory peptide of a protein

5 disclosed herein operably linked to another protein of interest. The secretory peptide can be used to direct the secretion of other proteins of interest by joining a polynucleotide sequence encoding it, in the correct reading frame, to the 5' end of a sequence encoding the other protein of interest. Those skilled in the art will recognize that the resulting fused sequence may encode additional residues of a protein of the

10 present invention at the amino terminus of the protein to be secreted. In the extreme case, the fusion may comprise an entire protein of the present invention fused to the amino terminus of a second protein, whereby secretion of the fusion protein is directed by the secretory peptide of the protein of the present invention. It will often be desirable to include a proteolytic cleavage site between the protein of the present

15 invention (or portion thereof) and the other protein of interest. The joined polynucleotide sequences are then introduced into a host cell, which is cultured according to conventional methods. The protein of interest is then recovered from the culture media. Methods for introducing DNA into host cells, culturing the cells, and isolating recombinant proteins are known in the art. Representative methods are

20 summarized below.

Within certain embodiments of the invention, the protein is selected from those listed in Table 2. Within related embodiments of the invention, the polynucleotide is selected from polynucleotides encoding the proteins listed in Table 2, i.e., for a protein of SEQ ID NO:M, the polynucleotide is SEQ ID NO:M-1.

5

Table 2

| SEQ ID NO: | Protein | SEQ ID NO: | Protein |
|------------|-----------|------------|-----------|
| 6 | AFP413680 | 234 | AFP117501 |
| 12 | AFP178828 | 236 | AFP194554 |
| 18 | AFP477303 | 240 | AFP313600 |
| 24 | AFP177000 | 242 | AFP262739 |
| 42 | AFP199200 | 252 | AFP250422 |
| 48 | AFP326051 | 254 | AFP198645 |
| 66 | AFP324422 | 258 | AFP460626 |
| 68 | AFP374312 | 270 | AFP266188 |
| 72 | AFP74517 | 272 | AFP275580 |
| 90 | AFP345861 | 288 | AFP236718 |
| 92 | AFP395942 | 294 | AFP280451 |
| 96 | AFP297548 | 300 | AFP277451 |
| 98 | AFP188135 | 306 | AFP138740 |
| 110 | AFP404202 | 324 | AFP195562 |
| 134 | AFP138504 | 338 | AFP229269 |
| 138 | AFP501809 | 342 | AFP237679 |
| 156 | AFP179530 | 344 | AFP249599 |
| 158 | AFP279267 | 348 | AFP290397 |
| 162 | AFP244615 | 350 | AFP306591 |
| 164 | AFP325761 | 366 | AFP347179 |
| 174 | AFP324816 | 374 | AFP372822 |
| 180 | AFP93743 | 378 | AFP375952 |
| 204 | AFP137186 | 386 | AFP404279 |
| 206 | AFP127023 | 396 | AFP436666 |
| 210 | AFP293220 | 398 | AFP448623 |
| 224 | AFP561930 | 408 | AFP545268 |
| 230 | AFP199044 | 416 | AFP71288 |

Higher order structures of the proteins of the present invention can be predicted by computer analysis using available software (e.g., the Insight II® viewer and homology modeling tools available from MSI, San Diego, CA; and King and Sternberg, *Protein Sci.* 5:2298-310, 1996). In addition, analytical algorithms permit the identification of homologies between newly discovered proteins and known proteins. Such homologies are indicative of related biological functions.

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AFP254653 is 49% identical in sequence to human lysozyme C. Lysozyme C is a secreted bacteriolytic enzyme with similarity to the alpha-lactalbumins. Both are small alpha + beta proteins with six conserved cysteines forming a disulfide core comprising three disulfide bonds. AFP254653 may also
5 exhibit bacteriolytic or other antimicrobial activity.

AFP581958 is 43% identical to wheat aluminum-induced protein, a member of the Bowman-Birk proteinase inhibitor family. All serine proteinases possess an exposed inhibitor loop that is stabilized by intermolecular interactions (usually disulfide bonds) between residues flanking the binding loop and the protein
10 core. Interaction between inhibitor and enzyme produces a stable complex that disassociates very slowly, producing either an unaffected or a modified inhibitor that is cleaved at the scissile bond of the binding loop. AFP581958 may be a secreted serine proteinase.

AFP220790 is 42% identical to chicken lysozyme G, a bacteriolytic
15 glycosyl hydrolase that hydrolizes peptidoglycan homopolymers of the prokaryote cell walls. AFP220790 may thus be a secreted bacteriolytic enzyme, and may exhibit other antimicrobial activity.

AFP271855 is 37% identical to bovine granulocyte peptide A precursor (antimicrobial BGP-A). Bovine and murine granulocyte peptide A precursor (also
20 called antimicrobial BGP-A) are disclosed in WIPO publication WO 97/29765. Bovine GP-A was isolated from a bone marrow library (WO 97/29765). GP-A exhibits activity against Gram-positive and Gram-negative bacteria, fungi and viruses. AFP271855 may exhibit antimicrobial (including one or more of anti-bacterial, anti-fungal, and anti-viral) activity.

AFP298054 is 24% identical to human T1/ST2 ligand. The T1 gene is
25 also known as ST2, DER4, and Fit-1. It encodes a member of the interleukin-1 (IL-1) receptor family. It is transcribed in two forms, a soluble form and a membrane-bound form. The classical IL-1 ligands (IL-1 α , IL-1 β , and IL-1ra) do not bind T1. A putative ligand for T1 was disclosed in 1996 (Gayle et al., *J. Biol. Chem.* 271:5784-5789, 1996).
30 This protein binds T1 but is unable to initiate signal transduction by the membrane-bound form. The ligand is apparently a type I membrane protein. It has a predicted molecular weight (excluding the signal sequence and transmembrane domain) of about 22 kD, and has no sequence or hydrophobicity profile similarity to the beta-trefoil cytokines IL-1 or the FGFs. AFP298054 may be an antagonist that binds the receptor
35 and regulates the activity of an as yet undiscovered IL-1 homolog.

Table 3 lists homologies between AFP sequences and sequences contained in the GenBank database, Derwent protein (PSP) or polynucleotide (PSN) databases, or Protein Identification Resource (PIR).

5

Table 3

| Locus | Accession Number & Description |
|-----------|--|
| AFP130852 | AE003823 (fly genomic) |
| AFP169968 | AE003515 (fly genomic) |
| AFP174843 | AF283518 (<i>Mus musculus</i> elongation factor sec) |
| AFP176427 | AE003808 (fly genomic) |
| AFP178828 | PSN_V61483 |
| AFP179530 | AE003708 (fly genomic) |
| AFP188135 | AE003677 (fly genomic) |
| AFP195042 | PIR_T41241 (yeast oxysterol-binding protein family) |
| AFP198645 | AE003718 (fly genomic) |
| AFP199200 | AF113691 (human clone FLB4739 PRO1238 mRNA) |
| AFP204736 | AC069237 (human chromosome 3 clone RP11-175M9) |
| AFP229269 | AF247177 (<i>Mus musculus</i> sphingosine-1-phosphate phosphohydrolase) |
| AFP230872 | AF150741 (<i>Rattus norvegicus</i> prolactin-like protein J mRNA) |
| AFP279267 | AE003559 (fly genomic) |
| AFP347179 | AE003499 (fly genomic) Z1041035F6P |
| AFP357958 | AF283518 (<i>Mus musculus</i> elongation factor sec mRNA) |
| AFP359196 | AE003530 (fly genomic) |
| AFP374312 | AE003538 (fly genomic) |
| AFP389687 | AE003831 (fly genomic) |
| AFP395942 | AB041564 (mouse brain cDNA; clone MNCb-0914) |
| AFP404202 | AL137255 (human mRNA; cDNA DKFZp434B1813) |
| AFP413680 | X14971 (mouse mRNA for alpha-adaptin, MMADAPA1) |
| AFP477303 | AE003778 (fly genomic) |
| AFP62060 | PSP_Y94938 (Human secreted protein clone ye78_1) |
| AFP71288 | AL161655 (human chromosome 20 clone RP11-116E13) |
| AFP74517 | PIR_T16263 (<i>C. elegans</i> hypothetical protein F35D11.3) |

Table 4 lists AFP proteins for which regions of identity have been found in the GenBank database.

Table 4

| Locus | Accession Number & Description |
|-----------|---|
| AFP127023 | SK000740 (human cDNA FLJ20733; clone HEP08550; by homology: molybdopterin cofactor sulfurase) |
| AFP134225 | AB020970 (human mRNA; partial cds and 3'UTR; up-regulated by BCG-CWS) |
| AFP195562 | AK000382 (human cDNA FLJ20375; clone HUV00942) |

| | |
|-----------|---|
| AFP199044 | HSU80813 (human nucleoside diphosphate kinase homolog DR-nm23) |
| AFP227032 | AK001848 (human cDNA FLJ10986; clone PLACE1001869; weakly similar to L-RIBULOKINASE; EC 2.7.1.16) |
| AFP237679 | AB000465 (human mRNA; exon 1; 2; 3; 4; clone:RES4-24B; in genomic region of Huntington's disease locus) |
| AFP262739 | AK000135 (human cDNA FLJ20128; clone COL06181) |
| AFP369635 | PSN_Z24827 (Human secreted protein gene 17 clone HNF1Y77) |
| AFP81957 | AF267730 (human 26S proteasome-associated UCH interacting protein 1; UIP1) |
| AFP93743 | AK000066 (human cDNA FLJ20059; clone COL01349) |

Table 5 lists AFP proteins for which longer regions of identity have been found in proteins contained in GenBank and other databases.

Table 5

| Locus | Accession Number & Description |
|-----------|---|
| AFP117501 | AK000505 (human cDNA FLJ20498; clone KAT08960) |
| AFP138740 | HSM802370 (human mRNA; cDNA DKFZp434M1511) |
| AFP170291 | AK000494 (human cDNA FLJ20487; clone KAT08245) |
| AFP170681 | AK001698 (human cDNA FLJ10836; clone NT2RP4001228 close paralogue of human Kelch-like 1 protein (KLHL1) mRNA: AF252283) |
| AFP177000 | AK000524 (human cDNA FLJ20517; clone KAT10235) |
| AFP193881 | AK000382 (human cDNA FLJ20375; clone HUV00942) |
| AFP195796 | AF251041 (human SGC32445 protein (SGC32445) mRNA; homology to PSP_W35393 Human TB2 gene product) |
| AFP202885 | AB037808 (human mRNA for KIAA1387 protein) |
| AFP207203 | AF250924 (human PNGase mRNA: peptide N-glycanase) |
| AFP226024 | AK001952 (human cDNA FLJ11090; clone PLACE1005308) |
| AFP227568 | AB019038 (human HMT-1 mRNA for beta-1;4 mannosyltransferase) |
| AFP244615 | AK001009 (human cDNA FLJ10147; clone HEMBA1003369; weak homology: CENE_HUMAN CENTROMERIC PROTEIN E) |
| AFP250422 | AF208849 (human BM-007 mRNA) |
| AFP266188 | AK000272 (human cDNA FLJ20265; clone COLF9334; homology to major facilitator protein homolog, fission yeast: PIR_S62432) |
| AFP277451 | AK001373 (human cDNA FLJ10511; clone NT2RP2000656) |
| AFP277752 | AK000453 (human cDNA FLJ20446; clone KAT05231; weak homology to dinitrogenase reductase activating glycohydrolase (draG) <i>Archaeoglobus fulgidus</i> : PIR_C69465) |
| AFP280451 | AL133355 (Human DNA sequence from clone RP11-541N10 on chromosome 10. Contains a novel gene and the 5' end of the gene for a novel protein; ortholog of mouse FISH protein) |
| AFP293220 | AK001441 (human cDNA FLJ10579; clone NT2RP2003446) |
| AFP297548 | AK000494 (human cDNA FLJ20487; clone KAT08245) |
| AFP306591 | AL359700 (human chromosome 6 clone RP11-802L12) |
| AFP324816 | AB032966 (human mRNA for KIAA1140 protein weak homology: Human O-linked GlcNAc transferase mRNA) |

| | |
|-----------|---|
| AFP356885 | AK001544 (human cDNA FLJ10682; clone NT2RP3000072) |
| AFP389012 | AK000428 (human cDNA FLJ20421; clone KAT02467; homologous to human bisphosphate 3'-nucleotidase mRNA: AF125042) |
| AFP436666 | AK001608 (human cDNA FLJ10746; clone NT2RP3001679; likely human orthologue of <i>Rattus norvegicus</i> small rec (srec) mRNA: AF228917) |
| AFP501809 | AK001963 (human cDNA FLJ11101; clone PLACE1005623) |
| AFP525341 | AF189692 (human non-kinase Cdc42 effector protein SPEC2 mRNA) |

A protein of the present invention can be prepared as a fusion protein by joining it to a second polypeptide or a plurality of additional polypeptides. Suitable second polypeptides include amino- or carboxyl-terminal extensions, such as linker peptides of up to about 20-25 residues and extensions that facilitate purification (affinity tags) as disclosed above. A protein of interest can be prepared as a fusion to a dimerizing protein as disclosed in U.S. Patents Nos. 5,155,027 and 5,567,584. Preferred dimerizing proteins in this regard include immunoglobulin constant region domains. Immunoglobulin-polypeptide fusions can be expressed in genetically engineered cells to produce a variety of multimeric analogs of a protein of interest. Fusion proteins can also comprise auxiliary domains that target the protein of interest to specific cells, tissues, or macromolecules (e.g., collagen). For example, a protein of interest can be targeted to a predetermined cell type by fusing it to a ligand that specifically binds to a receptor on the surface of a target cell. In this way, proteins can be targeted for therapeutic or diagnostic purposes. A protein can be fused to two or more moieties, such as an affinity tag for purification and a targeting domain. Protein fusions can also comprise one or more cleavage sites, particularly between domains. See, Tuan et al., *Connective Tissue Research* 34:1-9, 1996. Proteins of the present invention can also be used as targeting moieties within fusion proteins comprising, for example, cytokines, cytotoxins, or other biologically active polypeptide moieties.

Protein fusions of the present invention will usually contain not more than about 1,200 amino acid residues joined to the AFP protein. For example, an AFP protein can be fused to *E. coli* β -galactosidase (1,021 residues; see Casadaban et al., *J. Bacteriol.* 143:971-980, 1980), a 10-residue spacer, and a 4-residue factor Xa cleavage site. Such a protein comprising, for example, AFP345421 (SEQ ID NO:216), contains 2235 amino acid residues. In a second example, an AFP protein can be fused to maltose binding protein (approximately 370 residues), a 4-residue cleavage site, and a 6-residue polyhistidine tag.

As disclosed above, the proteins of the present invention or portions thereof can also be used to direct the secretion of a second protein. When such fusions

are designed so that the secreted protein retains a portion of the protein of the present invention, the fusion protein can be purified by means that exploit the properties of the protein of the present invention. Typical of such methods is immunoaffinity chromatography using an antibody directed against a protein of the present invention.

- 5 When such a fusion is engineered to contain a cleavage site at the fusion point, the fusion can be cleaved and the protein of interest recovered free of extraneous sequence.

The present invention also provides polynucleotide molecules, including DNA and RNA molecules, that encode the proteins disclosed above. Those skilled in the art will readily recognize that, in view of the degeneracy of the genetic code, 10 considerable sequence variation is possible among these polynucleotide molecules. The amino acid sequence information provided herein can be used by one of ordinary skill in the art to generate degenerate sequences comprising all nucleotide sequences encoding a particular polypeptide. Table 6 sets forth the one-letter codes used to denote degenerate nucleotide positions. "Resolutions" are the nucleotides denoted by a 15 code letter. "Complement" indicates the code for the complementary nucleotide(s). For example, the code Y denotes either C or T, and its complement R denotes A or G, A being complementary to T, and G being complementary to C.

TABLE 6

20

| Nucleotide | Resolutions | Complement | Resolutions |
|------------|-------------|------------|-------------|
| A | A | T | T |
| C | C | G | G |
| G | G | C | C |
| T | T | A | A |
| R | A G | Y | C T |
| Y | C T | R | A G |
| M | A C | K | G T |
| K | G T | M | A C |
| S | C G | S | C G |
| W | A T | W | A T |
| H | A C T | D | A G T |
| B | C G T | V | A C G |
| V | A C G | B | C G T |
| D | A G T | H | A C T |
| N | A C G T | N | A C G T |

Degenerate codons encompassing all possible codons for a given amino acid are set forth in Table 7, below.

TABLE 7

| Amino Acid | One-Letter Code | Codons | Degenerate Codon |
|------------|-----------------|-------------------------|------------------|
| Cys | C | TGC TGT | TGY |
| Ser | S | AGC AGT TCA TCC TCG TCT | WSN |
| Thr | T | ACA ACC ACG ACT | CAN |
| Pro | P | CCA CCC CCG CCT | CCN |
| Ala | A | GCA GCC GCG GCT | GCN |
| Gly | G | GGA GGC GGG GGT | GGN |
| Asn | N | AAC AAT | AAY |
| Asp | D | GAC GAT | GAY |
| Glu | E | GAA GAG | GAR |
| Gln | Q | CAA CAG | CAR |
| His | H | CAC CAT | CAY |
| Arg | R | AGA AGG CGA CGC CGG CGT | MGN |
| Lys | K | AAA AAG | AAR |
| Met | M | ATG | ATG |
| Ile | I | ATA ATC ATT | ATH |
| Leu | L | CTA CTC CTG CTT TTA TTG | YTN |
| Val | V | GTA GTC GTG GTT | GTN |
| Phe | F | TTC TTT | TTY |
| Tyr | Y | TAC TAT | TAY |
| Trp | W | TGG | TGG |
| Ter | . | TAA TAG TGA | TRR |
| Asn Asp | B | | RAY |
| Glu Gln | Z | | SAR |
| Any | X | | NNN |
| Gap | - | --- | |

5

One of ordinary skill in the art will appreciate that some ambiguity is introduced in determining a degenerate codon, representative of all possible codons encoding each amino acid. For example, the degenerate codon for serine (WSN) can, in some circumstances, encode arginine (AGR), and the degenerate codon for arginine (MGN) can, in some circumstances, encode serine (AGY). A similar relationship

10

exists between codons encoding phenylalanine and leucine. Thus, some polynucleotides encompassed by the degenerate sequences may encode variant amino acid sequences, but one of ordinary skill in the art can easily identify such variant sequences by reference to the amino acid sequences disclosed in the accompanying

5 Sequence Listing.

Methods for preparing DNA and RNA are well known in the art. Complementary DNA (cDNA) clones are prepared from RNA that is isolated from a tissue or cell that produces large amounts of the cognate mRNA. Such tissues and cells are identified by methods commonly known in the art, such as Northern blotting
10 (Thomas, *Proc. Natl. Acad. Sci. USA* 77:5201, 1980). Databases of expressed sequence tags (ESTs) can be analyzed to produce an "electronic Northern" wherein sequences are assigned to specific cell or tissue sources on the basis of their abundance within libraries. Table 8, below, shows the results of such an analysis when, as the minimum
15 significant abundance, it was required that at least 10% of all sequences for a given protein were from a single source and at least five individual clones had been identified from that source. Sequences shown in the accompanying Sequence Listing but not listed in Table 8 were widely distributed among various tissues or were represented by few clones.

Table 8

| | |
|-----------|---|
| AFP152733 | K562 cells |
| AFP169796 | T-cells |
| AFP173341 | testis |
| AFP17588 | fetal liver or spleen |
| AFP194554 | fetal liver or spleen |
| AFP199922 | testis |
| AFP229269 | placenta |
| AFP237679 | fetal liver or spleen |
| AFP257094 | adult brain |
| AFP258118 | epidermal breast keratinocytes |
| AFP263430 | breast |
| AFP276202 | infant brain |
| AFP287436 | testis |
| AFP290397 | testis |
| AFP306591 | fetal heart |
| AFP325761 | K562 cells |
| AFP352125 | testis |
| AFP359138 | infant brain |
| AFP369635 | germinal center B-cells |
| AFP409112 | kidney |
| AFP483037 | neonatal keratinocytes |
| AFP49026 | peripheral blood eosinophils of asthma patients |
| AFP545268 | K562 cells |
| AFP561930 | fetal liver or spleen |
| AFP62060 | testis |
| AFP62197 | pregnant uterus |
| AFP93743 | germinal center B-cells |
| AFP98983 | fetal heart |

A panel of cDNAs from human tissues was screened for AFP expression using PCR. The panel was made from first strand cDNAs obtained from Clontech laboratories, Inc., Palo Alto, CA and contained 20 first-strand cDNA samples from the human tissues shown in Table 9. The panel was set up in a 96-well format that further included a human genomic DNA (obtained from Clontech Laboratories, Inc.) positive control sample and a water-only well as a negative control sample. Each well contained approximately 0.2-100 pg/ μ l of cDNA, diluted with water to 17.5 μ l. The

- PCR reactions were set up by adding oligonucleotide primers, DNA polymerase (Ex Taq™; TAKARA Shuzo Co. Ltd. Biomedicals Group, Japan or Advantage™ 2 cDNA polymerase mix; Clontech Laboratories, Inc.) with the appropriate supplied buffer, dNTP mix (TAKARA Shuzo Co. Ltd.), and a density increasing agent and tracking dye
- 5 (RediLoad; Research Genetics, Inc., Huntsville, AL) to each sample on the panel. The amplification was carried out as follows: incubation at 94°C for 2 minutes; 35 cycles of 94°C for 30 seconds, 60°C for 20 seconds, and 72°C for 30 seconds; followed by incubation at 72°C for 5 minutes. About 10 µl of the PCR reaction product was subjected to standard agarose gel electrophoresis using a 4% agarose gel.

Table 9

| Protein | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 |
|-----------|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|----|----|----|----|----|----|
| AFP117501 | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | n | n |
| AFP127023 | y | y | y | y | y | y | y | y | y | y | n | y | y | y | y | n | y | y | n | y | n | n |
| AFP137186 | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | n | y |
| AFP138504 | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | n | y |
| AFP138740 | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | n | n |
| AFP177000 | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | n | y |
| AFP178828 | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | n | y |
| AFP179530 | y | y | y | y | y | y | y | y | y | y | n | y | y | y | y | y | y | y | y | y | n | y |
| AFP188135 | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | n | n |
| AFP194534 | y | y | y | y | y | y | y | y | n | y | y | y | y | y | y | y | y | y | y | y | n | y |
| AFP195502 | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | n | y |
| AFP198645 | n | n | n | n | n | n | n | n | n | n | n | n | n | n | n | n | n | n | n | n | n | n |
| AFP199044 | n | n | n | y | n | n | n | n | n | n | n | n | n | n | n | n | n | n | n | n | n | n |
| AFP199200 | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | n | y |
| AFP229269 | y | y | y | y | y | y | y | y | y | y | y | y | n | y | y | y | y | y | y | y | n | y |
| AFP236718 | n | y | y | y | y | y | y | n | n | y | n | n | n | y | n | n | n | y | y | y | n | y |
| AFP237679 | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | n | y |
| AFP244615 | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | n | n |
| AFP249599 | n | y | y | n | n | y | y | y | n | n | n | n | n | n | y | n | n | n | n | n | n | y |
| AFP250422 | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | n | y |
| AFP262739 | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | n | y |
| AFP266188 | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | n | y |
| AFP275580 | y | y | y | y | y | y | y | n | y | y | y | y | y | y | y | y | n | y | y | y | n | y |
| AFP277451 | y | y | y | y | y | y | y | y | y | y | nd | y | y | y | y | y | n | y | y | y | n | n |
| AFP279267 | y | y | y | y | y | y | y | y | n | y | y | y | n | y | y | y | y | y | y | y | n | n |
| AFP280451 | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | n | y |
| AFP290397 | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | n | y |
| AFP293220 | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | n | y |
| AFP297548 | y | y | y | y | y | y | y | y | y | y | y | y | n | y | y | y | y | y | y | y | n | y |
| AFP306591 | y | y | y | y | y | y | y | y | y | y | n | y | y | nd | y | nd | nd | y | y | y | n | y |
| AFP313600 | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | n | y |
| AFP324422 | n | n | y | n | n | n | n | n | n | n | n | n | n | n | n | n | n | n | y | n | n | y |

Table 9, continued

| Protein | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 |
|-----------|---|---|---|---|---|---|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|
| AFP324816 | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | n | y |
| AFP325761 | y | y | y | y | y | y | y | y | y | y | y | y | n | y | y | y | y | y | y | y | n | n |
| AFP326051 | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | n | y |
| AFP345861 | y | y | y | y | y | y | y | nd | nd | y | nd | y | nd | nd | y | y | y | y | y | y | n | n |
| AFP347179 | y | y | y | y | y | y | y | y | y | y | y | y | n | y | y | y | n | y | y | y | n | y |
| AFP372822 | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | n | y |
| AFP374312 | n | n | y | y | n | n | n | n | n | n | n | n | n | n | n | n | y | y | n | n | n | y |
| AFP375952 | n | n | n | n | n | n | n | n | n | n | n | n | n | n | n | n | n | n | n | n | n | y |
| AFP395942 | y | y | y | y | y | y | y | y | n | n | y | y | n | y | n | y | y | y | y | y | n | y |
| AFP404202 | y | y | y | y | y | y | y | n | y | y | y | y | n | y | y | y | y | y | y | y | n | n |
| AFP404279 | y | y | y | y | n | y | y | n | y | y | y | y | y | y | y | y | n | y | y | y | n | y |
| AFP413680 | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | nd | y | y | y | n | y |
| AFP436666 | y | y | y | y | y | y | y | y | n | y | y | y | n | y | y | y | y | y | y | y | n | y |
| AFP448623 | y | n | y | n | n | y | n | n | n | n | n | n | n | n | n | n | n | y | y | n | n | n |
| AFP460626 | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | nd | y | y | y | n | y |
| AFP477303 | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | n | y |
| AFP501809 | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | n | y |
| AFP545268 | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | n | y |
| AFP561930 | y | y | y | y | y | y | y | nd | y | y | n | y | y | nd | y | y | y | y | nd | y | n | y |
| AFP71288 | n | n | n | n | n | n | n | n | n | n | n | n | n | n | n | n | n | n | n | n | n | y |
| AFP74517 | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | n | n |
| AFP93743 | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | y | n | y |

Tissues screened were: 1, brain; 2, heart; 3, kidney; 4, liver; 5, lung; 6, pancreas; 7, placenta; 8, skeletal muscle; 9, colon; 10, ovary; 11, peripheral blood leukocytes; 12, prostate; 13, small intestine; 14, spleen; 15, testis; 16, thymus; 17, bone marrow; 18, fetal liver; 19, lymph node; 20, tonsil; 21, H₂O; 22, genomic DNA. Y=yes; n=no; nd=not determined.

Total RNA can be prepared using guanidine HCl extraction followed by isolation by centrifugation in a CsCl gradient (Chirgwin et al., *Biochemistry* 18:52-94, 1979). Poly (A)⁺ RNA is prepared from total RNA using the method of Aviv and Leder (*Proc. Natl. Acad. Sci. USA* 69:1408-1412, 1972). Complementary DNA (cDNA) is prepared from poly(A)⁺ RNA using known methods. In the alternative, genomic DNA can be isolated. For some applications (e.g., expression in transgenic animals) it may be preferable to use a genomic clone, or to modify a cDNA clone to include at least one genomic intron. Methods for identifying and isolating cDNA and genomic clones are well known and within the level of ordinary skill in the art, and include the use of the sequences disclosed herein, sequences complementary thereto, or parts thereof, for probing or priming a library. Such methods include, for example, hybridization or polymerase chain reaction ("PCR", Mullis, U.S. Patent 4,683,202). Expression libraries can be probed with antibodies to a protein of interest, receptor fragments, or other specific binding partners.

The polynucleotides of the present invention can also be prepared by automated synthesis. Synthesis of polynucleotides is within the level of ordinary skill in the art, and suitable equipment and reagents are available from commercial suppliers. See, in general, Glick and Pasternak, Molecular Biotechnology, Principles & Applications of Recombinant DNA, ASM Press, Washington, D.C., 1994; Itakura et al., *Ann. Rev. Biochem.* 53: 323-56, 1984; and Climie et al., *Proc. Natl. Acad. Sci. USA* 87:633-7, 1990.

The present invention further provides antisense polynucleotides that are complementary to a segment of a polynucleotide as set forth in one of SEQ ID NO:N, wherein N is an odd integer from 1 to 435. Such antisense polynucleotides are designed to bind to the corresponding mRNA and inhibit its translation. Antisense polynucleotides are used to inhibit gene expression in cell culture or in a patient, and can be used as probes or primers for research or diagnostic purposes.

Probes and primers of the present invention comprise a suitable fragment, and may comprise up to the complete sequence, of a polynucleotide as shown in SEQ ID NO:N or the complement thereof, wherein N is an odd integer from 1 to 421. Probes will generally be at least 20 nucleotides in length, although somewhat shorter probes (14-17 nucleotides) can be used. PCR primers are at least 5 nucleotides in length, preferably 15 or more nt, more preferably 20-30 nt. Shorter polynucleotide probes and primers are referred to in the art as "oligonucleotides," and can be DNA or RNA. Probes will generally comprise an oligonucleotide linked to a label, such as a radionuclide.

Probes and primers as disclosed herein can be used for cloning allelic, orthologous, and paralogous sequences. Allelic variants of the disclosed sequences can be cloned by probing cDNA or genomic libraries from different individuals according to standard procedures. Orthologous sequences can be cloned using information and compositions provided by the present invention in combination with conventional cloning techniques. For example, a cDNA can be cloned using mRNA obtained from a tissue or cell type that expresses the protein. Suitable sources of mRNA can be identified by probing Northern blots with probes designed from the sequences disclosed herein. A library is then prepared from mRNA of a positive tissue or cell line. A cDNA can then be isolated by a variety of methods, such as by probing with a complete or partial human cDNA or with one or more sets of degenerate probes based on the disclosed sequences. A cDNA can also be cloned by PCR using primers designed from the sequences disclosed herein. Within an additional method, the cDNA library can be used to transform or transfect host cells, and expression of the cDNA of interest can be detected with an antibody to the encoded protein. Similar techniques can also be applied to the isolation of genomic clones. Orthologous and paralogous sequences can be identified from libraries by probing blots at low stringency and washing the blots at successively higher stringency until background is suitably reduced.

Probes and primers disclosed herein can be used to clone 5' non-coding regions of a corresponding gene. In view of the tissue-specific expression observed for certain proteins of the invention (Tables 8 and 9), promoters of these genes are expected to provide tissue-specific expression. Such promoter elements can thus be used to direct the tissue-specific expression of heterologous genes in, for example, transgenic animals or patients treated with gene therapy. Cloning of 5' flanking sequences also facilitates production of a protein of interest by "gene activation" as disclosed in U.S. Patent No. 5,641,670. Briefly, expression of an endogenous gene in a cell is altered by introducing into its locus a DNA construct comprising at least a targeting sequence, a regulatory sequence, an exon, and an unpaired splice donor site. The targeting sequence is a 5' non-coding sequence that permits homologous recombination of the construct with the endogenous locus, whereby the sequences within the construct become operably linked with the endogenous coding sequence. In this way, an endogenous promoter can be replaced or supplemented with other regulatory sequences to provide enhanced, tissue-specific, or otherwise regulated expression.

The polynucleotides of the present invention further include polynucleotides encoding the fusion proteins, including signal peptide fusions, disclosed above.

The present invention further provides a computer-readable medium
5 encoded with a data structure that provides at least one of SEQ ID NO:1 through SEQ ID NO:436. Suitable forms of computer-readable media include magnetic media and optically-readable media. Examples of magnetic media include a hard or fixed drive, a random access memory (RAM) chip, a floppy disk, digital linear tape (DLT), a disk cache, and a ZIP® disk. Optically readable media are exemplified by compact discs
10 (e.g., CD-read only memory (ROM), CD-rewritable (RW), and CD-recordable), digital versatile/video discs (DVD) (e.g., DVD-ROM, DVD-RAM, and DVD+RW), and carrier waves.

The polypeptides of the present invention, including full-length proteins, biologically active fragments, immunogenic fragments, and fusion proteins,
15 can be produced in genetically engineered host cells according to conventional techniques. Suitable host cells are those cell types that can be transformed or transfected with exogenous DNA and grown in culture, and include bacteria, fungal cells, and cultured higher eukaryotic cells. Eukaryotic cells, particularly cultured cells of multicellular organisms, are generally preferred for the production of proteins
20 having higher eukaryotic-type post-translational modifications (e.g., γ -carboxylation) and for making proteins, especially secretory proteins, for pharmaceutical use in humans. Techniques for manipulating cloned DNA molecules and introducing exogenous DNA into a variety of host cells are disclosed by Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd ed., Cold Spring Harbor Laboratory
25 Press, Cold Spring Harbor, NY, 1989, and Ausubel et al., eds., *Current Protocols in Molecular Biology*, Green and Wiley and Sons, NY, 1993.

In general, a DNA sequence encoding a polypeptide of interest is operably linked to other genetic elements required for its expression, generally including a transcription promoter and terminator, within an expression vector. The
30 vector will also commonly contain one or more selectable markers and one or more origins of replication, although those skilled in the art will recognize that within certain systems selectable markers can be provided on separate vectors, and replication of the exogenous DNA can be achieved through integration into the host cell genome. Selection of promoters, terminators, selectable markers, vectors and other elements is a
35 matter of routine design within the level of ordinary skill in the art. Many such elements are described in the literature and are available through commercial suppliers.

To direct a polypeptide into the secretory pathway of a host cell, a secretory signal sequence (also known as a leader sequence, prepro sequence or pre sequence) is provided in the expression vector. The secretory signal sequence may be that of the protein of interest, or may be derived from another secreted protein (e.g., t-PA; see U.S. Patent No. 5,641,655) or synthesized *de novo*. The secretory signal sequence is operably linked to the DNA sequence encoding the protein of interest, i.e., the two sequences are joined in the correct reading frame and positioned to direct the newly synthesized protein into the secretory pathway of the host cell. Secretory signal sequences are commonly positioned 5' to the DNA sequence encoding the protein of interest, although certain secretory signal sequences may be positioned elsewhere in the DNA sequence of interest (see, e.g., Welch et al., U.S. Patent No. 5,037,743; Holland et al., U.S. Patent No. 5,143,830).

Cultured mammalian cells are suitable hosts for use within the present invention. Methods for introducing exogenous DNA into mammalian host cells include calcium phosphate-mediated transfection (Wigler et al., *Cell* 14:725, 1978; Corsaro and Pearson, *Somatic Cell Genetics* 7:603, 1981; Graham and Van der Eb, *Virology* 52:456, 1973), electroporation (Neumann et al., *EMBO J.* 1:841-845, 1982), DEAE-dextran mediated transfection (Ausubel et al., *ibid.*), and liposome-mediated transfection (Hawley-Nelson et al., *Focus* 15:73, 1993; Ciccarone et al., *Focus* 15:80, 1993). The production of recombinant polypeptides in cultured mammalian cells is disclosed by, for example, Levinson et al., U.S. Patent No. 4,713,339; Hagen et al., U.S. Patent No. 4,784,950; Palmiter et al., U.S. Patent No. 4,579,821; and Ringold, U.S. Patent No. 4,656,134. Suitable cultured mammalian cells include the COS-1 (ATCC No. CRL 1650), COS-7 (ATCC No. CRL 1651), BHK (ATCC No. CRL 1632), BHK 570 (ATCC No. CRL 10314), 293 (ATCC No. CRL 1573; Graham et al., *J. Gen. Virol.* 36:59-72, 1977) and Chinese hamster ovary (e.g. CHO-K1; ATCC No. CCL 61) cell lines. Additional suitable cell lines are known in the art and available from public depositories such as the American Type Culture Collection, Rockville, Maryland. In general, strong transcription promoters are preferred, such as promoters from SV-40 or cytomegalovirus. See, e.g., U.S. Patent No. 4,956,288. Other suitable promoters include those from metallothionein genes (U.S. Patent Nos. 4,579,821 and 4,601,978) and the adenovirus major late promoter. Within an alternative embodiment, adenovirus vectors can be employed. See, for example, Garnier et al., *Cytotechnol.* 15:145-55, 1994.

Drug selection is generally used to select for cultured mammalian cells into which foreign DNA has been inserted. Such cells are commonly referred to as "transfectants". Cells that have been cultured in the presence of the selective agent and

are able to pass the gene of interest to their progeny are referred to as "stable transfectants." An exemplary selectable marker is a gene encoding resistance to the antibiotic neomycin. Selection is carried out in the presence of a neomycin-type drug, such as G-418 or the like. Selection systems can also be used to increase the expression level of the gene of interest, a process referred to as "amplification." Amplification is carried out by culturing transfectants in the presence of a low level of the selective agent and then increasing the amount of selective agent to select for cells that produce high levels of the products of the introduced genes. An exemplary amplifiable selectable marker is dihydrofolate reductase, which confers resistance to methotrexate. Other drug resistance genes (e.g. hygromycin resistance, multi-drug resistance, puromycin acetyltransferase) can also be used.

Insect cells can be infected with recombinant baculovirus, commonly derived from *Autographa californica* nuclear polyhedrosis virus (AcNPV). See, King and Possee, The Baculovirus Expression System: A Laboratory Guide, London, Chapman & Hall; O'Reilly et al., Baculovirus Expression Vectors: A Laboratory Manual, New York, Oxford University Press., 1994; and Richardson, Ed., Baculovirus Expression Protocols. Methods in Molecular Biology, Humana Press, Totowa, NJ, 1995. Recombinant baculovirus can also be produced through the use of a transposon-based system described by Luckow et al. (*J. Virol.* 67:4566-4579, 1993). This system, which utilizes transfer vectors, is commercially available in kit form (Bac-to-Bac™ kit; Life Technologies, Rockville, MD). See also, Hill-Perkins and Possee, *J. Gen. Virol.* 71:971-976, 1990; Bonning et al., *J. Gen. Virol.* 75:1551-1556, 1994; and Chazenbalk and Rapoport, *J. Biol. Chem.* 270:1543-1549, 1995.

For protein production, the recombinant virus is used to infect host cells, typically a cell line derived from the fall armyworm, *Spodoptera frugiperda* (e.g., Sf9 or Sf21 cells) or *Trichoplusia ni* (e.g., High Five™ cells; Invitrogen, Carlsbad, CA). See, in general, Glick and Pasternak, Molecular Biotechnology: Principles and Applications of Recombinant DNA, ASM Press, Washington, D.C., 1994. See also, U.S. Patent No. 5,300,435. Serum-free media are used to grow and maintain the cells. Suitable media formulations are known in the art and can be obtained from commercial suppliers. The cells are grown up from an inoculation density of approximately 2.5×10^5 cells to a density of 1.2×10^6 cells, at which time a recombinant viral stock is added at a multiplicity of infection (MOI) of 0.1 to 10, more typically near 3. Procedures used are generally described in available laboratory manuals (e.g., King and Possee, *ibid.*; O'Reilly et al., *ibid.*; Richardson, *ibid.*). See also, Guarino et al., U.S. Patent No. 5,162,222 and WIPO publication WO 94/06463.

Fungal cells, including yeast cells, can also be used within the present invention. Yeast species of particular interest in this regard include *Saccharomyces cerevisiae*, *Pichia pastoris*, and *Pichia methanolica*. Methods for transforming *S. cerevisiae* cells with exogenous DNA and producing recombinant polypeptides therefrom are disclosed by, for example, Kawasaki, U.S. Patent No. 4,599,311; Kawasaki et al., U.S. Patent No. 4,931,373; Brake, U.S. Patent No. 4,870,008; Welch et al., U.S. Patent No. 5,037,743; and Murray et al., U.S. Patent No. 4,845,075. Transformed cells are selected by phenotype determined by the selectable marker, commonly drug resistance or the ability to grow in the absence of a particular nutrient (e.g., leucine). A preferred vector system for use in *Saccharomyces cerevisiae* is the *POT1* vector system disclosed by Kawasaki et al. (U.S. Patent No. 4,931,373), which allows transformed cells to be selected by growth in glucose-containing media. Suitable promoters and terminators for use in yeast include those from glycolytic enzyme genes (see, e.g., Kawasaki, U.S. Patent No. 4,599,311; Kingsman et al., U.S. Patent No. 4,615,974; and Bitter, U.S. Patent No. 4,977,092) and alcohol dehydrogenase genes. See also U.S. Patents Nos. 4,990,446; 5,063,154; 5,139,936 and 4,661,454.

Transformation systems for other yeasts, including *Hansenula polymorpha*, *Schizosaccharomyces pombe*, *Kluyveromyces lactis*, *Kluyveromyces fragilis*, *Ustilago maydis*, *Pichia pastoris*, *Pichia methanolica*, *Pichia guilliermondii* and *Candida maltosa* are known in the art. See, for example, Gleeson et al., *J. Gen. Microbiol.* 132:3459-3465, 1986 and Cregg, U.S. Patent No. 4,882,279. *Aspergillus* cells may be utilized according to the methods of McKnight et al., U.S. Patent No. 4,935,349. Methods for transforming *Acremonium chrysogenum* are disclosed by Sumino et al., U.S. Patent No. 5,162,228. Methods for transforming *Neurospora* are disclosed by Lambowitz, U.S. Patent No. 4,486,533. Production of recombinant proteins in *Pichia methanolica* is disclosed in U.S. Patents No. 5,716,808, 5,736,383, 5,854,039, and 5,888,768; and WIPO publications WO 99/14347 and WO 99/14320.

Other higher eukaryotic cells, including plant cells and avian cells, can also be used as hosts according to methods commonly known in the art. For example, the use of *Agrobacterium rhizogenes* as a vector for expressing genes in plant cells has been reviewed by Sinkar et al., *J. Biosci. (Bangalore)* 11:47-58, 1987.

Prokaryotic host cells, including strains of the bacteria *Escherichia coli*, *Bacillus* and other genera are also useful host cells within the present invention. Techniques for transforming these hosts and expressing foreign DNA sequences cloned therein are well known in the art (see, e.g., Sambrook et al., *ibid.*). When expressing a polypeptide in bacteria such as *E. coli*, the polypeptide may be retained in the

cytoplasm, typically as insoluble granules, or may be directed to the periplasmic space by a bacterial secretion sequence. In the former case, the cells are lysed, and the granules are recovered and denatured using, for example, guanidine isothiocyanate or urea. The denatured polypeptide can then be refolded and dimerized by diluting the
5 denaturant, such as by dialysis against a solution of urea and a combination of reduced and oxidized glutathione, followed by dialysis against a buffered saline solution. In the latter case, the polypeptide can be recovered from the periplasmic space in a soluble and functional form by disrupting the cells (by, for example, sonication or osmotic shock) to release the contents of the periplasmic space and recovering the protein,
10 thereby obviating the need for denaturation and refolding.

Transformed or transfected host cells are cultured according to conventional procedures in a culture medium containing nutrients and other components required for the growth of the chosen host cells. A variety of suitable media, including defined media and complex media, are known in the art and generally
15 include a carbon source, a nitrogen source, essential amino acids, vitamins and minerals. Media may also contain such components as growth factors or serum, as required. The growth medium will generally select for cells containing the exogenously added DNA by, for example, drug selection or deficiency in an essential nutrient which is complemented by the selectable marker carried on the expression
20 vector or co-transfected into the host-cell.

It is preferred to purify the polypeptides and proteins of the present invention to $\geq 80\%$ purity, more preferably to $\geq 90\%$ purity, even more preferably $\geq 95\%$ purity, and particularly preferred is a pharmaceutically pure state, that is greater than 99.9% pure with respect to contaminating macromolecules, particularly other proteins
25 and nucleic acids, and free of infectious and pyrogenic agents. Preferably, a purified polypeptide or protein is substantially free of other polypeptides or proteins, particularly those of animal origin.

Expressed recombinant proteins (including single polypeptide chains, chimeric polypeptides, and polypeptide multimers) are purified by conventional protein
30 purification methods, typically by a combination of chromatographic techniques. See, in general, Affinity Chromatography: Principles & Methods, Pharmacia LKB Biotechnology, Uppsala, Sweden, 1988; and Scopes, Protein Purification: Principles and Practice, Springer-Verlag, New York, 1994. Proteins comprising a polyhistidine affinity tag (typically about 6 histidine residues) are purified by affinity
35 chromatography on a nickel chelate resin. See, for example, Houchuli et al., *Bio/Technol.* 6: 1321-1325, 1988. Proteins comprising a glu-glu tag can be purified by immunoaffinity chromatography essentially as disclosed by Grussenmeyer et al., *ibid.*

Proteins comprising other affinity tags can be purified by appropriate affinity chromatography methods, which are known in the art.

Proteins of the present invention and fragments thereof can also be prepared through chemical synthesis according to methods known in the art, including
5 exclusive solid phase synthesis, partial solid phase methods, fragment condensation or classical solution synthesis. See, for example, Merrifield, *J. Am. Chem. Soc.* **85**:2149, 1963; Stewart et al., Solid Phase Peptide Synthesis (2nd edition), Pierce Chemical Co., Rockford, IL, 1984; Bayer and Rapp, *Chem. Pept. Prot.* **3**:3, 1986; and Atherton et al., Solid Phase Peptide Synthesis: A Practical Approach, IRL Press, Oxford, 1989.

10 Using methods known in the art, the proteins of the present invention can be prepared in a variety of modified or derivatized forms. For example, the proteins can be prepared glycosylated or non-glycosylated; pegylated or non-pegylated; and may or may not include an initial methionine amino acid residue.

Biological activities of the proteins of the present invention can be
15 measured *in vitro* using cultured cells or *in vivo* by administering molecules of the claimed invention to the appropriate animal model. Many such assays and models are known in the art. Guidance in initial assay selection is provided by structural predictions and sequence alignments. However, even if no functional prediction is made, the activity of a protein can be elucidated by known methods, including, for
20 example, screening a variety of target cells for a biological response, other *in vitro* assays, expression in a host animal, or through the use of transgenic and/or "knockout" animals. Through the application of robotics, many *in vitro* assays can be adapted to rapid, high-throughput screening of a large number of samples. Target cells for use in activity assays include, without limitation, vascular cells (especially endothelial cells
25 and smooth muscle cells), hematopoietic (myeloid and lymphoid) cells, liver cells (including hepatocytes, fenestrated endothelial cells, Kupffer cells, and Ito cells), fibroblasts (including human dermal fibroblasts and lung fibroblasts), neurite cells (including astrocytes, glial cells, dendritic cells, and PC-12 cells), fetal lung cells, articular synoviocytes, pericytes, chondrocytes, osteoblasts, adipocytes, and prostate
30 epithelial cells. Endothelial cells and hematopoietic cells are derived from a common ancestral cell, the hemangioblast (Choi et al., *Development* **125**:725-732, 1998).

Biological activity can be measured with a silicon-based biosensor microphysiometer that measures the extracellular acidification rate or proton excretion associated with receptor binding and subsequent physiologic cellular responses. An
35 exemplary such device is the Cytosensor™ Microphysiometer manufactured by Molecular Devices, Sunnyvale, CA. A variety of cellular responses, such as cell proliferation, ion transport, energy production, inflammatory response, regulatory and

receptor activation, and the like, can be measured by this method. See, for example, McConnell et al., *Science* 257:1906-1912, 1992; Pitchford et al., *Meth. Enzymol.* 228:84-108, 1997; Arimilli et al., *J. Immunol. Meth.* 212:49-59, 1998; and Van Liefde et al., *Eur. J. Pharmacol.* 346:87-95, 1998. The microphysiometer can be used for

5 assaying adherent or non-adherent eukaryotic or prokaryotic cells. By measuring extracellular acidification changes in cell media over time, the microphysiometer directly measures cellular responses to various stimuli, including agonistic and antagonistic stimuli. Preferably, the microphysiometer is used to measure responses of a eukaryotic cell known to be responsive to the protein of interest, compared to a

10 control eukaryotic cell that does not respond to the protein of interest. Responsive eukaryotic cells comprise cells into which a receptor for the protein of interest has been transfected, as well as naturally responsive cells. Differences in the response of cells exposed to the protein of interest, relative to a control not so exposed, are a direct measurement of protein-modulated cellular responses. Such responses can be assayed

15 under a variety of stimuli. The present invention thus provides methods of identifying agonists and antagonists of proteins of interest, comprising providing cells responsive to a selected protein, culturing a first portion of the cells in the absence of a test compound, culturing a second portion of the cells in the presence of a test compound, and detecting a change in a cellular response of the second portion of the cells as

20 compared to the first portion of the cells. The change in cellular response is shown as a measurable change in extracellular acidification rate. Culturing a third portion of the cells in the presence of the protein of interest and the absence of a test compound provides a positive control and a control to compare the agonist activity of a test compound with that of the protein of interest. Antagonists can be identified by

25 exposing the cells to the protein of interest in the presence and absence of the test compound, whereby a reduction in protein-stimulated activity is indicative of antagonist activity in the test compound.

Assays measuring cell proliferation or differentiation are well known in the art. For example, assays measuring proliferation include such assays as

30 chemosensitivity to neutral red dye (Cavanaugh et al., *Investigational New Drugs* 8:347-354, 1990), incorporation of radiolabelled nucleotides (as disclosed by, e.g., Raines and Ross, *Methods Enzymol.* 109:749-773, 1985; Wahl et al., *Mol. Cell Biol.* 8:5016-5025, 1988; and Cook et al., *Analytical Biochem.* 179:1-7, 1989), incorporation of 5-bromo-2'-deoxyuridine (BrdU) in the DNA of proliferating cells (Porstmann et al.,

35 *J. Immunol. Methods* 82:169-179, 1985), and use of tetrazolium salts (Mosmann, *J. Immunol. Methods* 65:55-63, 1983; Alley et al., *Cancer Res.* 48:589-601, 1988; Marshall et al., *Growth Reg.* 5:69-84, 1995; and Scudiero et al., *Cancer Res.* 48:4827-

4833, 1988). Differentiation can be assayed using suitable precursor cells that can be induced to differentiate into a more mature phenotype. Assays measuring differentiation include, for example, measuring cell-surface markers associated with stage-specific expression of a tissue, enzymatic activity, functional activity or morphological changes (Watt, *FASEB*, 5:281-284, 1991; Francis, *Differentiation* 57:63-75, 1994; Raes, *Adv. Anim. Cell Biol. Technol. Bioprocesses*, 161-171, 1989). Effects of a protein on tumor cell growth and metastasis can be analyzed using the Lewis lung carcinoma model, for example as described by Cao et al., *J. Exp. Med.* 182:2069-2077, 1995. Activity of a protein on cells of neural origin can be analyzed using assays that measure effects on neurite growth as disclosed below.

In vitro assays for pro- and anti-inflammatory activity are known in the art. Exemplary activity assays include mitogenesis assays in which IL-1 responsive cells (e.g., D10.N4.M cells) are incubated in the presence of IL-1 or a test protein for 72 hours at 37°C in a 5% CO₂ atmosphere. IL-2 (and optionally IL-4) is added to the culture medium to enhance sensitivity and specificity of the assay. ³H-thymidine is then added, and incubation is continued for six hours. The amount of label incorporated is indicative of agonist activity. See, Hopkins and Humphreys, *J. Immunol. Methods* 120:271-276, 1989; Greenfeder et al., *J. Biol. Chem.* 270:22460-22466, 1995. Stimulation of cell proliferation can also be measured using thymocytes cultured in a test protein in combination with phytohemagglutinin. IL-1 is used as a control. Proliferation is detected as ³H-thymidine incorporation or metabolic breakdown of (MTT) (Mosman, *ibid.*).

Protein activity may also be detected using assays designed to measure induction of one or more growth factors or other macromolecules. Preferred such assays include those for determining the presence of hepatocyte growth factor (HGF), epidermal growth factor (EGF), transforming growth factor alpha (TGF α), interleukin-6 (IL-6), VEGF, acidic fibroblast growth factor (aFGF), angiogenin, and other macromolecules produced by the liver. Suitable assays include mitogenesis assays using target cells responsive to the macromolecule of interest, receptor-binding assays, competition binding assays, immunological assays (e.g., ELISA), and other formats known in the art. Metalloprotease secretion is measured from treated primary human dermal fibroblasts, synoviocytes and chondrocytes. The relative levels of collagenase, gelatinase and stromalysin produced in response to culturing a target cell in the presence of a protein of interest is measured using zymogram gels (Loita and Stetler-Stevenson, *Cancer Biology* 1:96-106, 1990). Procollagen/collagen synthesis by dermal fibroblasts and chondrocytes in response to a test protein is measured using ³H-proline incorporation into nascent secreted collagen. ³H-labeled collagen is visualized by

SDS-PAGE followed by autoradiography (Unemori and Amento, *J. Biol. Chem.* 265: 10681-10685, 1990). Glycosaminoglycan (GAG) secretion from dermal fibroblasts and chondrocytes is measured using a 1,9-dimethylmethylen blue dye binding assay (Farndale et al., *Biochim. Biophys. Acta* 883:173-177, 1986). Collagen and GAG
5 assays are also carried out in the presence of IL-1 β or TGF- β to examine the ability of a protein to modify the established responses to these cytokines.

Monocyte activation assays are carried out (1) to look for the ability of a protein of interest to further stimulate monocyte activation, and (2) to examine the ability of a protein of interest to modulate attachment-induced or endotoxin-induced
10 monocyte activation (Fuhlbrigge et al., *J. Immunol.* 138: 3799-3802, 1987). IL-1 β and TNF α levels produced in response to activation are measured by ELISA (Biosource, Inc. Camarillo, CA). Monocyte/macrophage cells, by virtue of CD14 (LPS receptor), are exquisitely sensitive to endotoxin, and proteins with moderate levels of endotoxin-like activity will activate these cells.

15 Other metabolic effects of proteins can be measured by culturing target cells in the presence and absence of a protein and observing changes in adipogenesis, gluconeogenesis, glycogenolysis, lipogenesis, glucose uptake, or the like. Suitable assays are known in the art.

Hematopoietic activity of proteins can be assayed on various
20 hematopoietic cells in culture. Preferred assays include primary bone marrow colony assays and later stage lineage-restricted colony assays, which are known in the art (e.g., Holly et al., WIPO Publication WO 95/21920). Marrow cells plated on a suitable semi-solid medium (e.g., 50% methylcellulose containing 15% fetal bovine serum, 10% bovine serum albumin, and 0.6% PSN antibiotic mix) are incubated in the
25 presence of test polypeptide, then examined microscopically for colony formation. Known hematopoietic factors are used as controls. Mitogenic activity of a protein of interest on hematopoietic cell lines can be measured as disclosed above.

Cell migration is assayed essentially as disclosed by Kähler et al. (*Arteriosclerosis, Thrombosis, and Vascular Biology* 17:932-939, 1997). A protein is
30 considered to be chemotactic if it induces migration of cells from an area of low protein concentration to an area of high protein concentration. A typical assay is performed using modified Boyden chambers with a polystyrene membrane separating the two chambers (Transwell; Corning Costar Corp.). The test sample, diluted in medium containing 1% BSA, is added to the lower chamber of a 24-well plate
35 containing Transwells. Cells are then placed on the Transwell insert that has been pretreated with 0.2% gelatin. Cell migration is measured after 4 hours of incubation at 37°C. Non-migrating cells are wiped off the top of the Transwell membrane, and cells

attached to the lower face of the membrane are fixed and stained with 0.1% crystal violet. Stained cells are then extracted with 10% acetic acid and absorbance is measured at 600 nm. Migration is then calculated from a standard calibration curve. Cell migration can also be measured using the matrigel method of Grant et al.

5 ("Angiogenesis as a component of epithelial-mesenchymal interactions" in Goldberg and Rosen, *Epithelial-Mesenchymal Interaction in Cancer*, Birkhäuser Verlag, 1995, 235-248; Baatout, *Anticancer Research* 17:451-456, 1997).

Proteins can be assayed for the ability to modulate axon guidance and growth. Suitable assays that detect changes in neuron growth patterns include, for

10 example, those disclosed in Hastings, WIPO Publication WO 97/29189 and Walter et al., *Development* 101:685-96, 1987. Assays to measure the effects on neuron growth are well known in the art. For example, the C assay (e.g., Raper and Kapfhammer, *Neuron* 4:21-9, 1990 and Luo et al., *Cell* 75:217-27, 1993) can be used to determine collapsing activity of a protein of interest on growing neurons. Other methods that can

15 assess protein-induced inhibition of neurite extension or divert such extension are also known. See, Goodman, *Annu. Rev. Neurosci.* 19:341-77, 1996. Conditioned media from cells expressing a protein of interest, or aggregates of such cells, can be placed in a gel matrix near suitable neural cells, such as dorsal root ganglia (DRG) or sympathetic ganglia explants, which have been co-cultured with nerve growth factor.

20 Compared to control cells, protein-induced changes in neuron growth can be measured (as disclosed by, for example, Messersmith et al., *Neuron* 14:949-59, 1995 and Puschel et al., *Neuron* 14:941-8, 1995). Neurite outgrowth can be measured using neuronal cell suspensions grown in the presence of molecules of the present invention. See, for example, O'Shea et al., *Neuron* 7:231-7, 1991 and DeFreitas et al., *Neuron* 15:333-43,

25 1995.

Cell adhesion activity is assayed essentially as disclosed by LaFleur et al. (*J. Biol. Chem.* 272:32798-32803, 1997). Briefly, microtiter plates are coated with the test protein, non-specific sites are blocked with BSA, and cells (such as smooth muscle cells, leukocytes, or endothelial cells) are plated at a density of approximately

30 10^4 - 10^5 cells/well. The wells are incubated at 37°C (typically for about 60 minutes), then non-adherent cells are removed by gentle washing. Adhered cells are quantitated by conventional methods (e.g., by staining with crystal violet, lysing the cells, and determining the optical density of the lysate). Control wells are coated with a known adhesive protein, such as fibronectin or vitronectin.

35 Assays for angiogenic activity are also known in the art. For example, the effect of a protein of interest on primordial endothelial cells in angiogenesis can be assayed in the chick chorioallantoic membrane angiogenesis assay (Leung, *Science*

246:1306-1309, 1989; Ferrara, *Ann. NY Acad. Sci.* 752:246-256, 1995). Briefly, a small window is cut into the shell of an eight-day old fertilized egg, and a test substance is applied to the chorioallantoic membrane. After 72 hours, the membrane is examined for neovascularization. Other suitable assays include microinjection of early stage quail (*Coturnix coturnix japonica*) embryos as disclosed by Drake et al. (*Proc. Natl. Acad. Sci. USA* 92:7657-7661, 1995); the rodent model of corneal neovascularization disclosed by Muthukkaruppan and Auerbach (*Science* 205:1416-1418, 1979), wherein a test substance is inserted into a pocket in the cornea of an inbred mouse; and the hamster cheek pouch assay (Höckel et al., *Arch. Surg.* 128:423-429, 1993). Induction of vascular permeability, which is indicative of angiogenic activity, is measured in assays designed to detect leakage of protein from the vasculature of a test animal (e.g., mouse or guinea pig) after administration of a test compound (Miles and Miles, *J. Physiol.* 118:228-257, 1952; Feng et al., *J. Exp. Med.* 183:1981-1986, 1996). *In vitro* assays for angiogenic activity include the tridimensional collagen gel matrix model (Pepper et al. *Biochem. Biophys. Res. Comm.* 189:824-831, 1992 and Ferrara et al., *Ann. NY Acad. Sci.* 732:246-256, 1995), which measures the formation of tube-like structures by microvascular endothelial cells; and matrigel models (Grant et al., "Angiogenesis as a component of epithelial-mesenchymal interactions" in Goldberg and Rosen, *Epithelial-Mesenchymal Interaction in Cancer*, Birkhäuser Verlag, 1995, 235-248; Baatout, *Anticancer Research* 17:451-456, 1997), which are used to determine effects on cell migration and tube formation by endothelial cells seeded in matrigel, a basement membrane extract enriched in laminin. It is preferred to carry out angiogenesis assays in the presence and absence of vascular endothelial growth factor (VEGF) to assess possible combinatorial effects. It is also preferred to use VEGF as a control within *in vivo* assays.

Receptor binding can be measured by the competition binding method of Labriola-Tompkins et al., *Proc. Natl. Acad. Sci. USA* 88:11182-11186, 1991. In an exemplary assay for IL-1 receptor binding, membranes prepared from EL-4 thymoma cells (Paganelli et al., *J. Immunol.* 138:2249-2253, 1987) are incubated in the presence of the test protein for 30 minutes at 37°C. Labeled IL-1 α or IL-1 β is then added and the incubation is continued for 60 minutes. The assay is terminated by membrane filtration. The amount of bound label is determined by conventional means (e.g., γ counter). In an alternative assay, the ability of a test protein to compete with labeled IL-1 for binding to cultured human dermal fibroblasts is measured according to the method of Dower et al. (*Nature* 324:266-268, 1986). Briefly, cells are incubated in a round-bottomed, 96-well plate in a suitable culture medium (e.g., RPMI 1640 containing 1% BSA, 0.1% Na azide, and 20 mM HEPES pH 7.4) at 8°C on a rocker

platform in the presence of labeled IL-1. Various concentrations of test protein are added. After the incubation (typically about two hours), cells are separated from unbound label by centrifuging 60- μ l aliquots through 200 μ l of phthalate oils in 400- μ l polyethylene centrifuge tubes and excising the tips of the tubes with a razor blade as disclosed by Segal and Hurwitz, *J. Immunol.* 118:1338-1347, 1977. Receptor binding assays for other cell types are known in the art. See, for example, Bowen-Pope and Ross, *Methods Enzymol.* 109:69-100, 1985.

Receptor binding can also be measured using immobilized receptors or ligand-binding receptor fragments. For example, an immobilized receptor can be exposed to its labeled ligand and unlabeled test protein, whereby a reduction in labeled ligand binding compared to a control is indicative of receptor-binding activity in the test protein. Within another format, a receptor or ligand-binding receptor fragment is immobilized on a biosensor (e.g., BLACore™, Pharmacia Biosensor, Piscataway, NJ) and binding is determined. Antagonists of the native ligand will exhibit receptor binding but will exhibit essentially no activity in appropriate activity assays or will reduce the ligand-mediated response when combined with the native ligand. In view of the low level of receptor occupancy required to produce a response to some ligands (e.g., IL-1), a large excess of antagonist (typically a 10- to 1000-fold molar excess) may be necessary to neutralize ligand activity.

Receptor activation can be detected in target cells by: (1) measurement of adenylate cyclase activity (Salomon et al., *Anal. Biochem.* 58:541-48, 1974; Alvarez and Daniels, *Anal. Biochem.* 187:98-103, 1990); (2) measurement of change in intracellular cAMP levels using conventional radioimmunoassay methods (Steiner et al., *J. Biol. Chem.* 247:1106-13, 1972; Harper and Brooker, *J. Cyc. Nucl. Res.* 1:207-18, 1975); or (3) through use of a cAMP scintillation proximity assay (SPA) method (such as available from Amersham Corp., Arlington Heights, IL).

Proteins can be tested for serine protease activity or proteinase inhibitory activity using conventional assays. Substrate cleavage is conveniently assayed using a tetrapeptide that mimics the cleavage site of the natural substrate and which is linked, via a peptide bond, to a carboxyl-terminal para-nitro-anilide (pNA) group. The protease hydrolyzes the bond between the fourth amino acid residue and the pNA group, causing the pNA group to undergo a dramatic increase in absorbance at 405 nm. Suitable substrates can be synthesized according to known methods or obtained from commercial suppliers. Inhibitory activity is measured by adding a test sample to a reaction mixture containing enzyme and substrate, and comparing the observed enzyme activity to a control (without the test sample). A variety of such assays are known in the art, including assays measuring inhibition of trypsin,

chymotrypsin, plasmin, cathepsin G, and human leukocyte elastase. See, for example, Petersen et al., *Eur. J. Biochem.* 235:310-316, 1996. In a typical procedure, the inhibitory activity of a test compound is measured by incubating the test compound with the proteinase, then adding an appropriate substrate, typically a chromogenic peptide substrate. See, for example, Norris et al. (*Biol. Chem. Hoppe-Seyler* 371:37-42, 1990). Various concentrations of the inhibitor are incubated in the presence of trypsin, plasmin, and plasma kallikrein in a low-salt buffer at pH 7.4, 25°C. After 30 minutes, the residual enzymatic activity is measured by the addition of a chromogenic substrate (e.g., S2251 (D-Val-Leu-Lys-Nan) or S2302 (D-Pro-Phe-Arg-Nan), available from Kabi, Stockholm, Sweden) and a 30-minute incubation. Inhibition of enzyme activity is indicated by a decrease in absorbance at 405 nm or fluorescence Em at 460 nm. From the results, the apparent inhibition constant K_i is calculated. When a serine protease is prepared as an active precursor (e.g., comprising N-terminal residues 1-109 of SEQ ID NO:2), it is activated by cleavage with a suitable protease (e.g., furin (Steiner et al., *J. Biol. Chem.* 267:23435-23438, 1992)) prior to assay. Assays of this type are well known in the art. See, for example, Lottenberg et al., *Thrombosis Research* 28:313-332, 1982; Cho et al., *Biochem.* 23:644-650, 1984; Foster et al., *Biochem.* 26:7003-7011, 1987). The inhibition of coagulation factors (e.g., factor VIIa, factor Xa) can be measured using chromogenic substrates or in conventional coagulation assays (e.g., clotting time of normal human plasma; Dennis et al., *J. Biol. Chem.* 270:25411-25417, 1995).

Blood coagulation and chromogenic assays, which can be used to detect both procoagulant, anticoagulant, and thrombolytic activities, are known in the art. For example, pro- and anticoagulant activities can be measured in a one-stage clotting assay using platelet-poor or factor-deficient plasma (Levy and Edgington, *J. Exp. Med.* 151:1232-1243, 1980; Schwartz et al., *J. Clin. Invest.* 67:1650-1658, 1981). As disclosed by Anderson et al. (*Proc. Natl. Acad. Sci. USA* 96:11189-11193, 1999), the effect of a test compound on platelet activation can be determined by a change in turbidity, and the procoagulant activity of activated platelets can be determined in a phospholipid-dependent coagulation assay. Activation of thrombin can be determined by hydrolysis of peptide p-nitroanilide substrates as disclosed by Lottenberg et al. (*Thrombosis Res.* 28:313-332, 1982). Other procoagulant, anticoagulant, and thrombolytic activities can be measured using appropriate chromogenic substrates, a variety of which are available from commercial suppliers. See, for example, Kettner and Shaw, *Methods Enzymol.* 80:826-842, 1981.

Anti-microbial activity of proteins is evaluated by techniques that are known in the art. For example, anti-microbial activity can be assayed by evaluating the

sensitivity of microbial cell cultures to test agents and by evaluating the protective effect of test agents on infected mice. See, for example, Musiek et al., *Antimicrob. Agents Chemother.* 3:40, 1973. Antiviral activity can also be assessed by protection of mammalian cell cultures. Known techniques for evaluating anti-microbial activity include, for example, Barsum et al., *Eur. Respir. J.* 8:709-714, 1995; Sandovsky-Losica et al., *J. Med. Vet. Mycol (England)* 28:279-287, 1990; Mehentee et al., *J. Gen. Microbiol (England)* 135:2181-2188, 1989; and Segal and Savage, *J. Med. Vet. Mycol.* 24:477-479, 1986. Assays specific for anti-viral activity include, for example, those described by Daher et al., *J. Virol.* 60:1068-1074, 1986.

10 The assays disclosed above can be modified by those skilled in the art to detect the presence of agonists and antagonists of a selected protein of interest.

 Expression of a polynucleotide encoding a protein of interest in animals provides models for further study of the biological effects of overproduction or inhibition of protein activity *in vivo*. Polynucleotides and antisense polynucleotides can be introduced into test animals, such as mice, using viral vectors or naked DNA, or transgenic animals can be produced.

 One *in vivo* approach for assaying proteins of the present invention utilizes viral delivery systems. Exemplary viruses for this purpose include adenovirus, herpesvirus, retroviruses, vaccinia virus, and adeno-associated virus (AAV). Adenovirus, a double-stranded DNA virus, is currently the best studied gene transfer vector for delivery of heterologous nucleic acids. For review, see Becker et al., *Meth. Cell Biol.* 43:161-89, 1994; and Douglas and Curiel, *Science & Medicine* 4:44-53, 1997. The adenovirus system offers several advantages. Adenovirus can (i) accommodate relatively large DNA inserts; (ii) be grown to high-titer; (iii) infect a broad range of mammalian cell types; and (iv) be used with many different promoters including ubiquitous, tissue specific, and regulatable promoters. Because adenoviruses are stable in the bloodstream, they can be administered by intravenous injection.

 By deleting portions of the adenovirus genome, larger inserts (up to 7 kb) of heterologous DNA can be accommodated. These inserts can be incorporated into the viral DNA by direct ligation or by homologous recombination with a co-transfected plasmid. In an exemplary system, the essential E1 gene is deleted from the viral vector, and the virus will not replicate unless the E1 gene is provided by the host cell (e.g., the human 293 cell line). When intravenously administered to intact animals, adenovirus primarily targets the liver. If the adenoviral delivery system has an E1 gene deletion, the virus cannot replicate in the host cells. However, the host's tissue (e.g., liver) will express and process (and, if a signal sequence is present, secrete) the

heterologous protein. Secreted proteins will enter the circulation in the highly vascularized liver, and effects on the infected animal can be determined.

An alternative method of gene delivery comprises removing cells from the body and introducing a vector into the cells as a naked DNA plasmid. The transformed cells are then re-implanted in the body. Naked DNA vectors are introduced into host cells by methods known in the art, including transfection, electroporation, microinjection, transduction, cell fusion, DEAE dextran, calcium phosphate precipitation, use of a gene gun, or use of a DNA vector transporter. See, Wu et al., *J. Biol. Chem.* 263:14621-14624, 1988; Wu et al., *J. Biol. Chem.* 267:963-967, 1992; and Johnston and Tang, *Meth. Cell Biol.* 43:353-365, 1994.

Transgenic mice, engineered to express a gene encoding a protein of interest, and mice that exhibit a complete absence of gene function, referred to as "knockout mice" (Snouwaert et al., *Science* 257:1083, 1992), can also be generated (Lowell et al., *Nature* 366:740-742, 1993). These mice can be employed to study the gene of interest and the protein encoded thereby in an *in vivo* system. Transgenic mice are particularly useful for investigating the role of proteins in early development in that they allow the identification of developmental abnormalities or blocks resulting from the over- or underexpression of a specific factor. See also, Maisonpierre et al., *Science* 277:55-60, 1997 and Hanahan, *Science* 277:48-50, 1997. Preferred promoters for transgenic expression include promoters from metallothionein and albumin genes. As disclosed above, the human sequences provided herein can be used to clone orthologous polynucleotides, which may be preferred for use in generating transgenic and knockout animals.

Antisense methodology can be used to inhibit gene transcription to examine the effects of such inhibition *in vivo*. Polynucleotides that are complementary to a segment of a protein-encoding polynucleotide are designed to bind to the encoding mRNA and to inhibit translation of such mRNA. Such antisense oligonucleotides can also be used to inhibit expression of protein-encoding genes in cell culture.

Biological activities of test proteins can also be measured in animal models by administering the test protein, by itself or in combination with other agents, including other proteins. Using such models facilitates the assay of the test protein by itself or as an inhibitor or modulator of another agent, and also facilitates the measurement of combinatorial effects of bioactive compounds.

Anti-inflammatory activity can be tested in animal models of inflammatory disease. For example, animal models of psoriasis include the analysis of histological alterations in adult mouse tail epidermis (Hofbauer et al, *Brit. J. Dermatol.*

118:85-89, 1988; Bladon et al., *Arch Dermatol. Res.* 277:121-125, 1985). In this model, anti-psoriatic activity is indicated by the induction of a granular layer and orthokeratosis in areas of scale between the hinges of the tail epidermis. Typically, a topical ointment comprising a test compound is applied daily for seven consecutive
5 days, then the animal is sacrificed, and tail skin is examined histologically. An additional model is provided by grafting psoriatic human skin to congenitally athymic (nude) mice (Krueger et al., *J. Invest. Dermatol.* 64:307-312, 1975). Such grafts have been shown to retain the characteristic histology for up to eleven weeks. As in the mouse tail model, the test composition is applied to the skin at predetermined intervals
10 for a period of one to several weeks, at which time the animals are sacrificed and the skin grafts examined histologically. A third model has been disclosed by Fretland et al. (*Inflammation* 14:727-739, 1990). Briefly, inflammation is induced in guinea pig epidermis by topically applying phorbol ester (phorbol-12-myristate-13-acetate; PMA), typically at ca. 2 g/ml in acetone, to one ear and vehicle to the contralateral ear. Test
15 compounds are applied concurrently with the PMA, or may be given orally. Histological analysis is performed at 96 hours after application of PMA. This model duplicates many symptoms of human psoriasis, including edema, inflammatory cell diapedesis and infiltration, high LTB₄ levels and epidermal proliferation.

Cerebral ischemia can be studied in a rat model as disclosed by Relton
20 et al. (*ibid.*) and Loddick et al. (*ibid.*).

The effect of a test protein on primordial endothelial cells in angiogenesis can be assayed in the chick chorioallantoic membrane angiogenesis assay (Leung, *Science* 246:1306-1309, 1989; Ferrara, *Ann. NY Acad. Sci.* 752:246-256, 1995). Briefly, a small window is cut into the shell of an eight-day old fertilized egg,
25 and a test substance is applied to the chorioallantoic membrane. After 72 hours, the membrane is examined for neovascularization. Embryo microinjection of early stage quail (*Coturnix coturnix japonica*) embryos can also be used (Drake et al., *Proc. Natl. Acad. Sci. USA* 92:7657-7661, 1995). Briefly, a solution containing the protein is injected into the interstitial space between the endoderm and the splanchnic mesoderm
30 of early-stage embryos using a micropipette and micromanipulator system. After injection, embryos are placed ventral side down on a nutrient agar medium and incubated for 7 hours at 37°C in a humidified CO₂/air mixture (10%/90%). Vascular development is assessed by microscopy of fixed, whole-mounted embryos and sections.

35 Stimulation of coronary collateral growth can be measured in known animal models, including a rabbit model of peripheral limb ischemia and hind limb ischemia and a pig model of chronic myocardial ischemia (Ferrara et al., *Endocrine*

Reviews 18:4-25, 1997). Test proteins are assayed in the presence and absence of VEGF and basic FGF to test for combinatorial effects. These models can be modified by the use of adenovirus or naked DNA for gene delivery as disclosed in more detail above, resulting in local expression of the test protein(s).

5 Angiogenic activity can also be tested in a rodent model of corneal neovascularization as disclosed by Muthukkaruppan and Auerbach, *Science* 205:1416-1418, 1979, wherein a test substance is inserted into a pocket in the cornea of an inbred mouse. For use in this assay, proteins are combined with a solid or semi-solid, biocompatible carrier, such as a polymer pellet. Angiogenesis is followed
10 microscopically. Vascular growth into the corneal stroma can be detected in about 10 days.

 Angiogenic activity can also be tested in the hamster cheek pouch assay (Höckel et al., *Arch. Surg.* 128:423-429, 1993). A test substance is injected subcutaneously into the cheek pouch, and after five days the pouch is examined under
15 low magnification to determine the extent of neovascularization. Tissue sections can also be examined histologically.

 Induction of vascular permeability is measured in assays designed to detect leakage of protein from the vasculature of a test animal (e.g., mouse or guinea pig) after administration of a test compound (Miles and Miles, *J. Physiol.* 118:228-257,
20 1952; Feng et al., *J. Exp. Med.* 183:1981-1986, 1996).

 Wound-healing models include the linear skin incision model of Mustoe et al. (*Science* 237:1333, 1987). In a typical procedure, a 6-cm incision is made in the dorsal pelt of an adult rat, then closed with wound clips. Test substances and controls (in solution, gel, or powder form) are applied before primary closure. It is preferred to
25 limit administration to a single application, although additional applications can be made on succeeding days by careful injection at several sites under the incision. Wound breaking strength is evaluated between 3 and 21 days post wounding. In a second model, multiple, small, full-thickness excisions are made on the ear of a rabbit. The cartilage in the ear splints the wound, removing the variable of wound contraction
30 from the evaluation of closure. Experimental treatments and controls are applied. The geometry and anatomy of the wound site allow for reliable quantification of cell ingrowth and epithelial migration, as well as quantitative analysis of the biochemistry of the wounds (e.g., collagen content). See, Mustoe et al., *J. Clin. Invest.* 87:694, 1991. The rabbit ear model can be modified to create an ischemic wound environment,
35 which more closely resembles the clinical situation (Ahn et al., *Ann. Plast. Surg.* 24:17, 1990). Within a third model, healing of partial-thickness skin wounds in pigs or guinea pigs is evaluated (LeGrand et al., *Growth Factors* 8:307, 1993). Experimental

treatments are applied daily on or under dressings. Seven days after wounding, granulation tissue thickness is determined. This model is preferred for dose-response studies, as it is more quantitative than other *in vivo* models of wound healing. A full thickness excision model can also be employed. Within this model, the epidermis and dermis are removed down to the panniculus carnosum in rodents or the subcutaneous fat in pigs. Experimental treatments are applied topically on or under a dressing, and can be applied daily if desired. The wound closes by a combination of contraction and cell ingrowth and proliferation. Measurable endpoints include time to wound closure, histologic score, and biochemical parameters of wound tissue. Impaired wound healing models are also known in the art (e.g., Cromack et al., *Surgery* 113:36, 1993; Pierce et al., *Proc. Natl. Acad. Sci. USA* 86:2229, 1989; Greenhalgh et al., *Amer. J. Pathol.* 136:1235, 1990). Delay or prolongation of the wound healing process can be induced pharmacologically by treatment with steroids, irradiation of the wound site, or by concomitant disease states (e.g., diabetes). Linear incisions or full-thickness excisions are most commonly used as the experimental wound. Endpoints are as disclosed above for each type of wound. Subcutaneous implants can be used to assess compounds acting in the early stages of wound healing (Broadley et al., *Lab. Invest.* 61:571, 1985; Sprugel et al., *Amer. J. Pathol.* 129: 601, 1987). Implants are prepared in a porous, relatively non-inflammatory container (e.g., polyethylene sponges or expanded polytetrafluoroethylene implants filled with bovine collagen) and placed subcutaneously in mice or rats. The interior of the implant is empty of cells, producing a "wound space" that is well-defined and separable from the preexisting tissue. This arrangement allows the assessment of cell influx and cell type as well as the measurement of vasculogenesis/angiogenesis and extracellular matrix production.

Inhibition of tumor metastasis can be assessed in mice into which cancerous cells or tumor tissue have been introduced by implantation or injection (e.g., Brown, *Advan. Enzyme Regul.* 35:293-301, 1995; Conway et al., *Clin. Exp. Metastasis* 14:115-124, 1996).

Effects on fibrinolysis can be measured in a rat model wherein the enzyme batroxobin and radiolabeled fibrinogen are administered to test animals. Inhibition of fibrinogen activation by a test compound is seen as a reduction in the circulating level of the label as compared to animals not receiving the test compound. See, Lenfors and Gustafsson, *Semin. Thromb. Hemost.* 22:335-342, 1996.

The invention further provides polypeptides that comprise an epitope-bearing portion of a protein as shown in SEQ ID NO:M, wherein M is an even integer from 2 to 436. An "epitope" is a region of a protein to which an antibody can bind. See, for example, Geysen et al., *Proc. Natl. Acad. Sci. USA* 81:3998-4002, 1984.

Epitopes can be linear or conformational, the latter being composed of discontinuous regions of the protein that form an epitope upon folding of the protein. Linear epitopes are generally at least 6 amino acid residues in length. Relatively short synthetic peptides that mimic part of a protein sequence are routinely capable of eliciting an antiserum that reacts with the partially mimicked protein. See, for example, Sutcliffe et al., *Science* 219:660-666, 1983. Antibodies that recognize short, linear epitopes are particularly useful in analytic and diagnostic applications that employ denatured protein, such as Western blotting (Tobin, *Proc. Natl. Acad. Sci. USA* 76:4350-4356, 1979). Antibodies to short peptides may also recognize proteins in native conformation and will thus be useful for monitoring protein expression and protein isolation, and in detecting proteins in solution, such as by ELISA or in immunoprecipitation studies.

Antigenic, epitope-bearing polypeptides of the present invention are useful for raising antibodies, including monoclonal antibodies, that specifically bind to the corresponding protein. Antigenic, epitope-bearing polypeptides contain a sequence of at least six, preferably at least nine, more preferably from 15 to about 30 contiguous amino acid residues of a protein. Within certain embodiments of the invention, the polypeptides comprise 40, 50, 100, or more contiguous residues of a protein as shown in SEQ ID NO:M, up to the entire predicted mature protein or the primary translation product. It is preferred that the amino acid sequence of the epitope-bearing polypeptide is selected to provide substantial solubility in aqueous solvents, that is the sequence includes relatively hydrophilic residues, and hydrophobic residues are substantially avoided. Table 10 lists preferred hexapeptides for use as antigens. Within Table 10, each the amino termini of the hexapeptides are specified. Those skilled in the art will recognize that longer polypeptides comprising these hexapeptides can also be used and will often be preferred.

Table 10

| Protein | | Hexapeptide N-termini | | | |
|-----------|-----|-----------------------|-----|-----|-----|
| AFP210015 | 389 | 405 | 97 | 388 | 359 |
| AFP170681 | 51 | 334 | 113 | 49 | 140 |
| AFP413680 | 221 | 207 | 220 | 206 | 198 |
| AFP483037 | 219 | 218 | 82 | 216 | 215 |
| AFP230872 | 189 | 188 | 73 | 156 | 68 |
| AFP178828 | 211 | 210 | 209 | 208 | 207 |
| AFP200134 | 150 | 149 | 146 | 132 | 145 |
| AFP195796 | 99 | 97 | 111 | 208 | 240 |

| | | | | | |
|-----------|-----|-----|-----|-----|-----|
| AFP477303 | 64 | 126 | 63 | 54 | 112 |
| AFP354334 | 269 | 268 | 267 | 266 | 265 |
| AFP250287 | 34 | 33 | 48 | 2 | 143 |
| AFP177000 | 133 | 132 | 104 | 37 | 68 |
| AFP278176 | 234 | 145 | 284 | 91 | 291 |
| AFP202885 | 134 | 244 | 170 | 133 | 243 |
| AFP221312 | 31 | 29 | 28 | 51 | 43 |
| AFP239757 | 329 | 200 | 556 | 107 | 328 |
| AFP226311 | 293 | 74 | 250 | 86 | 184 |
| AFP305901 | 340 | 194 | 451 | 192 | 120 |
| AFP325549 | 293 | 74 | 250 | 86 | 184 |
| AFP81988 | 151 | 167 | 147 | 165 | 173 |
| AFP199200 | 150 | 149 | 148 | 92 | 147 |
| AFP290395 | 31 | 29 | 28 | 329 | 326 |
| AFP212675 | 67 | 66 | 65 | 204 | 396 |
| AFP326051 | 49 | 56 | 23 | 78 | 95 |
| AFP512441 | 94 | 93 | 41 | 39 | 38 |
| AFP55098 | 140 | 34 | 139 | 120 | 32 |
| AFP169796 | 177 | 173 | 156 | 32 | 155 |
| AFP280706 | 33 | 54 | 32 | 31 | 53 |
| AFP383165 | 25 | 82 | 52 | 24 | 178 |
| AFP195467 | 113 | 112 | 71 | 2 | 80 |
| AFP134225 | 114 | 280 | 113 | 455 | 417 |
| AFP261193 | 120 | 66 | 65 | 85 | 119 |
| AFP324422 | 147 | 145 | 66 | 65 | 85 |
| AFP374312 | 125 | 124 | 79 | 123 | 77 |
| AFP258118 | 64 | 63 | 116 | 115 | 62 |
| AFP74517 | 1 | 72 | 124 | 123 | 22 |
| AFP254653 | 134 | 36 | 62 | 14 | 23 |
| AFP108666 | 79 | 76 | 74 | 49 | 48 |
| AFP8766 | 140 | 34 | 139 | 120 | 298 |
| AFP397185 | 265 | 35 | 264 | 34 | 48 |
| AFP195042 | 192 | 535 | 191 | 259 | 533 |
| AFP310695 | 49 | 75 | 190 | 5 | 94 |
| AFP70022 | 38 | 64 | 179 | 83 | 37 |
| AFP121670 | 184 | 183 | 121 | 118 | 182 |
| AFP345861 | 151 | 89 | 75 | 135 | 149 |

| | | | | | |
|-----------|-----|-----|-----|-----|-----|
| AFP395942 | 60 | 14 | 59 | 13 | 21 |
| AFP170291 | 144 | 72 | 56 | 55 | 63 |
| AFP297548 | 145 | 73 | 57 | 56 | 64 |
| AFP188135 | 152 | 148 | 158 | 147 | 144 |
| AFP302388 | 478 | 431 | 416 | 414 | 429 |
| AFP263430 | 92 | 23 | 64 | 91 | 110 |
| AFP201273 | 373 | 384 | 163 | 372 | 44 |
| AFP98983 | 3 | 2 | 35 | 34 | 32 |
| AFP581958 | 71 | 66 | 80 | 26 | 25 |
| AFP404202 | 1 | 31 | 115 | 30 | 92 |
| AFP207203 | 427 | 258 | 204 | 426 | 48 |
| AFP220790 | 139 | 92 | 51 | 187 | 91 |
| AFP536326 | 87 | 146 | 105 | 73 | 103 |
| AFP257473 | 270 | 205 | 203 | 245 | 244 |
| AFP248380 | 283 | 62 | 54 | 272 | 100 |
| AFP276202 | 50 | 48 | 35 | 46 | 33 |
| AFP227568 | 199 | 23 | 238 | 363 | 224 |
| AFP229039 | 226 | 91 | 116 | 161 | 225 |
| AFP176297 | 261 | 382 | 183 | 119 | 182 |
| AFP356885 | 622 | 45 | 525 | 175 | 466 |
| AFP226938 | 118 | 108 | 117 | 79 | 107 |
| AFP138504 | 77 | 255 | 75 | 254 | 292 |
| AFP359196 | 4 | 76 | 3 | 2 | 37 |
| AFP501809 | 141 | 139 | 9 | 169 | 2 |
| AFP152733 | 258 | 204 | 48 | 47 | 257 |
| AFP541394 | 31 | 29 | 28 | 235 | 232 |
| AFP243183 | 272 | 110 | 106 | 3 | 2 |
| AFP80739 | 398 | 397 | 224 | 223 | 155 |
| AFP361806 | 4 | 78 | 139 | 3 | 76 |
| AFP483930 | 107 | 124 | 123 | 88 | 45 |
| AFP257336 | 124 | 42 | 122 | 182 | 158 |
| AFP195800 | 40 | 39 | 65 | 38 | 96 |
| AFP179530 | 57 | 251 | 249 | 315 | 55 |
| AFP279267 | 106 | 62 | 216 | 187 | 59 |
| AFP299766 | 127 | 168 | 165 | 29 | 126 |
| AFP244615 | 171 | 196 | 326 | 255 | 179 |
| AFP325761 | 138 | 137 | 2 | 144 | 109 |

| | | | | | |
|-----------|-----|-----|-----|-----|-----|
| AFP226024 | 79 | 317 | 159 | 140 | 45 |
| AFP257094 | 71 | 116 | 115 | 3 | 144 |
| AFP197103 | 200 | 198 | 215 | 195 | 177 |
| AFP271855 | 92 | 44 | 42 | 18 | 27 |
| AFP324816 | 9 | 252 | 120 | 8 | 63 |
| AFP407963 | 202 | 201 | 156 | 200 | 155 |
| AFP369635 | 98 | 398 | 255 | 97 | 254 |
| AFP93743 | 4 | 254 | 3 | 294 | 293 |
| AFP243230 | 28 | 129 | 128 | 127 | 44 |
| AFP169316 | 294 | 170 | 293 | 36 | 157 |
| AFP130852 | 82 | 59 | 117 | 145 | 66 |
| AFP194191 | 363 | 112 | 271 | 69 | 267 |
| AFP213472 | 103 | 102 | 69 | 2 | 37 |
| AFP360430 | 177 | 75 | 183 | 74 | 130 |
| AFP491309 | 107 | 106 | 69 | 2 | 37 |
| AFP193428 | 129 | 87 | 343 | 60 | 128 |
| AFP366534 | 72 | 4 | 2 | 59 | 39 |
| AFP22706 | 229 | 227 | 65 | 64 | 188 |
| AFP389012 | 216 | 27 | 289 | 34 | 17 |
| AFP137186 | 2 | 1 | 182 | 216 | 43 |
| AFP127023 | 86 | 56 | 131 | 178 | 55 |
| AFP389687 | 57 | 56 | 117 | 370 | 369 |
| AFP293220 | 186 | 194 | 105 | 146 | 182 |
| AFP425535 | 264 | 181 | 163 | 370 | 149 |
| AFP301494 | 159 | 4 | 2 | 84 | 25 |
| AFP345421 | 500 | 592 | 639 | 652 | 849 |
| AFP216667 | 92 | 435 | 329 | 422 | 47 |
| AFP247951 | 27 | 34 | 33 | 25 | 94 |
| AFP4464 | 365 | 363 | 362 | 55 | 209 |
| AFP561930 | 108 | 107 | 104 | 52 | 66 |
| AFP192851 | 300 | 276 | 299 | 298 | 496 |
| AFP252759 | 311 | 310 | 64 | 21 | 157 |
| AFP199044 | 143 | 2 | 209 | 206 | 125 |
| AFP357958 | 167 | 338 | 165 | 324 | 362 |
| AFP117501 | 135 | 87 | 362 | 86 | 418 |
| AFP194554 | 318 | 170 | 54 | 105 | 169 |
| AFP371069 | 332 | 1 | 283 | 365 | 279 |

| | | | | | |
|-----------|-----|-----|-----|-----|-----|
| AFP313600 | 341 | 340 | 240 | 48 | 176 |
| AFP262739 | 25 | 24 | 142 | 23 | 207 |
| AFP180730 | 58 | 37 | 30 | 27 | 36 |
| AFP287227 | 596 | 592 | 591 | 374 | 525 |
| AFP75785 | 128 | 127 | 136 | 99 | 71 |
| AFP174843 | 152 | 323 | 150 | 309 | 347 |
| AFP250422 | 100 | 140 | 99 | 138 | 182 |
| AFP198645 | 145 | 144 | 143 | 64 | 56 |
| AFP238111 | 123 | 50 | 20 | 137 | 35 |
| AFP460626 | 153 | 151 | 71 | 150 | 70 |
| AFP271081 | 68 | 112 | 39 | 202 | 67 |
| AFP277752 | 109 | 106 | 220 | 238 | 92 |
| AFP291338 | 347 | 342 | 97 | 362 | 339 |
| AFP551038 | 134 | 131 | 186 | 130 | 173 |
| AFP301579 | 105 | 153 | 130 | 152 | 67 |
| AFP266188 | 121 | 235 | 61 | 180 | 120 |
| AFP275580 | 193 | 77 | 192 | 2 | 148 |
| AFP298054 | 148 | 234 | 146 | 233 | 144 |
| AFP348226 | 148 | 103 | 85 | 309 | 59 |
| AFP349106 | 208 | 118 | 117 | 207 | 116 |
| AFP288248 | 376 | 342 | 340 | 339 | 312 |
| AFP436476 | 18 | 39 | 139 | 38 | 99 |
| AFP352125 | 53 | 59 | 163 | 142 | 104 |
| AFP62060 | 247 | 187 | 73 | 426 | 72 |
| AFP236718 | 100 | 99 | 249 | 248 | 184 |
| AFP75775 | 201 | 90 | 239 | 173 | 199 |
| AFP407487 | 148 | 103 | 85 | 59 | 58 |
| AFP280451 | 141 | 294 | 6 | 209 | 139 |
| AFP11675 | 58 | 56 | 90 | 64 | 89 |
| AFP348656 | 160 | 159 | 158 | 103 | 149 |
| AFP277451 | 118 | 2 | 1 | 146 | 241 |
| AFP287436 | 53 | 59 | 223 | 142 | 104 |
| AFP116043 | 212 | 239 | 138 | 186 | 183 |
| AFP138740 | 264 | 263 | 31 | 72 | 232 |
| AFP15192 | 47 | 46 | 216 | 85 | 212 |
| AFP169968 | 64 | 117 | 63 | 2 | 81 |
| AFP173341 | 65 | 64 | 102 | 101 | 100 |

| | | | | | |
|-----------|-----|-----|-----|-----|-----|
| AFP17588 | 43 | 42 | 2 | 41 | 1 |
| AFP176427 | 311 | 290 | 308 | 155 | 288 |
| AFP192633 | 58 | 56 | 162 | 349 | 44 |
| AFP193013 | 47 | 90 | 87 | 46 | 68 |
| AFP193881 | 274 | 295 | 402 | 273 | 292 |
| AFP195562 | 274 | 295 | 339 | 473 | 273 |
| AFP199922 | 57 | 55 | 74 | 180 | 50 |
| AFP204736 | 89 | 58 | 43 | 28 | 23 |
| AFP206179 | 74 | 80 | 73 | 71 | 70 |
| AFP221877 | 32 | 31 | 30 | 50 | 75 |
| AFP222758 | 44 | 43 | 75 | 42 | 19 |
| AFP227032 | 47 | 55 | 46 | 65 | 54 |
| AFP229269 | 147 | 127 | 146 | 63 | 60 |
| AFP232213 | 44 | 41 | 28 | 27 | 40 |
| AFP237679 | 2 | 1 | 34 | 58 | 55 |
| AFP249599 | 48 | 47 | 45 | 43 | 42 |
| AFP275215 | 82 | 80 | 70 | 2 | 55 |
| AFP290397 | 149 | 148 | 2 | 1 | 29 |
| AFP306591 | 45 | 44 | 84 | 83 | 65 |
| AFP310297 | 23 | 31 | 37 | 47 | 30 |
| AFP314720 | 47 | 44 | 26 | 25 | 23 |
| AFP318671 | 55 | 54 | 51 | 64 | 63 |
| AFP323575 | 75 | 73 | 72 | 70 | 18 |
| AFP327160 | 37 | 68 | 47 | 67 | 96 |
| AFP329002 | 78 | 77 | 76 | 75 | 74 |
| AFP345415 | 41 | 40 | 133 | 106 | 39 |
| AFP347179 | 30 | 4 | 29 | 86 | 177 |
| AFP359138 | 77 | 2 | 76 | 75 | 74 |
| AFP365372 | 13 | 1 | 62 | 69 | 79 |
| AFP367284 | 61 | 60 | 36 | 5 | 59 |
| AFP372822 | 49 | 48 | 25 | 8 | 24 |
| AFP374595 | 154 | 153 | 165 | 3 | 56 |
| AFP375952 | 36 | 35 | 53 | 52 | 69 |
| AFP382913 | 67 | 32 | 30 | 20 | 66 |
| AFP389184 | 24 | 31 | 78 | 30 | 39 |
| AFP404208 | 69 | 68 | 67 | 39 | 36 |
| AFP404279 | 81 | 31 | 72 | 30 | 62 |

| | | | | | |
|-----------|-----|-----|-----|-----|-----|
| AFP409112 | 97 | 96 | 56 | 94 | 55 |
| AFP413111 | 65 | 85 | 96 | 64 | 94 |
| AFP415635 | 35 | 26 | 25 | 34 | 32 |
| AFP421092 | 27 | 1 | 46 | 57 | 35 |
| AFP436666 | 5 | 95 | 59 | 4 | 58 |
| AFP448623 | 14 | | | | |
| AFP454192 | 106 | 104 | 83 | 114 | 112 |
| AFP49026 | 49 | 104 | 76 | 48 | 138 |
| AFP51688 | 51 | 86 | 50 | 85 | 43 |
| AFP525341 | 18 | 17 | 16 | 79 | 14 |
| AFP545268 | 65 | 64 | 75 | 21 | 74 |
| AFP592620 | 22 | 21 | 29 | 20 | 28 |
| AFP62197 | 134 | 84 | 133 | 20 | 104 |
| AFP68229 | 161 | 171 | 192 | 170 | 232 |
| AFP71288 | 67 | 49 | 65 | 48 | 46 |
| AFP77851 | 123 | 121 | 33 | 103 | 53 |
| AFP81957 | 89 | 66 | 63 | 25 | 40 |
| AFP85168 | 61 | 31 | 39 | 27 | 46 |

As used herein, the term "antibodies" includes polyclonal antibodies, monoclonal antibodies, antigen-binding fragments thereof such as F(ab')₂ and Fab fragments, single chain antibodies, and the like, including genetically engineered antibodies. Non-human antibodies can be humanized by grafting only non-human CDRs onto human framework and constant regions, or by incorporating the entire non-human variable domains (optionally "cloaking" them with a human-like surface by replacement of exposed residues, wherein the result is a "veneered" antibody). In some instances, humanized antibodies may retain non-human residues within the human variable region framework domains to enhance proper binding characteristics. Through humanizing antibodies, biological half-life may be increased, and the potential for adverse immune reactions upon administration to humans is reduced. One skilled in the art can generate humanized antibodies with specific and different constant domains (i.e., different Ig subclasses) to facilitate or inhibit various immune functions associated with particular antibody constant domains.

Alternative techniques for generating or selecting antibodies useful herein include *in vitro* exposure of lymphocytes to an immunogenic polypeptide, and selection of antibody display libraries in phage or similar vectors (for instance, through use of an immobilized or labeled polypeptide). Human antibodies can be produced in

transgenic, non-human animals that have been engineered to contain human immunoglobulin genes as disclosed in WIPO Publication WO 98/24893. It is preferred that the endogenous immunoglobulin genes in these animals be inactivated or eliminated, such as by homologous recombination.

5 Antibodies are defined to be specifically binding if they bind to a target polypeptide with an affinity at least 10-fold greater than the binding affinity to control (non-target) polypeptide. It is preferred that the antibodies exhibit a binding affinity (K_d) of $10^6 M^{-1}$ or greater, preferably $10^7 M^{-1}$ or greater, more preferably $10^8 M^{-1}$ or greater, and most preferably $10^9 M^{-1}$ or greater. The affinity of a monoclonal antibody
10 can be readily determined by one of ordinary skill in the art (see, for example, Scatchard, *Ann. NY Acad. Sci.* 51: 660-672, 1949).

 Methods for preparing polyclonal and monoclonal antibodies are well known in the art (see for example, Hurrell, J. G. R., Ed., *Monoclonal Hybridoma Antibodies: Techniques and Applications*, CRC Press, Inc., Boca Raton, FL, 1982). As
15 would be evident to one of ordinary skill in the art, polyclonal antibodies can be generated from a variety of warm-blooded animals such as horses, cows, goats, sheep, dogs, chickens, rabbits, mice, and rats. The immunogenicity of a polypeptide immunogen may be increased through the use of an adjuvant such as alum (aluminum hydroxide) or Freund's complete or incomplete adjuvant. Polypeptides useful for
20 immunization also include fusion polypeptides, such as fusions of a polypeptide of interest or a portion thereof with an immunoglobulin polypeptide or with maltose binding protein. The polypeptide immunogen may be a full-length molecule or a portion thereof. If the polypeptide portion is "hapten-like", such portion may be advantageously joined or linked to a macromolecular carrier (such as keyhole limpet
25 hemocyanin (KLH), bovine serum albumin (BSA) or tetanus toxoid) for immunization.

 A variety of assays known to those skilled in the art can be utilized to detect antibodies that specifically bind to a polypeptide of interest. Exemplary assays are described in detail in *Antibodies: A Laboratory Manual*, Harlow and Lane (Eds.), Cold Spring Harbor Laboratory Press, 1988. Representative examples of such assays
30 include concurrent immunoelectrophoresis, radio-immunoassays, radio-immunoprecipitations, enzyme-linked immunosorbent assays (ELISA), dot blot assays, Western blot assays, inhibition or competition assays, and sandwich assays.

 Antibodies can be used, for example, to isolate target polypeptides by affinity purification, for diagnostic assays for determining circulating or localized
35 levels of target polypeptides, for tissue typing, for cell sorting, for screening expression libraries; for generating anti-idiotypic antibodies, and as neutralizing antibodies or as antagonists to block protein activity *in vitro* and *in vivo*.

The present invention also provides reagents for use in diagnostic and therapeutic applications. Such reagents include polynucleotide probes and primers; antibodies, including antibody fragments, single-chain antibodies, and other genetically engineered forms; soluble receptors and other polypeptide binding partners; and the proteins of the invention themselves, including fragments thereof. Those skilled in the art will recognize that diagnostic reagents will commonly be labeled to provide a detectable signal or other second function. Thus, polypeptides, antibodies, receptors, and other binding partners disclosed herein can be directly or indirectly conjugated to drugs, toxins, radionuclides, enzymes, enzyme substrates, cofactors, inhibitors, fluorescent markers, chemiluminescent markers, magnetic particles, and the like, and these conjugates used for *in vivo* diagnostic or therapeutic applications. Cytotoxic molecules, for example, can be directly or indirectly attached to the binding partner (e.g., by chemical coupling or as a fusion protein), and include bacterial or plant toxins (e.g., diphtheria toxin, *Pseudomonas* exotoxin, ricin, saporin, abrin, and the like); therapeutic radionuclides (e.g., iodine-131, rhenium-188 or yttrium-90) which can be directly attached to a polypeptide or antibody or indirectly attached through means of a chelating moiety; and cytotoxic drugs (e.g., adriamycin). Methods for preparing labeled reagents are known in the art. Within an alternative embodiment, the detectable signal or other function can be provided by a second member of a complement-anticomplement pair, which second member binds to the diagnostic reagent. For example, a first (unlabeled) antibody can be used to bind to a cell-surface polypeptide, after which a second, labeled antibody which binds to the first antibody is added. Other complement-anticomplement pairs are known in the art and include biotin/streptavidin.

Diagnostic reagents as disclosed herein can be used *in vivo* or *in vitro*. *In vitro* diagnostic assays include assays of tissue and fluid samples. Assays for protein in serum, for example, may be used to detect metabolic abnormalities characterized by over- or under-production of the protein, such as cancers, immune system abnormalities, infections, organ failure, metabolic imbalances, inborn errors of metabolism and other disease states. Proteins of the present invention can also be used in the detection of circulating autoantibodies, which are indicative of autoimmune disorders. Those skilled in the art will recognize that conditions related to protein underexpression or overexpression may be amenable to treatment by therapeutic manipulation of the relevant protein level(s). Proteins in serum can be quantitated by known methods known in the art, which include the use of antibodies in a variety of formats. Non-antibody binding partners, such as ligand-binding receptor fragments (commonly referred to as "soluble receptors") can also be used.

In general, diagnostic methods employing oligonucleotide probes or primers comprise the steps of (a) obtaining a genetic sample from a patient; (b) incubating the genetic sample with an oligonucleotide probe or primer as disclosed above, under conditions wherein the probe or primer will hybridize to a complementary polynucleotide sequence, to produce a first reaction product; and (c) comparing the first reaction product to a control reaction product. A difference between the first reaction product and the control reaction product is indicative of a genetic abnormality in the patient. Genetic samples for use within such methods include genomic DNA, cDNA, and RNA. Suitable assay methods in this regard include molecular genetic techniques known to those in the art, such as restriction fragment length polymorphism (RFLP) analysis, short tandem repeat (STR) analysis employing PCR techniques, ligation chain reaction (Barany, *PCR Methods and Applications* 1:5-16, 1991), ribonuclease protection assays, and other genetic linkage analysis techniques known in the art (Sambrook et al., *ibid.*; Ausubel et. al., *ibid.*; A.J. Marian, *Chest* 108:255-65, 1995). Ribonuclease protection assays (see, e.g., Ausubel et al., *ibid.*, ch. 4) comprise the hybridization of an RNA probe to a patient RNA sample, after which the reaction product (RNA-RNA hybrid) is exposed to RNase. Hybridized regions of the RNA are protected from digestion. Within PCR assays, a patient genetic sample is incubated with a pair of oligonucleotide primers, and the region between the primers is amplified and recovered. Changes in size, amount, or sequence of recovered product are indicative of mutations in the patient. Another PCR-based technique that can be employed is single strand conformational polymorphism (SSCP) analysis (Hayashi, *PCR Methods and Applications* 1:34-38, 1991). Chromosomal localization data can be used to correlate AFP gene locations with known genetic disorders using, for example, the OMIM™ Database, Johns Hopkins University, 2000 (<http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=OMIM>).

Relative chromosomal sublocalization shown in Table 11 was determined using the Draft Human Genome Browser (Kent, J., University of California Santa Cruz, <http://genome.ucsc.edu/goldenPath/hgTracks.html>) displaying the draft assembly of the July 17, 2000 version of the human genome. Table 11 also correlates AFP sequences with corresponding sequences in public databases by GenBank Accession Number, source clone ID number, and EST accession number. Also see Table 5, above.

Table 11

| AFP | GenBank Acc. No. | Source Clone ID No. | EST Acc. No. | Chr. | Band | Start | Stop |
|-----------|---------------------|-----------------------------------|------------------|------|-----------|-----------|-----------|
| AFP127023 | AP001155 | RP11-594B10 | * | 18 | 18q12 | 35729370 | 35952786 |
| AFP138504 | AP001931 | RP11-691N7 | * | 11 | 11p11.11 | 53438038 | 53888802 |
| AFP138740 | AC024059 | RP11-79j21 | AW580814 | 15 | 15q22.1 | 58185489 | 58481462 |
| AFP177000 | AL118506 | RP4-591C20 | AW580814 | 15 | | 58258653 | 58308652 |
| AFP178828 | AC007686 | CTD-2289B16;RP11-116N21;RP11-7F17 | * | 20 | 20q12 | 48950838 | 49160243 |
| AFP179530 | AC011475 | CTC-539A10 | * | 14 | 14q23.3 | 62132030 | 62313415 |
| AFP188135 | AC013740 | * | * | 12 | 12q12 | 41234876 | 41456630 |
| AFP194554 | AC024888 | RP11-901L | * | 9 | 9q31.2 | 91150313 | 91361876 |
| AFP199044 | AC012180 | RP11-31110 | * | 16 | 16q22.1 | 71944378 | 72167142 |
| AFP199200 | CNS01DV7 | BAC-R-1070N10 | * | 16 | 16q11.2 | 44574019 | 44904017 |
| AFP229269 | AL161670 | BAC-R-804M7 | * | 14 | | 82330266 | 82541053 |
| AFP236718 | AC010319 | CTD-2521M24 | * | 14 | 14q21.3 | 46135365 | 46299284 |
| AFP237679 | Z69709 | * | * | 19 | 19p13.3 | 4839920 | 5087628 |
| AFP244615 | * | * | AI494556;AW85055 | 4 | 4p16.3 | 4521455 | 4544888 |
| | | | 3 | 3 | 3q13.12 | 116466893 | 116517043 |
| AFP249599 | AL157714 | RP11-541H12 | * | 1 | 1q22-23.3 | 161893354 | 162136704 |
| AFP250422 | AC012046 | RP11-312P12 | * | 10 | 10q22.1 | 81289799 | 81650062 |
| AFP262739 | AC005884 | hRPK.264_B_14 | * | 17 | 17q23.3 | 64245127 | 64365313 |
| AFP275580 | AC016773 | * | * | 3 | 3q21.3 | 141329005 | 141513510 |
| AFP277451 | AC055822 | RP11-707M3 | * | 8 | 8q13.3 | 75395740 | 75583383 |
| AFP279267 | * | * | AI566086 | 10 | 10q11.1 | 52859924 | 52861338 |
| AFP280451 | AL133355 | RP11-541N10 | * | 10 | 10q24.32 | 115276306 | 115467187 |
| AFP290397 | * | * | AA421069 | 15 | 15q15.3 | 48427462 | 48427830 |
| AFP293220 | AC012476 | RP11-532F12 | * | 15 | 15p11.1 | 17263661 | 17480097 |
| AFP297548 | * | * | W52728 | 11 | 11q11 | 57918740 | 57927327 |
| AFP306591 | AQ079258 | 236B89 | AW118928 | 6 | 6p22.3 | 19812023 | 19812791 |
| AFP313600 | AC005037 | NH0469M07 | * | 2 | 2q33.1 | 205320800 | 205511307 |
| AFP324816 | AC011687 | RP11-15120 | * | 2 | 2p21 | 49054619 | 49249783 |
| AFP325761 | AC012485 | RP11-5024 | * | 2 | 2p24.3 | 17554756 | 17765537 |

| | | | | | | | |
|-----------|----------|---------------|----------|----|--------------|-----------|-----------|
| AFP326051 | AL132639 | BAC-R-407N17 | AI525611 | 14 | 14p11.1 | 19959493 | 20153358 |
| AFP345861 | AC015936 | CTD-2534121 | * | 17 | 17q21.2 | 44087441 | 44286594 |
| AFP347179 | AC025740 | * | * | 12 | 12q24.23 | 125918909 | 126134148 |
| AFP372822 | AL022240 | 3.28E+21 | * | 1 | 1q12-21.2 | 138667522 | 138765140 |
| AFP374312 | * | * | AI253088 | 11 | 11q23.3 | 128134250 | 128134589 |
| AFP375952 | * | * | AI741157 | 16 | 16p13.3 | 3479999 | 3500834 |
| AFP395942 | AC004235 | * | * | 16 | 16p13.3 | 4189155 | 4222465 |
| AFP404202 | * | * | AI133727 | 7 | | 142961410 | 143641730 |
| AFP404279 | * | * | AI341602 | 4 | 4p16.3 | 1512179 | 1514256 |
| AFP413680 | AC006942 | cosmid-R31181 | * | 19 | 19q13.33 | 59897688 | 59940397 |
| AFP436666 | * | * | AI814257 | 8 | 8p21.3 | 18993217 | 19003942 |
| AFP448623 | * | * | AI140615 | 5 | 5q33.1 | 173540737 | 173547400 |
| AFP460626 | AC009131 | RP11-502K10 | * | 16 | 16q22.1 | 70222075 | 70471703 |
| AFP477303 | AC008686 | CTB-5E10 | * | 19 | 19p13.13 | 16491516 | 16677574 |
| AFP501809 | * | * | AW583171 | 6 | 6p21.1 | 50554924 | 50564907 |
| AFP545268 | AL138695 | RP11-342J4 | * | 13 | 13q21.1 | 60450247 | 60714738 |
| AFP561930 | AL136221 | RP11-391H12 | * | 13 | 13q34 | 108494503 | 108794286 |
| AFP71288 | * | * | AA493506 | 6 | 6q22.33 | 137477811 | 137478427 |
| AFP74517 | HS1056L3 | RP5-1056L3 | * | 1 | 1p35.1-36.13 | * | * |
| AFP93743 | AC067942 | RP11-791G16 | * | 4 | 4q21.22 | 77419530 | 77633569 |

If a mammal has an insufficiency of a protein of interest (due to, for example, a mutated or absent gene), the corresponding wild-type gene can be introduced into the cells of the mammal. In one embodiment, a gene encoding a protein of interest is introduced into the animal using a viral vector. Such vectors include an attenuated or defective DNA virus, such as, but not limited to, herpes simplex virus (HSV), papillomavirus, Epstein Barr virus (EBV), adenovirus, adeno-associated virus (AAV), and the like. Defective viruses, which entirely or almost entirely lack viral genes, are preferred. A defective virus is not infective after introduction into a cell. Use of defective viral vectors allows for administration to cells in a specific, localized area, without concern that the vector can infect other cells. Examples of particular vectors include, but are not limited to, a defective herpes simplex virus 1 (HSV1) vector (Kaplit et al., *Molec. Cell. Neurosci.* 2:320-30, 1991); an attenuated adenovirus vector, such as the vector described by Stratford-Perricaudet et al. (*J. Clin. Invest.* 90:626-30, 1992); and a defective adeno-associated virus vector (Samulski et al., *J. Virol.* 61:3096-101, 1987; Samulski et al., *J. Virol.* 63:3822-28, 1989).

Within another embodiment, a gene of interest is introduced into an animal by liposome-mediated transfection ("lipofection") essentially as disclosed above. Lipofection can be used to introduce exogenous genes into specific organs.

A gene of interest can also be introduced into an animal for gene therapy as a naked DNA plasmid using the methods disclosed above.

In another embodiment, polypeptide-toxin fusion proteins or antibody/fragment-toxin fusion proteins may be used for targeted cell or tissue inhibition or ablation, such as in cancer therapy. Of particular interest in this regard are conjugates of an AFP protein and a cytotoxin, which can be used to target the cytotoxin to a tumor or other tissue that is undergoing undesired angiogenesis or neovascularization.

In another embodiment, AFP-cytokine fusion proteins or antibody/fragment-cytokine fusion proteins may be used for enhancing *in vitro* cytotoxicity (for instance, that mediated by monoclonal antibodies against tumor targets) and for enhancing *in vivo* killing of target tissues (for example, blood and bone marrow cancers). See, generally, Hornick et al., *Blood* 89:4437-4447, 1997). In general, cytokines are toxic if administered systemically. The described fusion proteins enable targeting of a cytokine to a desired site of action, such as a cell having binding sites for an AFP protein, thereby providing an elevated local concentration of cytokine. Polypeptides, antibodies, or receptors target an undesirable cell or tissue

(e.g., a tumor), and the fused cytokine mediates improved target cell lysis by effector cells. Suitable cytokines for this purpose include, for example, interleukin-2 and granulocyte-macrophage colony-stimulating factor (GM-CSF).

In another embodiment, polypeptide-toxin fusion proteins or other
5 binding partner-linked toxins may be used for targeted cell or tissue inhibition or ablation (for instance, to treat cancer cells or tissues). Target cells (i.e., those displaying a receptor for a polypeptide of interest) bind the polypeptide-toxin conjugate, which is then internalized, killing the cell. The effects of receptor-specific cell killing (target ablation) are revealed by changes in whole animal physiology or
10 through histological examination. Thus, ligand-dependent, receptor-directed cytotoxicity can be used to enhance understanding of the physiological significance of a protein ligand. A preferred such toxin is saporin. Mammalian cells have no receptor for saporin, which is non-toxic when it remains extracellular. Alternatively, if the polypeptide of interest has multiple functional domains (i.e., an activation domain or a
15 ligand binding domain, plus a targeting domain), a fusion protein including only the targeting domain may be suitable for directing a detectable molecule, a cytotoxic molecule or a complementary molecule to a cell or tissue type of interest. In instances where the domain-only fusion protein includes a complementary molecule, the anti-complementary molecule can be conjugated to a detectable or cytotoxic molecule.
20 Such domain-complementary molecule fusion proteins thus represent a generic targeting vehicle for cell- or tissue-specific delivery of generic anti-complementary-detectable/cytotoxic molecule conjugates.

The bioactive conjugates described herein can be delivered intravenously, intraarterially or intraductally, or may be introduced locally at the
25 intended site of action.

For pharmaceutical use, the proteins of the present invention are formulated according to conventional methods. Routes of delivery include topical, mucosal, and parenteral, the latter including intravenous and subcutaneous delivery. Intravenous administration will be by bolus injection or infusion over a typical period
30 of one to several hours. In general, pharmaceutical formulations will include a protein of the present invention in combination with a pharmaceutically acceptable vehicle, such as saline, buffered saline, 5% dextrose in water or the like. Formulations may further include one or more excipients, diluents, fillers, emulsifiers, preservatives, solubilizers, buffering agents, wetting agents, stabilizers, colorings, penetration
35 enhancers, albumin to prevent protein loss on vial surfaces, etc. Topical formulations are typically provided as liquids, ointments, salves, gels, emulsions and the like. Methods of formulation are well known in the art and are disclosed, for example, in

Remington: The Science and Practice of Pharmacy, Gennaro, ed., Mack Publishing Co., Easton, PA, 19th ed., 1995. Therapeutic doses will be determined by the clinician according to accepted standards, taking into account the nature and severity of the condition to be treated, patient traits, etc. Proteins of the present invention will
5 generally be formulated to provide a dose of from 0.01 μ g to 100 mg per kg patient weight per day, more commonly from 0.1 μ g to 10 mg/kg/day, still more commonly from 0.1 μ g to 1.0 mg/kg/day. Determination of dose is within the level of ordinary skill in the art. The proteins may be administered for acute treatment, over one week or less, often over a period of one to three days or may be used in chronic treatment, over
10 several months or years. In general, a therapeutically effective amount is an amount sufficient to produce a clinically significant change in the targetted condition.

Within the laboratory research field, the proteins of the present invention can be used as molecular weight standards, or as standards in the analysis of cell phenotype, and as reagents for the study of cells, receptors, and other binding
15 molecules. Such reagents will generally further comprise a second moiety, such as a label, binding partner, or toxin, that facilitates the detection of the protein when bound to its target. Many such systems are known in the art and are summarized above. Receptors and other cell-surface binding sites for proteins of the present invention can be identified by exposing a population of cells to a labelled protein under physiologic
20 conditions, whereby the protein binds to the surface of the cell. Cells bearing receptors for a protein of interest can also be identified using the protein joined to a toxin, whereby receptor-bearing cells are killed by the toxin.

AFP proteins and antagonists thereof can be used as standards in assays of protein and protein inhibitors in both clinical and research settings. Such assays can
25 comprise any of a number of standard formats, include radioreceptor assays and ELISAs. Protein standards can be prepared in labeled form using a radioisotope, enzyme, fluorophore, or other compound that produces a detectable signal. The proteins can be packaged in kit form, such kits comprising one or more vials containing the AFP protein and, optionally, a diluent, an antibody, a labeled binding protein, etc.
30 Assay kits can be used in the research laboratory to detect protein and inhibitor activities produced by cultured cells or test animals.

Proteins of the present invention may also be used as protein and amino acid supplements, including hydrolysates. Specific uses in this regard include use as
35 animal feed supplements and as cell culture components. Proteins rich in a particular amino acid can be used as a source of that amino acid.

Polynucleotides and polypeptides of the present invention will additionally find use as educational tools as a laboratory practicum kits for courses

related to genetics and molecular biology, protein chemistry and antibody production and analysis. Due to their unique polynucleotide and polypeptide sequences, molecules of AFP protein or polynucleotide can be used as standards or as "unknowns" for testing purposes. For example, AFP polynucleotides can be used as aids in

5 teaching students how to prepare expression constructs for bacterial, viral, and/or mammalian expression, including fusion constructs, wherein an AFP polynucleotide is the gene to be expressed; for determining the restriction endonuclease cleavage sites of the polynucleotides (which can be determined from the sequence using conventional computer software, such as MapDraw™ (DNASTAR, Madison, WI)); determining

10 mRNA and DNA localization of AFP polynucleotides in tissues (e.g., by Northern and Southern blotting as well as polymerase chain reaction); and for identifying related polynucleotides and polypeptides by nucleic acid hybridization.

AFP polypeptides can be used educationally as aids to teach preparation of antibodies; identifying proteins by Western blotting; protein purification;

15 determining the weight of expressed AFP polypeptides as a ratio to total protein expressed; identifying peptide cleavage sites; coupling amino and carboxyl terminal tags; amino acid sequence analysis, as well as, but not limited to monitoring biological activities of both the native and tagged protein (i.e., receptor binding, signal transduction, proliferation, and differentiation) *in vitro* and *in vivo*. AFP polypeptides

20 can also be used to teach analytical skills such as mass spectrometry, circular dichroism to determine conformation, in particular the locations of the disulfide bonds, x-ray crystallography to determine the three-dimensional structure in atomic detail, nuclear magnetic resonance spectroscopy to reveal the structure of proteins in solution. For example, a kit containing an AFP protein can be given to the student to analyze.

25 Since the amino acid sequence would be known by the professor, the protein can be given to the student as a test to determine the skills or develop the skills of the student, the teacher would then know whether or not the student has correctly analyzed the polypeptide. Since every polypeptide is unique, the educational utility of zcub5 would be unique unto itself.

30 Antibodies that bind specifically to an AFP polypeptide can be used as a teaching aid to instruct students how to prepare affinity chromatography columns to purify the cognate polypeptide, cloning and sequencing the polynucleotide that encodes an antibody and thus as a practicum for teaching a student how to design humanized antibodies. The AFP polynucleotide, polypeptide or antibody would then be packaged

35 by reagent companies and sold to universities so that the students gain skill in art of molecular biology. Because each polynucleotide and protein is unique, each polynucleotide and protein creates unique challenges and learning experiences for

students in a lab practicum. Such educational kits containing an AFP polynucleotide, polypeptide or antibody are considered within the scope of the present invention.

The invention is further illustrated by the following non-limiting examples.

5

EXAMPLES

Example 1

A protein of the present invention ("AFP") is produced in *E. coli* using a His₆ tag/maltose binding protein (MBP) double affinity fusion system as generally disclosed by Pryor and Leiting, *Prot. Expr. Pur.* 10:309-319, 1997. A thrombin cleavage site is placed at the junction between the affinity tag and AFP sequences.

The fusion construct is assembled in the vector pTAP98, which comprises sequences for replication and selection in *E. coli* and yeast, the *E. coli* *tac* promoter, and a unique SmaI site just downstream of the MBP-His₆-thrombin site coding sequences. The AFP cDNA is amplified by PCR using primers each comprising 40 bp of sequence homologous to vector sequence and 25 bp of sequence that anneals to the cDNA. The reaction is run using Taq DNA polymerase (Boehringer Mannheim, Indianapolis, IN) for 30 cycles of 94°C, 30 seconds; 60°C, 60 seconds; and 72°C, 60 seconds. One microgram of the resulting fragment is mixed with 100 ng of SmaI-cut pTAP98, and the mixture is transformed into yeast to assemble the vector by homologous recombination (Oldenburg et al., *Nucl. Acids. Res.* 25:451-452, 1997). Ura⁺ transformants are selected.

Plasmid DNA is prepared from yeast transformants and transformed into *E. coli* MC1061. Pooled plasmid DNA is then prepared from the MC1061 transformants by the miniprep method after scraping an entire plate. Plasmid DNA is analyzed by restriction digestion.

E. coli strain BL21 is used for expression of AFP. Cells are transformed by electroporation and grown on minimal glucose plates containing casamino acids and ampicillin.

Protein expression is analyzed by gel electrophoresis. Cells are grown in liquid glucose media containing casamino acids and ampicillin. After one hour at 37°C, IPTG is added to a final concentration of 1mM, and the cells are grown for an additional 2-3 hours at 37°C. Cells are disrupted using glass beads, and extracts are prepared.

35

Example 2

Larger scale cultures of AFP transformants are prepared by the method of Pryor and Leiting (*ibid.*). 100-ml cultures in minimal glucose media containing casamino acids and 100 µg/ml ampicillin are grown at 37°C in 500-ml baffled flasks to
5 OD₆₀₀ ≈ 0.5. Cells are harvested by centrifugation and resuspended in 100 ml of the same media at room temperature. After 15 minutes, IPTG is added to 0.5 mM, and cultures are incubated at room temperature (ca. 22.5°C) for 16 to 20 hours with shaking at 125 rpm. The culture is harvested by centrifugation, and cell pellets are stored at -70°C.

10

Example 3

For larger-scale protein preparation, 500-ml cultures of *E. coli* BL21 expressing the AFP-MBP-His₆ fusion protein are prepared essentially as disclosed in Example 2. Cell pellets are resuspended in 100 ml of binding buffer (20 mM Tris, pH
15 7.58, 100 mM NaCl, 20 mM NaH₂PO₄, 0.4 mM 4-(2-Aminoethyl)-benzenesulfonyl fluoride hydrochloride [Pefabloc® SC; Boehringer-Mannheim], 2 µg/ml Leupeptin, 2 µg/ml Aprotinin). The cells are lysed in a French press at 30,000 psi, and the lysate is centrifuged at 18,000 x g for 45 minutes at 4°C to clarify it. Protein concentration is estimated by gel electrophoresis with a BSA standard.

20

Recombinant AFP fusion protein is purified from the lysate by affinity chromatography. Immobilized cobalt resin (Talon® resin; Clontech Laboratories, Inc., Palo Alto, CA) is equilibrated in binding buffer. One ml of packed resin per 50 mg protein is combined with the clarified supernatant in a tube, and the tube is capped and sealed, then placed on a rocker overnight at 4°C. The resin is then pelleted by
25 centrifugation at 4°C and washed three times with binding buffer. Protein is eluted with binding buffer containing 0.2 M imidazole. The resin and elution buffer are mixed for at least one hour at 4°C, the resin is pelleted, and the supernatant is removed. An aliquot is analyzed by gel electrophoresis, and concentration is estimated. Amylose resin is equilibrated in amylose binding buffer (20 mM Tris-HCl, pH 7.0, 100 mM
30 NaCl, 10 mM EDTA) and combined with the supernatant from the Talon resin at a ratio of 2 mg fusion protein per ml of resin. Binding and washing steps are carried out as disclosed above. Protein is eluted with amylose binding buffer containing 10 mM maltose using as small a volume as possible to minimize the need for subsequent concentration. The eluted protein is analyzed by gel electrophoresis and staining with
35 Coomassie blue using a BSA standard, and by Western blotting using an anti-MBP antibody.

Example 4

An expression plasmid containing all or part of a polynucleotide encoding AFP is constructed via homologous recombination. An AFP coding sequence comprising the ORF with 5' and 3' ends corresponding to the vector sequences flanking the insertion point is prepared by PCR. The primers for PCR each include from 5' to 3' end: 40 bp of flanking sequence from the vector and 17 bp corresponding to the amino or carboxyl termini from the open reading frame of AFP.

Ten μ l of the 100 μ l PCR reaction mixture is run on a 0.8% low-melting-temperature agarose (SeaPlaque GTG®; FMC BioProducts, Rockland, ME) gel with 1 x TBE buffer for analysis. The remaining 90 μ l of the reaction mixture is precipitated with the addition of 5 μ l 1 M NaCl and 250 μ l of absolute ethanol. The plasmid pZMP6, which has been cut with SmaI, is used for recombination with the PCR fragment. Plasmid pZMP6 is a mammalian expression vector containing an expression cassette having the cytomegalovirus immediate early promoter, multiple restriction sites for insertion of coding sequences, a stop codon, and a human growth hormone terminator; an *E. coli* origin of replication; a mammalian selectable marker expression unit comprising an SV40 promoter, enhancer and origin of replication, a DHFR gene, and the SV40 terminator; and URA3 and CEN-ARS sequences required for selection and replication in *S. cerevisiae*. It was constructed from pZP9 (deposited at the American Type Culture Collection, 10801 University Boulevard, Manassas, VA 20110-2209, under Accession No. 98668) with the yeast genetic elements taken from pRS316 (available from the American Type Culture Collection, 10801 University Boulevard, Manassas, VA, under Accession No. 77145), an internal ribosome entry site (IRES) element from poliovirus, and the extracellular domain of CD8 truncated at the C-terminal end of the transmembrane domain.

One hundred microliters of competent yeast (*S. cerevisiae*) cells are independently combined with 10 μ l of the various DNA mixtures from above and transferred to a 0.2-cm electroporation cuvette. The yeast/DNA mixtures are electropulsed using power supply (BioRad Laboratories, Hercules, CA) settings of 0.75 kV (5 kV/cm), ∞ ohms, 25 μ F. To each cuvette is added 600 μ l of 1.2 M sorbitol, and the yeast is plated in two 300- μ l aliquots onto two URA-D plates (1.8% agar in 2% D-glucose, 0.67% yeast nitrogen base without amino acids, 0.056% -Ura -Trp -Thr powder [made by combining 4.0 g L-adenine, 3.0 g L-arginine, 5.0 g L-aspartic acid, 2.0 g L-histidine, 6.0 g L-isoleucine, 8.0 g L-leucine, 4.0 g L-lysine, 2.0 g L-methionine, 6.0 g L-phenylalanine, 5.0 g L-serine, 5.0 g L-tyrosine, and 6.0 g L-valine], and 0.5% 200X tryptophan, threonine solution [3.0% L-threonine, 0.8% L-tryptophan in H₂O]) and incubated at 30°C. After about 48 hours, the Ura⁺ yeast

transformants from a single plate are resuspended in 1 ml H₂O and spun briefly to pellet the yeast cells. The cell pellet is resuspended in 1 ml of lysis buffer (2% Triton X-100, 1% SDS, 100 mM NaCl, 10 mM Tris, pH 8.0, 1 mM EDTA). Five hundred microliters of the lysis mixture is added to an Eppendorf tube containing 300 µl acid-washed glass beads and 200 µl phenol-chloroform, vortexed for 1 minute intervals two or three times, and spun for 5 minutes in an Eppendorf centrifuge at maximum speed. Three hundred microliters of the aqueous phase is transferred to a fresh tube, and the DNA is precipitated with 600 µl ethanol (EtOH), followed by centrifugation for 10 minutes at 4°C. The DNA pellet is resuspended in 10 µl H₂O.

Transformation of electrocompetent *E. coli* host cells (Electromax DH10B™ cells; obtained from Life Technologies, Inc., Gaithersburg, MD) is done with 0.5-2 ml yeast DNA prep and 40 µl of cells. The cells are electropulsed at 1.7 kV, 25 µF, and 400 ohms. Following electroporation, 1 ml SOC (2% Bacto™ Tryptone (Difco, Detroit, MI), 0.5% yeast extract (Difco), 10 mM NaCl, 2.5 mM KCl, 10 mM MgCl₂, 10 mM MgSO₄, 20 mM glucose) is plated in 250-µl aliquots on four LB AMP plates (LB broth (Lennox), 1.8% Bacto™ Agar (Difco), 100 mg/L Ampicillin).

Individual clones harboring the correct expression construct for AFP are identified by restriction digest to verify the presence of the AFP insert and to confirm that the various DNA sequences have been joined correctly to one another. The inserts of positive clones are subjected to sequence analysis. Larger scale plasmid DNA is isolated using a commercially available kit (QIAGEN Plasmid Maxi Kit, Qiagen, Valencia, CA) according to manufacturer's instructions. The correct construct is designated pZMP6/AFP.

Recombinant protein is produced in BHK cells transfected with pZMP6/AFP. BHK 570 cells (ATCC CRL-10314) are plated in 10-cm tissue culture dishes and allowed to grow to approximately 50 to 70% confluence overnight at 37°C, 5% CO₂, in DMEM/FBS media (DMEM, Gibco/BRL High Glucose; Life Technologies), 5% fetal bovine serum (Hyclone, Logan, UT), 1 mM L-glutamine (JRH Biosciences, Lenexa, KS), 1 mM sodium pyruvate (Life Technologies). The cells are then transfected with pZMP6/AFP by liposome-mediated transfection using a 3:1 (w/w) liposome formulation of the polycationic lipid 2,3-dioleoyloxy-N-[2(sperminecarboxamido)ethyl]-N,N-dimethyl-1-propaniminium-trifluoroacetate and the neutral lipid dioleoyl phosphatidylethanolamine in membrane-filtered water (Lipofectamine™ Reagent; Life Technologies, Gaithersburg, MD), in serum free (SF) media (DMEM supplemented with 10 mg/ml transferrin, 5 mg/ml insulin, 2 mg/ml fetuin, 1% L-glutamine and 1% sodium pyruvate). The plasmid is diluted into 15-ml tubes to a total final volume of 640 µl with SF media. 35 µl of the lipid mixture is

mixed with 605 μ l of SF medium, and the resulting mixture is allowed to incubate approximately 30 minutes at room temperature. Five milliliters of SF media is then added to the DNA:lipid mixture. The cells are rinsed once with 5 ml of SF media, aspirated, and the DNA:lipid mixture is added. The cells are incubated at 37°C for five
5 hours, then 6.4 ml of DMEM/10% FBS, 1% PSN media is added to each plate. The plates are incubated at 37°C overnight, and the DNA:lipid mixture is replaced with fresh 5% FBS/DMEM media the next day. On day 5 post-transfection, the cells are split into T-162 flasks in selection medium (DMEM + 5% FBS, 1% L-Gln, 1% NaPyr, 1 μ M methotrexate). Approximately 10 days post-transfection, two 150-mm culture
10 dishes of methotrexate-resistant colonies from each transfection are trypsinized, and the cells are pooled and plated into a T-162 flask and transferred to large-scale culture.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for purposes of illustration,
15 various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the invention is not limited except as by the appended claims.

CLAIMS

We claim:

1. An isolated polypeptide comprising fifteen contiguous amino acid residues of a polypeptide as shown in SEQ ID NO:M, wherein M is an even integer from 2 to 422.
2. The isolated polypeptide of claim 1 wherein M is 6, 8, 12, 18, 24, 42, 48, 54, 66, 68, 70, 72, 90, 92, 96, 98, 102, 106, 110, 122, 134, 138, 140, 156, 158, 162, 164, 168, 174, 178, 180, 204, 206, 210, 224, 230, 234, 236, 240, 242, 252, 254, 258, 270, 272, 284, 286, 288, 294, 300, 302, 306, 312, 314, 324, 326, 338, 342, 344, 348, 350, 366, 368, 374, 378, 386, 388, 396, 398, 402, 408, 412, or 416.
3. The isolated polypeptide of claim 1 or claim 2 which is from 15 to 2235 amino acid residues in length.
4. The isolated polypeptide of claim 3 which is operably linked via a peptide bond or polypeptide linker to a second polypeptide selected from the group consisting of maltose binding protein, an immunoglobulin constant region, a polyhistidine tag, and a peptide as shown in SEQ ID NO:423.
5. The isolated polypeptide of any of claims 1-4 comprising at least 30 contiguous residues of SEQ ID NO:M.
6. The isolated polypeptide of any of claims 1-5 comprising at least 47 contiguous residues of SEQ ID NO:M.
7. An isolated, mature protein encoded by a sequence selected from the group consisting of SEQ ID NO:N, wherein N is an odd integer from 1 to 421.
8. The protein of claim 7 wherein N is 5, 7, 11, 17, 23, 41, 47, 53, 65, 67, 69, 71, 89, 91, 95, 97, 101, 105, 109, 121, 133, 137, 139, 155, 157, 161, 163, 167, 173, 177, 179, 203, 205, 209, 223, 229, 233, 235, 239, 241, 251, 253, 257, 269, 271, 283, 285, 287, 293, 299, 301, 305, 311, 313, 323, 325, 337, 341, 343, 347, 349, 365, 367, 373, 377, 385, 387, 395, 397, 401, 407, 411, or 415.
9. An isolated polynucleotide comprising a sequence of nucleotides as shown in SEQ ID NO:N, wherein N is an odd integer from 1 to 421.

10. The isolated polynucleotide of claim 9 wherein N is 5, 7, 11, 17, 23, 41, 47, 53, 65, 67, 69, 71, 89, 91, 95, 97, 101, 105, 109, 121, 133, 137, 139, 155, 157, 161, 163, 167, 173, 177, 179, 203, 205, 209, 223, 229, 233, 235, 239, 241, 251, 253, 257, 269, 271, 283, 285, 287, 293, 299, 301, 305, 311, 313, 323, 325, 337, 341, 343, 347, 349, 365, 367, 373, 377, 385, 387, 395, 397, 401, 407, 411, or 415.
11. An expression vector comprising the following operably linked elements:
a transcription promoter;
a DNA segment encoding a polypeptide as shown in SEQ ID NO:M, wherein M is an even integer from 2 to 422; and
a transcription terminator.
12. The expression vector of claim 11 wherein M is 6, 8, 12, 18, 24, 42, 48, 54, 66, 68, 70, 72, 90, 92, 96, 98, 102, 106, 110, 122, 134, 138, 140, 156, 158, 162, 164, 168, 174, 178, 180, 204, 206, 210, 224, 230, 234, 236, 240, 242, 252, 254, 258, 270, 272, 284, 286, 288, 294, 300, 302, 306, 312, 314, 324, 326, 338, 342, 344, 348, 350, 366, 368, 374, 378, 386, 388, 396, 398, 402, 408, 412, or 416.
13. A cultured cell comprising the expression vector of claim 11 or claim 12.
14. A method of producing a polypeptide comprising culturing the cell of claim 13 under conditions whereby said sequence of nucleotides is expressed, and recovering said polypeptide.
15. A polypeptide produced by the method of claim 14.
16. An isolated polynucleotide encoding a fusion protein, said protein comprising a secretory peptide selected from the group consisting of secretory peptides shown in SEQ ID NO:M, wherein M is an even integer from 2 to 422, operably linked to a second polypeptide.
17. An expression vector comprising the following operably linked elements:

a transcription promoter;
a DNA segment encoding a fusion protein, said protein comprising a secretory peptide selected from the group consisting of secretory peptides shown in SEQ ID NO:M, wherein M is an even integer from 2 to 422, operably linked to a second polypeptide; and
a transcription terminator.

18. A cultured cell comprising the expression vector of claim 17, wherein the cell expresses the DNA segment and produces the encoded fusion protein.

19. A method of producing a protein comprising culturing the cell of claim 18 under conditions whereby said DNA segment is expressed, and recovering said second polypeptide.

20. An antibody that specifically binds to a protein selected from of the group consisting of SEQ ID NO:M, wherein M is an even integer from 2 to 422.

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| atg | tgc | tct | ctg | ggg | ttg | ttc | cct | cct | cca | ccg | cct | cgg | ggg | caa | gtc | 48 |
| Met | Cys | Ser | Leu | Gly | Leu | Phe | Pro | Pro | Pro | Pro | Pro | Arg | Gly | Gln | Val | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| acc | cta | tat | gag | cac | aat | aac | gag | ctg | gtg | acg | ggc | agt | agc | tat | gag | 96 |
| Thr | Leu | Tyr | Glu | His | Asn | Asn | Glu | Leu | Val | Thr | Gly | Ser | Ser | Tyr | Glu | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| agc | ccg | ccc | ccc | gac | ttc | cgg | ggc | cag | tgg | atc | aat | ctt | cct | gtc | cta | 144 |
| Ser | Pro | Pro | Pro | Asp | Phe | Arg | Gly | Gln | Trp | Ile | Asn | Leu | Pro | Val | Leu | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| caa | ctg | aca | aag | gat | ccc | cta | aag | acc | cct | gga | agg | ctg | gac | cat | ggc | 192 |
| Gln | Leu | Thr | Lys | Asp | Pro | Leu | Lys | Thr | Pro | Gly | Arg | Leu | Asp | His | Gly | |
| | 50 | | | | | 55 | | | | 60 | | | | | | |
| aca | aga | act | gcc | ttc | atc | cat | cac | cgg | gag | caa | gtg | tgg | aag | aga | tgc | 240 |
| Thr | Arg | Thr | Ala | Phe | Ile | His | His | Arg | Glu | Gln | Val | Trp | Lys | Arg | Cys | |
| 65 | | | | | 70 | | | | 75 | | | | | | 80 | |

| | |
|--|-----|
| atc aac att tgg cgt gat gtg ggc ctt ttt ggg gtg cta aat gaa att Ile Asn Ile Trp Arg Asp Val Gly Leu Phe Gly Val Leu Asn Glu Ile | 288 |
| 85 90 95 | |
| gca aac tca gaa gaa gag gtg ttt gag tgg gtg aag acg gca tcc ggc Ala Asn Ser Glu Glu Glu Val Phe Glu Trp Val Lys Thr Ala Ser Gly | 336 |
| 100 105 110 | |
| tgg gcc ctg gca ctc tgt cga tgg gcc tct tcc ctc cat ggg tcc ctg Trp Ala Leu Ala Leu Cys Arg Trp Ala Ser Ser Leu His Gly Ser Leu | 384 |
| 115 120 125 | |
| ttc ccc cat ctg tct ctc agg agc gaa gat ctg atc gct gaa ttt gcc Phe Pro His Leu Ser Leu Arg Ser Glu Asp Leu Ile Ala Glu Phe Ala | 432 |
| 130 135 140 | |
| caa gtc acā aat tgg tcc agc tgc tgc ttg cgt gtc ttt gca tgg cac Gln Val Thr Asn Trp Ser Ser Cys Cys Leu Arg Val Phe Ala Trp His | 480 |
| 145 150 155 160 | |
| ccc cac acc aac aag ttt gca gtg gcc ctg cta gat gac tca gtc cgt Pro His Thr Asn Lys Phe Ala Val Ala Leu Leu Asp Asp Ser Val Arg | 528 |
| 165 170 175 | |
| gtg tat aat gcc agc agc acc ata gtc ccc tcc ctg aag cac cgg ctg Val Tyr Asn Ala Ser Ser Thr Ile Val Pro Ser Leu Lys His Arg Leu | 576 |
| 180 185 190 | |
| cag cga aat gtg gcg tct ctg gcc tgg aag ccc ctt agt gcc tct gtc Gln Arg Asn Val Ala Ser Leu Ala Trp Lys Pro Leu Ser Ala Ser Val | 624 |
| 195 200 205 | |
| ttg gct gtg gcc tgc cag agc tgc att ctt atc tgg acc ctg gac cct Leu Ala Val Ala Cys Gln Ser Cys Ile Leu Ile Trp Thr Leu Asp Pro | 672 |
| 210 215 220 | |
| acc tcc ttg tct acc cga ccc tct tct ggc tgt gcc caa gtg ctg tct Thr Ser Leu Ser Thr Arg Pro Ser Ser Gly Cys Ala Gln Val Leu Ser | 720 |
| 225 230 235 240 | |
| cac cct ggg cat aca cct gtt acc agc ttg gcc tgg gcc ccc agt ggg His Pro Gly His Thr Pro Val Thr Ser Leu Ala Trp Ala Pro Ser Gly | 768 |
| 245 250 255 | |

| | |
|---|------|
| ggg cgg ctg ctc tca gct tca ccc gtg gat gct gct atc cgg gta tgg Gly Arg Leu Leu Ser Ala Ser Pro Val Asp Ala Ala Ile Arg Val Trp 260 265 270 | 816 |
| gat gtc tca aca gag acc tgt gtc ccc ctt ccc tgg ttt cga gga ggt Asp Val Ser Thr Glu Thr Cys Val Pro Leu Pro Trp Phe Arg Gly Gly 275 280 285 | 864 |
| ggg gtg acc aac ctg ctc tgg tcc cca gac ggc agc aaa atc ctg gct Gly Val Thr Asn Leu Leu Trp Ser Pro Asp Gly Ser Lys Ile Leu Ala 290 295 300 | 912 |
| acc act cct tca gct gtc ttt cga gtc tgg gag gcc cag atg tgg act Thr Thr Pro Ser Ala Val Phe Arg Val Trp Glu Ala Gln Met Trp Thr 305 310 315 320 | 960 |
| tgt gag agg tgg cct act cta tca ggg cgc tgt cag act ggc tgc tgg Cys Glu Arg Trp Pro Thr Leu Ser Gly Arg Cys Gln Thr Gly Cys Trp 325 330 335 | 1008 |
| agc cca gat ggc agc cga ctg ctg ttc act gta ttg gga gag cca ctg Ser Pro Asp Gly Ser Arg Leu Leu Phe Thr Val Leu Gly Glu Pro Leu 340 345 350 | 1056 |
| att tac tcc ctg tct ttt cca gaa cgt tgt ggt gag gga aag ggg tgc Ile Tyr Ser Leu Ser Phe Pro Glu Arg Cys Gly Glu Gly Lys Gly Cys 355 360 365 | 1104 |
| gtt gga ggt gca aag tca gca acg att gtg gca gat ctg tct gag aca Val Gly Gly Ala Lys Ser Ala Thr Ile Val Ala Asp Leu Ser Glu Thr 370 375 380 | 1152 |
| aca ata cag aca cca gat ggt gag gag agg ctt ggg gga gag gct cac Thr Ile Gln Thr Pro Asp Gly Glu Glu Arg Leu Gly Gly Glu Ala His 385 390 395 400 | 1200 |
| tcc atg gtc tgg gac ccc agt ggg gaa cgt ctg gct gtg ctt atg aaa Ser Met Val Trp Asp Pro Ser Gly Glu Arg Leu Ala Val Leu Met Lys 405 410 415 | 1248 |
| gga aag cca agg gta cag gat ggt aaa cca gtc atc ctc ctt ttt cgc Gly Lys Pro Arg Val Gln Asp Gly Lys Pro Val Ile Leu Leu Phe Arg 420 425 430 | 1296 |

act cga aac agc cct gtg ttt gag ctc ctt ccc tgt ggc att atc cag 1344
 Thr Arg Asn Ser Pro Val Phe Glu Leu Leu Pro Cys Gly Ile Ile Gln
 435 440 445

ggg gag cca gga gcc cag ccc cag ctc atc act ttc cat cct tcc ttc 1392
 Gly Glu Pro Gly Ala Gln Pro Gln Leu Ile Thr Phe His Pro Ser Phe
 450 455 460

aac aaa ggg gcc ctg ctc agt gtg ggc tgg tcc aca ggc cga att gcc 1440
 Asn Lys Gly Ala Leu Leu Ser Val Gly Trp Ser Thr Gly Arg Ile Ala
 465 470 475 480

cac atc ccg ctg tac ttt gtc aat gcc cag ttt cca cgt ttt agc cca 1488
 His Ile Pro Leu Tyr Phe Val Asn Ala Gln Phe Pro Arg Phe Ser Pro
 485 490 495

gtg ctt ggg cgg gcc cag gaa ccc cct gct ggg ggt gga ggc tct att 1536
 Val Leu Gly Arg Ala Gln Glu Pro Pro Ala Gly Gly Gly Gly Ser Ile
 500 505 510

cat gac ctg ccc ctc ttt act gag aca tcc cca acc tct gcc cct tgg 1584
 His Asp Leu Pro Leu Phe Thr Glu Thr Ser Pro Thr Ser Ala Pro Trp
 515 520 525

gac cct ctc cca ggg cca cca cct gtt ctg ccc cac tcc cca cat tcc 1632
 Asp Pro Leu Pro Gly Pro Pro Pro Val Leu Pro His Ser Pro His Ser
 530 535 540

cac ctc taa 1641
 His Leu *
 545

<210> 2

<211> 546

<212> PRT

<213> Homo sapiens

<400> 2

Met Cys Ser Leu Gly Leu Phe Pro Pro Pro Pro Pro Arg Gly Gln Val
 1 5 10 15
 Thr Leu Tyr Glu His Asn Asn Glu Leu Val Thr Gly Ser Ser Tyr Glu
 20 25 30

Ser Pro Pro Pro Asp Phe Arg Gly Gln Trp Ile Asn Leu Pro Val Leu
 35 40 45
 Gln Leu Thr Lys Asp Pro Leu Lys Thr Pro Gly Arg Leu Asp His Gly
 50 55 60
 Thr Arg Thr Ala Phe Ile His His Arg Glu Gln Val Trp Lys Arg Cys
 65 70 75 80
 Ile Asn Ile Trp Arg Asp Val Gly Leu Phe Gly Val Leu Asn Glu Ile
 85 90 95
 Ala Asn Ser Glu Glu Glu Val Phe Glu Trp Val Lys Thr Ala Ser Gly
 100 105 110
 Trp Ala Leu Ala Leu Cys Arg Trp Ala Ser Ser Leu His Gly Ser Leu
 115 120 125
 Phe Pro His Leu Ser Leu Arg Ser Glu Asp Leu Ile Ala Glu Phe Ala
 130 135 140
 Gln Val Thr Asn Trp Ser Ser Cys Cys Leu Arg Val Phe Ala Trp His
 145 150 155 160
 Pro His Thr Asn Lys Phe Ala Val Ala Leu Leu Asp Asp Ser Val Arg
 165 170 175
 Val Tyr Asn Ala Ser Ser Thr Ile Val Pro Ser Leu Lys His Arg Leu
 180 185 190
 Gln Arg Asn Val Ala Ser Leu Ala Trp Lys Pro Leu Ser Ala Ser Val
 195 200 205
 Leu Ala Val Ala Cys Gln Ser Cys Ile Leu Ile Trp Thr Leu Asp Pro
 210 215 220
 Thr Ser Leu Ser Thr Arg Pro Ser Ser Gly Cys Ala Gln Val Leu Ser
 225 230 235 240
 His Pro Gly His Thr Pro Val Thr Ser Leu Ala Trp Ala Pro Ser Gly
 245 250 255
 Gly Arg Leu Leu Ser Ala Ser Pro Val Asp Ala Ala Ile Arg Val Trp
 260 265 270
 Asp Val Ser Thr Glu Thr Cys Val Pro Leu Pro Trp Phe Arg Gly Gly
 275 280 285
 Gly Val Thr Asn Leu Leu Trp Ser Pro Asp Gly Ser Lys Ile Leu Ala
 290 295 300
 Thr Thr Pro Ser Ala Val Phe Arg Val Trp Glu Ala Gln Met Trp Thr
 305 310 315 320
 Cys Glu Arg Trp Pro Thr Leu Ser Gly Arg Cys Gln Thr Gly Cys Trp
 325 330 335
 Ser Pro Asp Gly Ser Arg Leu Leu Phe Thr Val Leu Gly Glu Pro Leu
 340 345 350
 Ile Tyr Ser Leu Ser Phe Pro Glu Arg Cys Gly Glu Gly Lys Gly Cys
 355 360 365
 Val Gly Gly Ala Lys Ser Ala Thr Ile Val Ala Asp Leu Ser Glu Thr
 370 375 380

Thr Ile Gln Thr Pro Asp Gly Glu Glu Arg Leu Gly Gly Glu Ala His
 385 390 395 400
 Ser Met Val Trp Asp Pro Ser Gly Glu Arg Leu Ala Val Leu Met Lys
 405 410 415
 Gly Lys Pro Arg Val Gln Asp Gly Lys Pro Val Ile Leu Leu Phe Arg
 420 425 430
 Thr Arg Asn Ser Pro Val Phe Glu Leu Leu Pro Cys Gly Ile Ile Gln
 435 440 445
 Gly Glu Pro Gly Ala Gln Pro Gln Leu Ile Thr Phe His Pro Ser Phe
 450 455 460
 Asn Lys Gly Ala Leu Leu Ser Val Gly Trp Ser Thr Gly Arg Ile Ala
 465 470 475 480
 His Ile Pro Leu Tyr Phe Val Asn Ala Gln Phe Pro Arg Phe Ser Pro
 485 490 495
 Val Leu Gly Arg Ala Gln Glu Pro Pro Ala Gly Gly Gly Gly Ser Ile
 500 505 510
 His Asp Leu Pro Leu Phe Thr Glu Thr Ser Pro Thr Ser Ala Pro Trp
 515 520 525
 Asp Pro Leu Pro Gly Pro Pro Pro Val Leu Pro His Ser Pro His Ser
 530 535 540
 His Leu
 545

<210> 3

<211> 1233

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1233)

<221> misc_feature

<222> (1)...(1233)

<223> n = A,T,C or G

<400> 3

atg gag cat ttc atg gaa gta atc aga aac cag gaa ttt gta tta tta
 Met Glu His Phe Met Glu Val Ile Arg Asn Gln Glu Phe Val Leu Leu
 1 5 10 15

48

cca gcc agc gaa att gca aag ctc ttg gct agt gat gac atg aac att
 Pro Ala Ser Glu Ile Ala Lys Leu Leu Ala Ser Asp Asp Met Asn Ile
 20 25 30

96

| | |
|---|-----|
| cct aat gag gag aca ata ttg aat gca ctt ctt act tgg gtc cgt cat | 144 |
| Pro Asn Glu Glu Thr Ile Leu Asn Ala Leu Leu Thr Trp Val Arg His | |
| 35 40 45 | |
| gat ttg gaa cag aga cgg aaa gat cta agt aaa ctt ttg gct tat att | 192 |
| Asp Leu Glu Gln Arg Arg Lys Asp Leu Ser Lys Leu Leu Ala Tyr Ile | |
| 50 55 60 | |
| agg cta cct ctt ctt gca cca cag ttc ctg gca gac atg gaa aat aat | 240 |
| Arg Leu Pro Leu Leu Ala Pro Gln Phe Leu Ala Asp Met Glu Asn Asn | |
| 65 70 75 80 | |
| gta ctt ttt cgg gat gat ata gaa tgt cag aaa ctc att atg gaa gca | 288 |
| Val Leu Phe Arg Asp Asp Ile Glu Cys Gln Lys Leu Ile Met Glu Ala | |
| 85 90 95 | |
| atg aag tac cat tta tta cca gag aga cga ccc atg tta caa agt cct | 336 |
| Met Lys Tyr His Leu Leu Pro Glu Arg Arg Pro Met Leu Gln Ser Pro | |
| 100 105 110 | |
| cgg aca aaa cct agg aag tca act gtt ggt aca tta ttt gca gtt ggg | 384 |
| Arg Thr Lys Pro Arg Lys Ser Thr Val Gly Thr Leu Phe Ala Val Gly | |
| 115 120 125 | |
| gga atg gat tca aca aaa gga gca aca agc att gaa aag tat gat ctc | 432 |
| Gly Met Asp Ser Thr Lys Gly Ala Thr Ser Ile Glu Lys Tyr Asp Leu | |
| 130 135 140 | |
| cgt aca aat atg tgg act cca gta gca aat atg aat ggg agg ngg cta | 480 |
| Arg Thr Asn Met Trp Thr Pro Val Ala Asn Met Asn Gly Arg Xaa Leu | |
| 145 150 155 160 | |
| cag ttc ggt gtt gca gtg cta gat gac aaa ctg tat gtg gtt gga gga | 528 |
| Gln Phe Gly Val Ala Val Leu Asp Asp Lys Leu Tyr Val Val Gly Gly | |
| 165 170 175 | |
| aga gat gga ctg aag act ttg aat act gta gag tgc tac aac ccc aaa | 576 |
| Arg Asp Gly Leu Lys Thr Leu Asn Thr Val Glu Cys Tyr Asn Pro Lys | |
| 180 185 190 | |
| aca aaa act tgg agt gtg atg cca cct atg tcc aca cat aga cat ggc | 624 |
| Thr Lys Thr Trp Ser Val Met Pro Pro Met Ser Thr His Arg His Gly | |
| 195 200 205 | |

| | |
|---|------|
| ctt ggt gtg gct gta ctg gaa ggt ccc atg tat gcc gta gga gga cat Leu Gly Val Ala Val Leu Glu Gly Pro Met Tyr Ala Val Gly Gly His 210 215 220 | 672 |
| gat ggc tgg agc tat ctg aac aca gtg gaa aga tgg gac cct cag gct Asp Gly Trp Ser Tyr Leu Asn Thr Val Glu Arg Trp Asp Pro Gln Ala 225 230 235 240 | 720 |
| cgc cag tgg aat ttt gtt gcc act atg tct acc cct agg agt aca gta Arg Gln Trp Asn Phe Val Ala Thr Met Ser Thr Pro Arg Ser Thr Val 245 250 255 | 768 |
| ggt gtg gca gta cta agt gga aaa ctt tat gca gtt ggt ggt cgt gat Gly Val Ala Val Leu Ser Gly Lys Leu Tyr Ala Val Gly Gly Arg Asp 260 265 270 | 816 |
| gga agt tct tgt ctc aaa tca gta gaa tgt ttt gat cct cat act aat Gly Ser Ser Cys Leu Lys Ser Val Glu Cys Phe Asp Pro His Thr Asn 275 280 285 | 864 |
| aag tgg aca ctg tgt gca cag atg tca aaa agg aga ggt ggc gta gga Lys Trp Thr Leu Cys Ala Gln Met Ser Lys Arg Arg Gly Gly Val Gly 290 295 300 | 912 |
| gtg acg acc tgg aat gga ctg ctg tat gct ata ggg ggg cac gat gct Val Thr Thr Trp Asn Gly Leu Leu Tyr Ala Ile Gly Gly His Asp Ala 305 310 315 320 | 960 |
| ccc gca tcc aac ttg act tcc aga ctc tca gac tgt gtg gaa aga tat Pro Ala Ser Asn Leu Thr Ser Arg Leu Ser Asp Cys Val Glu Arg Tyr 325 330 335 | 1008 |
| gat ccc aaa aca gac atg tgg act gca gta gca tcc atg agc atc agc Asp Pro Lys Thr Asp Met Trp Thr Ala Val Ala Ser Met Ser Ile Ser 340 345 350 | 1056 |
| aga gat gca gtg ggg gtc tgt tta ctt ggt gat aag tta tat gct gtt Arg Asp Ala Val Gly Val Cys Leu Leu Gly Asp Lys Leu Tyr Ala Val 355 360 365 | 1104 |
| ggg ggg tat gat gga cag gca tac ctt aat acc gtg gag gct tat gat Gly Gly Tyr Asp Gly Gln Ala Tyr Leu Asn Thr Val Glu Ala Tyr Asp 370 375 380 | 1152 |

```

ccc cag aca aat gag tgg acc cag gtt gct cca ctg tgc cta gga aga      1200
Pro Gln Thr Asn Glu Trp Thr Gln Val Ala Pro Leu Cys Leu Gly Arg
385                      390                      395                      400

```

```

gct gga gct tgt gtt gtg act gta aaa tta taa      1233
Ala Gly Ala Cys Val Val Thr Val Lys Leu *
                      405                      410

```

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<210> 4
<211> 410
<212> PRT
<213> Homo sapiens

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<220>
<221> VARIANT
<222> (1)...(410)
<223> Xaa = Any Amino Acid

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<400> 4
Met Glu His Phe Met Glu Val Ile Arg Asn Gln Glu Phe Val Leu Leu
 1              5              10              15
Pro Ala Ser Glu Ile Ala Lys Leu Leu Ala Ser Asp Asp Met Asn Ile
                20              25              30
Pro Asn Glu Glu Thr Ile Leu Asn Ala Leu Leu Thr Trp Val Arg His
                35              40              45
Asp Leu Glu Gln Arg Arg Lys Asp Leu Ser Lys Leu Leu Ala Tyr Ile
                50              55              60
Arg Leu Pro Leu Leu Ala Pro Gln Phe Leu Ala Asp Met Glu Asn Asn
65              70              75              80
Val Leu Phe Arg Asp Asp Ile Glu Cys Gln Lys Leu Ile Met Glu Ala
                85              90              95
Met Lys Tyr His Leu Leu Pro Glu Arg Arg Pro Met Leu Gln Ser Pro
                100             105             110
Arg Thr Lys Pro Arg Lys Ser Thr Val Gly Thr Leu Phe Ala Val Gly
                115             120             125
Gly Met Asp Ser Thr Lys Gly Ala Thr Ser Ile Glu Lys Tyr Asp Leu
                130             135             140
Arg Thr Asn Met Trp Thr Pro Val Ala Asn Met Asn Gly Arg Xaa Leu
145             150             155             160
Gln Phe Gly Val Ala Val Leu Asp Asp Lys Leu Tyr Val Val Gly Gly
                165             170             175
Arg Asp Gly Leu Lys Thr Leu Asn Thr Val Glu Cys Tyr Asn Pro Lys

```

| 180 | | | | | | | | | | 185 | | | | 190 | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Thr | Lys | Thr | Trp | Ser | Val | Met | Pro | Met | Ser | Thr | His | Arg | His | Gly | | | |
| 195 | | | | | | | | | | 200 | | | | 205 | | | |
| Leu | Gly | Val | Ala | Val | Leu | Glu | Gly | Pro | Met | Tyr | Ala | Val | Gly | Gly | His | | |
| 210 | | | | | | | | | | 215 | | | | 220 | | | |
| Asp | Gly | Trp | Ser | Tyr | Leu | Asn | Thr | Val | Glu | Arg | Trp | Asp | Pro | Gln | Ala | | |
| 225 | | | | | | | | | | 230 | | | | 235 | | | |
| Arg | Gln | Trp | Asn | Phe | Val | Ala | Thr | Met | Ser | Thr | Pro | Arg | Ser | Thr | Val | | |
| 245 | | | | | | | | | | 250 | | | | 255 | | | |
| Gly | Val | Ala | Val | Leu | Ser | Gly | Lys | Leu | Tyr | Ala | Val | Gly | Gly | Arg | Asp | | |
| 260 | | | | | | | | | | 265 | | | | 270 | | | |
| Gly | Ser | Ser | Cys | Leu | Lys | Ser | Val | Glu | Cys | Phe | Asp | Pro | His | Thr | Asn | | |
| 275 | | | | | | | | | | 280 | | | | 285 | | | |
| Lys | Trp | Thr | Leu | Cys | Ala | Gln | Met | Ser | Lys | Arg | Arg | Gly | Gly | Val | Gly | | |
| 290 | | | | | | | | | | 295 | | | | 300 | | | |
| Val | Thr | Thr | Trp | Asn | Gly | Leu | Leu | Tyr | Ala | Ile | Gly | Gly | His | Asp | Ala | | |
| 305 | | | | | | | | | | 310 | | | | 315 | | | |
| Pro | Ala | Ser | Asn | Leu | Thr | Ser | Arg | Leu | Ser | Asp | Cys | Val | Glu | Arg | Tyr | | |
| 325 | | | | | | | | | | 330 | | | | 335 | | | |
| Asp | Pro | Lys | Thr | Asp | Met | Trp | Thr | Ala | Val | Ala | Ser | Met | Ser | Ile | Ser | | |
| 340 | | | | | | | | | | 345 | | | | 350 | | | |
| Arg | Asp | Ala | Val | Gly | Val | Cys | Leu | Leu | Gly | Asp | Lys | Leu | Tyr | Ala | Val | | |
| 355 | | | | | | | | | | 360 | | | | 365 | | | |
| Gly | Gly | Tyr | Asp | Gly | Gln | Ala | Tyr | Leu | Asn | Thr | Val | Glu | Ala | Tyr | Asp | | |
| 370 | | | | | | | | | | 375 | | | | 380 | | | |
| Pro | Gln | Thr | Asn | Glu | Trp | Thr | Gln | Val | Ala | Pro | Leu | Cys | Leu | Gly | Arg | | |
| 385 | | | | | | | | | | 390 | | | | 395 | | | |
| Ala | Gly | Ala | Cys | Val | Val | Thr | Val | Lys | Leu | | | | | | | | |
| 405 | | | | | | | | | | 410 | | | | | | | |

```
<220>  
<221> CDS  
<222> (1)...(1644)
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48

11

| | |
|---|-----|
| gtc ctg aag gtg gcc atc ctg gcc gag aag tac gcc gtg gac tac agc Val Leu Lys Val Ala Ile Leu Ala Glu Lys Tyr Ala Val Asp Tyr Ser 20 25 30 | 96 |
| tgg tac gtg gac acc atc ctc aac ctc atc cgc att gcg ggc gac tac Trp Tyr Val Asp Thr Ile Leu Asn Leu Ile Arg Ile Ala Gly Asp Tyr 35 40 45 | 144 |
| gtg agt gag gag gtg tgg tac cgt gtg cta cag atc gtc acc aac cgt Val Ser Glu Glu Val Trp Tyr Arg Val Leu Gln Ile Val Thr Asn Arg 50 55 60 | 192 |
| gat gac gtc cag ggc tat gcc gcc aag acc gtc ttt gag gcg ctc cag Asp Asp Val Gln Gly Tyr Ala Ala Lys Thr Val Phe Glu Ala Leu Gln 65 70 75 80 | 240 |
| gcc cct gcc tgt cac gag aac atg gtg aag gtt ggc ggc tac atc ctt Ala Pro Ala Cys His Glu Asn Met Val Lys Val Gly Gly Tyr Ile Leu 85 90 95 | 288 |
| ggg gag ttt ggg aac ctg att gct ggg gac ccc cgc tcc agc ccc cca Gly Glu Phe Gly Asn Leu Ile Ala Gly Asp Pro Arg Ser Ser Pro Pro 100 105 110 | 336 |
| gtg cag ttc tcc ctg ctc cac tcc aag ttc cat ctg tgc agc gtg gcc Val Gln Phe Ser Leu Leu His Ser Lys Phe His Leu Cys Ser Val Ala 115 120 125 | 384 |
| acg cgg gcg ctg ctg ctg tcc acc tac atc aag ttc atc aac ctc ttc Thr Arg Ala Leu Leu Leu Ser Thr Tyr Ile Lys Phe Ile Asn Leu Phe 130 135 140 | 432 |
| ccc gag acc aag gcc acc atc cag ggc gtc ctg cgg gcc ggc tcc cag Pro Glu Thr Lys Ala Thr Ile Gln Gly Val Leu Arg Ala Gly Ser Gln 145 150 155 160 | 480 |
| ctg cgc aat gct gac gtg gag ctg cag cag cga gcc gtg gag tac ctc Leu Arg Asn Ala Asp Val Glu Leu Gln Gln Arg Ala Val Glu Tyr Leu 165 170 175 | 528 |
| acc ctc agc tca gtg gcc agc acc gac gtc ctg gcc acg gtg ctg gag Thr Leu Ser Ser Val Ala Ser Thr Asp Val Leu Ala Thr Val Leu Glu 180 185 190 | 576 |

| | |
|---|------|
| gag atg ccg ccc ttc ccc gag cgc gag tcg tcc atc ctg gcc aag ctg Glu Met Pro Pro Phe Pro Glu Arg Glu Ser Ser Ile Leu Ala Lys Leu 195 200 205 | 624 |
| aaa cgc aag aag ggg cca ggg gcc ggc agc gcc ctg gac gat ggc cgg Lys Arg Lys Lys Gly Pro Gly Ala Gly Ser Ala Leu Asp Asp Gly Arg 210 215 220 | 672 |
| agg gac ccc agc agc aac gac atc aac ggg ggc atg gag ccc acc ccc Arg Asp Pro Ser Ser Asn Asp Ile Asn Gly Gly Met Glu Pro Thr Pro 225 230 235 240 | 720 |
| agc act gtg tcg acg ccc tcg ccc tcc gcc gac ctc ctg ggg ctg cgg Ser Thr Val Ser Thr Pro Ser Pro Ser Ala Asp Leu Leu Gly Leu Arg 245 250 255 | 768 |
| gca gcc cct ccc ccg gca gca ccc ccg gct tct gca gga gca ggg aac Ala Ala Pro Pro Pro Ala Ala Pro Pro Ala Ser Ala Gly Ala Gly Asn 260 265 270 | 816 |
| ctt ctg gtg gac gtc ttc gat ggc ccg gcc gcc cag ccc agc ctg ggg Leu Leu Val Asp Val Phe Asp Gly Pro Ala Ala Gln Pro Ser Leu Gly 275 280 285 | 864 |
| ccc acc ccc gag gag gcc ttc ctc agc cca ggt cct gag gac atc ggc Pro Thr Pro Glu Glu Ala Phe Leu Ser Pro Gly Pro Glu Asp Ile Gly 290 295 300 | 912 |
| cct ccc att ccg gaa gcc gat gag ttg ctg aat aag ttt gtg tgt aag Pro Pro Ile Pro Glu Ala Asp Glu Leu Leu Asn Lys Phe Val Cys Lys 305 310 315 320 | 960 |
| aac aac ggg gtc ctg ttc gag aac cag ctg ctg cag atc gga gtc aag Asn Asn Gly Val Leu Phe Glu Asn Gln Leu Leu Gln Ile Gly Val Lys 325 330 335 | 1008 |
| tca gag ttc cga cag aac ctg ggc cgc atg tat ctc ttc tat ggc aac Ser Glu Phe Arg Gln Asn Leu Gly Arg Met Tyr Leu Phe Tyr Gly Asn 340 345 350 | 1056 |
| aag acc tcg gtg cag ttc cag aat ttc tca ccc act gtg gtt cac ccg Lys Thr Ser Val Gln Phe Gln Asn Phe Ser Pro Thr Val Val His Pro 355 360 365 | 1104 |

| | |
|---|------|
| gga gac ctc cag act cag ctg gct gtg cag acc aag cgc gtg gcg gcg Gly Asp Leu Gln Thr Gln Leu Ala Val Gln Thr Lys Arg Val Ala Ala 370 375 380 | 1152 |
| cag gtg gac ggc ggc gcg cag gtg cag cag gtg ctc aat atc gag tgc Gln Val Asp Gly Gly Ala Gln Val Gln Gln Val Leu Asn Ile Glu Cys 385 390 395 400 | 1200 |
| ctg cgg gac ttc ctg acg ccc ccg ctg ctg tcc gtg cgc ttc cgg tac Leu Arg Asp Phe Leu Thr Pro Pro Leu Leu Ser Val Arg Phe Arg Tyr 405 410 415 | 1248 |
| ggt ggc gcc ccc cag gcc ctc acc ctg aag ctc cca gtg acc atc aac Gly Gly Ala Pro Gln Ala Leu Thr Leu Lys Leu Pro Val Thr Ile Asn 420 425 430 | 1296 |
| aag ttc ttc cag ccc acc gag atg gcg gcc cag gat ttc ttc cag cgc Lys Phe Phe Gln Pro Thr Glu Met Ala Ala Gln Asp Phe Phe Gln Arg 435 440 445 | 1344 |
| tgg aag cag ctg agc ctc cct caa cag gag gcg cag aaa atc ttc aaa Trp Lys Gln Leu Ser Leu Pro Gln Gln Glu Ala Gln Lys Ile Phe Lys 450 455 460 | 1392 |
| gcc aac cac ccc atg gac gca gaa gtt act aag gcc aag ctt ctg ggg Ala Asn His Pro Met Asp Ala Glu Val Thr Lys Ala Lys Leu Leu Gly 465 470 475 480 | 1440 |
| ttt ggc tct gct ctc ctg gac aat gtg gac ccc aac cct gag aac ttc Phe Gly Ser Ala Leu Leu Asp Asn Val Asp Pro Asn Pro Glu Asn Phe 485 490 495 | 1488 |
| gtg ggg gcg ggg atc atc cag act aaa gcc ctg cag gtg ggc tgt ctg Val Gly Ala Gly Ile Ile Gln Thr Lys Ala Leu Gln Val Gly Cys Leu 500 505 510 | 1536 |
| ctt cgg ctg gag ccc aat gcc cag gcc cag atg tac cgg ctg acc ctg Leu Arg Leu Glu Pro Asn Ala Gln Ala Gln Met Tyr Arg Leu Thr Leu 515 520 525 | 1584 |
| cgc acc agc aag gag ccc gtc tcc cgt cac ctg tgt gag ctg ctg gca Arg Thr Ser Lys Glu Pro Val Ser Arg His Leu Cys Glu Leu Leu Ala 530 535 540 | 1632 |

cag cag ttc tga
Gln Gln Phe *
545

1644

<210> 6
<211> 547
<212> PRT
<213> Homo sapiens

<400> 6
Met Leu Arg Tyr Leu Glu Thr Ala Asp Tyr Ala Ile Arg Glu Glu Ile
1 5 10 15
Val Leu Lys Val Ala Ile Leu Ala Glu Lys Tyr Ala Val Asp Tyr Ser
20 25 30
Trp Tyr Val Asp Thr Ile Leu Asn Leu Ile Arg Ile Ala Gly Asp Tyr
35 40 45
Val Ser Glu Glu Val Trp Tyr Arg Val Leu Gln Ile Val Thr Asn Arg
50 55 60
Asp Asp Val Gln Gly Tyr Ala Ala Lys Thr Val Phe Glu Ala Leu Gln
65 70 75 80
Ala Pro Ala Cys His Glu Asn Met Val Lys Val Gly Gly Tyr Ile Leu
85 90 95
Gly Glu Phe Gly Asn Leu Ile Ala Gly Asp Pro Arg Ser Ser Pro Pro
100 105 110
Val Gln Phe Ser Leu Leu His Ser Lys Phe His Leu Cys Ser Val Ala
115 120 125
Thr Arg Ala Leu Leu Leu Ser Thr Tyr Ile Lys Phe Ile Asn Leu Phe
130 135 140
Pro Glu Thr Lys Ala Thr Ile Gln Gly Val Leu Arg Ala Gly Ser Gln
145 150 155 160
Leu Arg Asn Ala Asp Val Glu Leu Gln Gln Arg Ala Val Glu Tyr Leu
165 170 175
Thr Leu Ser Ser Val Ala Ser Thr Asp Val Leu Ala Thr Val Leu Glu
180 185 190
Glu Met Pro Pro Phe Pro Glu Arg Glu Ser Ser Ile Leu Ala Lys Leu
195 200 205
Lys Arg Lys Lys Gly Pro Gly Ala Gly Ser Ala Leu Asp Asp Gly Arg
210 215 220
Arg Asp Pro Ser Ser Asn Asp Ile Asn Gly Gly Met Glu Pro Thr Pro
225 230 235 240
Ser Thr Val Ser Thr Pro Ser Pro Ser Ala Asp Leu Leu Gly Leu Arg
245 250 255
Ala Ala Pro Pro Pro Ala Ala Pro Pro Ala Ser Ala Gly Ala Gly Asn

15

260 265 270
 Leu Leu Val Asp Val Phe Asp Gly Pro Ala Ala Gln Pro Ser Leu Gly
 275 280 285
 Pro Thr Pro Glu Glu Ala Phe Leu Ser Pro Gly Pro Glu Asp Ile Gly
 290 295 300
 Pro Pro Ile Pro Glu Ala Asp Gly Leu Leu Asn Lys Phe Val Cys Lys
 305 310 315 320
 Asn Asn Gly Val Leu Phe Glu Asn Gln Leu Leu Gln Ile Gly Val Lys
 325 330 335
 Ser Glu Phe Arg Gln Asn Leu Gly Arg Met Tyr Leu Phe Tyr Gly Asn
 340 345 350
 Lys Thr Ser Val Gln Phe Gln Asn Phe Ser Pro Thr Val Val His Pro
 355 360 365
 Gly Asp Leu Gln Thr Gln Leu Ala Val Gln Thr Lys Arg Val Ala Ala
 370 375 380
 Gln Val Asp Gly Gly Ala Gln Val Gln Gln Val Leu Asn Ile Glu Cys
 385 390 395 400
 Leu Arg Asp Phe Leu Thr Pro Pro Leu Leu Ser Val Arg Phe Arg Tyr
 405 410 415
 Gly Gly Ala Pro Gln Ala Leu Thr Leu Lys Leu Pro Val Thr Ile Asn
 420 425 430
 Lys Phe Phe Gln Pro Thr Glu Met Ala Ala Gln Asp Phe Phe Gln Arg
 435 440 445
 Trp Lys Gln Leu Ser Leu Pro Gln Gln Glu Ala Gln Lys Ile Phe Lys
 450 455 460
 Ala Asn His Pro Met Asp Ala Glu Val Thr Lys Ala Lys Leu Leu Gly
 465 470 475 480
 Phe Gly Ser Ala Leu Asp Asn Val Asp Pro Asn Pro Glu Asn Phe
 485 490 495
 Val Gly Ala Gly Ile Ile Gln Thr Lys Ala Leu Gln Val Gly Cys Leu
 500 505 510
 Leu Arg Leu Glu Pro Asn Ala Gln Ala Gln Met Tyr Arg Leu Thr Leu
 515 520 525
 Arg Thr Ser Lys Glu Pro Val Ser Arg His Leu Cys Glu Leu Leu Ala
 530 535 540
 Gln Gln Phe
 545

<210> 7

<211> 711

<212> DNA

<213> Homo sapiens

<220>

| | |
|---|-----|
| atg gca gcc ttt gca gtg gaa cct cag ggg ccc gcg tta gga tct gaa | 48 |
| Met Ala Ala Phe Ala Val Glu Pro Gln Gly Pro Ala Leu Gly Ser Glu | |
| 1 5 10 15 | |
| cca atg atg ctg ggt tca ccc aca tct cca aag cca gga gtt aat gcc | 96 |
| Pro Met Met Leu Gly Ser Pro Thr Ser Pro Lys Pro Gly Val Asn Ala | |
| 20 25 30 | |
| cag ttc tta cct gga ttt tta atg ggg gat ttg cca gct ccg gtg act | 144 |
| Gln Phe Leu Pro Gly Phe Leu Met Gly Asp Leu Pro Ala Pro Val Thr | |
| 35 40 45 | |
| cca caa cct cga tca att agt ggc cct tca gta gga gta atg gaa atg | 192 |
| Pro Gln Pro Arg Ser Ile Ser Gly Pro Ser Val Gly Val Met Glu Met | |
| 50 55 60 | |
| aga tca cct tta ctt gca ggt ggg tca cca cca caa cca gtt gta cca | 240 |
| Arg Ser Pro Leu Leu Ala Gly Gly Ser Pro Pro Gln Pro Val Val Pro | |
| 65 70 75 80 | |
| gct cat aaa gat aaa agt ggc gct cca cca gtt aga agt ata tat gat | 288 |
| Ala His Lys Asp Lys Ser Gly Ala Pro Pro Val Arg Ser Ile Tyr Asp | |
| 85 90 95 | |
| gac att tct agc cca gga ctt gga tca aca cct tta act tca aga aga | 336 |
| Asp Ile Ser Ser Pro Gly Leu Gly Ser Thr Pro Leu Thr Ser Arg Arg | |
| 100 105 110 | |
| cag atg tct aat aca gga aat tgg atg cat att cgt tat caa tct aaa | 384 |
| Gln Met Ser Asn Thr Gly Asn Trp Met His Ile Arg Tyr Gln Ser Lys | |
| 115 120 125 | |
| ctg cag gct cgg aaa gcc tta agc aaa gat ggg agg att ttt gga gaa | 432 |
| Leu Gln Ala Arg Lys Ala Leu Ser Lys Asp Gly Arg Ile Phe Gly Glu | |
| 130 135 140 | |
| tcc atc atg att ggt gta aaa cca tgt att gac aaa agt gtt atg gaa | 480 |
| Ser Ile Met Ile Gly Val Lys Pro Cys Ile Asp Lys Ser Val Met Glu | |
| 145 150 155 160 | |

17

agc agt gac aga tgt gct tta tca tct cca tct tta gcc ttt aca cca 528
 Ser Ser Asp Arg Cys Ala Leu Ser Ser Pro Ser Leu Ala Phe Thr Pro
 165 170 175
 cca atc aaa act cta ggt aca cca aca caa cct gga agt act cct agg 576
 Pro Ile Lys Thr Leu Gly Thr Pro Thr Gln Pro Gly Ser Thr Pro Arg
 180 185 190
 att tct acc atg aga cct ctt gct aca gca tac aaa gcc tct act agt 624
 Ile Ser Thr Met Arg Pro Leu Ala Thr Ala Tyr Lys Ala Ser Thr Ser
 195 200 205
 gat tat cag gtt att tct gac aga caa acg cca aaa aaa gat gaa agt 672
 Asp Tyr Gln Val Ile Ser Asp Arg Gln Thr Pro Lys Lys Asp Glu Ser
 210 215 220
 ctt gta tcc aaa gca atg gag tac atg ttt ggc tgg tag 711
 Leu Val Ser Lys Ala Met Glu Tyr Met Phe Gly Trp *
 225 230 235

<210> 8

<211> 236

<212> PRT

<213> Homo sapiens

<400> 8

Met Ala Ala Phe Ala Val Glu Pro Gln Gly Pro Ala Leu Gly Ser Glu
 1 5 10 15
 Pro Met Met Leu Gly Ser Pro Thr Ser Pro Lys Pro Gly Val Asn Ala
 20 25 30
 Gln Phe Leu Pro Gly Phe Leu Met Gly Asp Leu Pro Ala Pro Val Thr
 35 40 45
 Pro Gln Pro Arg Ser Ile Ser Gly Pro Ser Val Gly Val Met Glu Met
 50 55 60
 Arg Ser Pro Leu Leu Ala Gly Gly Ser Pro Pro Gln Pro Val Val Pro
 65 70 75 80
 Ala His Lys Asp Lys Ser Gly Ala Pro Pro Val Arg Ser Ile Tyr Asp
 85 90 95
 Asp Ile Ser Ser Pro Gly Leu Gly Ser Thr Pro Leu Thr Ser Arg Arg
 100 105 110
 Gln Met Ser Asn Thr Gly Asn Trp Met His Ile Arg Tyr Gln Ser Lys
 115 120 125
 Leu Gln Ala Arg Lys Ala Leu Ser Lys Asp Gly Arg Ile Phe Gly Glu

18

130 135 140
 Ser Ile Met Ile Gly Val Lys Pro Cys Ile Asp Lys Ser Val Met Glu
 145 150 155 160
 Ser Ser Asp Arg Cys Ala Leu Ser Ser Pro Ser Leu Ala Phe Thr Pro
 165 170 175
 Pro Ile Lys Thr Leu Gly Thr Pro Thr Gln Pro Gly Ser Thr Pro Arg
 180 185 190
 Ile Ser Thr Met Arg Pro Leu Ala Thr Ala Tyr Lys Ala Ser Thr Ser
 195 200 205
 Asp Tyr Gln Val Ile Ser Asp Arg Gln Thr Pro Lys Lys Asp Glu Ser
 210 215 220
 Leu Val Ser Lys Ala Met Glu Tyr Met Phe Gly Trp
 225 230 235

<210> 9
 <211> 636
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(636)

<400> 9
 atg cag cta tca ctg act caa gcg cgc acc tgg aag ggt ctg ttg ctg 48
 Met Gln Leu Ser Leu Thr Gln Ala Arg Thr Trp Lys Gly Leu Leu Leu
 1 5 10 15

 ttg gtg tca tgc atg atc ctg tgg ata tct gtg act ccc aca cca tat 96
 Leu Val Ser Cys Met Ile Leu Trp Ile Ser Val Thr Pro Thr Pro Tyr
 20 25 30

 gac cag atg tcc aat gag gag ctg tat gac aat ctg ctt tcc tgt tct 144
 Asp Gln Met Ser Asn Glu Glu Leu Tyr Asp Asn Leu Leu Ser Cys Ser
 35 40 45

 cat cgc acc cat gta gtt gcc cga aaa atg tat aaa att tta gac tta 192
 His Arg Thr His Val Val Ala Arg Lys Met Tyr Lys Ile Leu Asp Leu
 50 55 60

 aat gta gct gag aga aga tgt ttt aag aat aaa aga aac aac acc tgc 240
 Asn Val Ala Glu Arg Arg Cys Phe Lys Asn Lys Arg Asn Asn Thr Cys
 65 70 75 80

19

cac acc act tct acc cat act gca aaa aca aat gaa gat ctt ctg aaa 288
 His Thr Thr Ser Thr His Thr Ala Lys Thr Asn Glu Asp Leu Leu Lys
 85 90 95

gtc atc atc agt gtt tcg aat gca tgg ata tat cca ctg aaa atg ctc 336
 Val Ile Ile Ser Val Ser Asn Ala Trp Ile Tyr Pro Leu Lys Met Leu
 100 105 110

ata cct gca gtg ttg act cat ttg ggc tcc tat gat ggt atg atg gca 384
 Ile Pro Ala Val Leu Thr His Leu Gly Ser Tyr Asp Gly Met Met Ala
 115 120 125

aga gcc ata gag ctt aac tat gga aat caa aaa att ctg gag gga gca 432
 Arg Ala Ile Glu Leu Asn Tyr Gly Asn Gln Lys Ile Leu Glu Gly Ala
 130 135 140

aaa ttt tta ctc agc agg att cag cct gga att gaa gaa aat gac tat 480
 Lys Phe Leu Leu Ser Arg Ile Gln Pro Gly Ile Glu Glu Asn Asp Tyr
 145 150 155 160

cct gtc tgg tca agc tta aaa gaa ttg agg tct tcc aat aaa agc att 528
 Pro Val Trp Ser Ser Leu Lys Glu Leu Arg Ser Ser Asn Lys Ser Ile
 165 170 175

cac ctt ttt gca ttt tgt aaa ttc ttc tac tgc ttg cgc aaa gat aca 576
 His Leu Phe Ala Phe Cys Lys Phe Phe Tyr Cys Leu Arg Lys Asp Thr
 180 185 190

aag aag att aag gat tat ctc cag atc ttg agg cct aac att att aaa 624
 Lys Lys Ile Lys Asp Tyr Leu Gln Ile Leu Arg Pro Asn Ile Ile Lys
 195 200 205

aac aag tgg taa 636
 Asn Lys Trp *
 210

<210> 10

<211> 211

<212> PRT

<213> Homo sapiens

<400> 10

Met Gln Leu Ser Leu Thr Gln Ala Arg Thr Trp Lys Gly Leu Leu Leu

20

1 5 10 15
 Leu Val Ser Cys Met Ile Leu Trp Ile Ser Val Thr Pro Thr Pro Tyr
 20 25 30
 Asp Gln Met Ser Asn Glu Glu Leu Tyr Asp Asn Leu Leu Ser Cys Ser
 35 40 45
 His Arg Thr His Val Val Ala Arg Lys Met Tyr Lys Ile Leu Asp Leu
 50 55 60
 Asn Val Ala Glu Arg Arg Cys Phe Lys Asn Lys Arg Asn Asn Thr Cys
 65 70 75 80
 His Thr Thr Ser Thr His Thr Ala Lys Thr Asn Glu Asp Leu Leu Lys
 85 90 95
 Val Ile Ile Ser Val Ser Asn Ala Trp Ile Tyr Pro Leu Lys Met Leu
 100 105 110
 Ile Pro Ala Val Leu Thr His Leu Gly Ser Tyr Asp Gly Met Met Ala
 115 120 125
 Arg Ala Ile Glu Leu Asn Tyr Gly Asn Gln Lys Ile Leu Glu Gly Ala
 130 135 140
 Lys Phe Leu Leu Ser Arg Ile Gln Pro Gly Ile Glu Glu Asn Asp Tyr
 145 150 155 160
 Pro Val Trp Ser Ser Leu Lys Glu Leu Arg Ser Ser Asn Lys Ser Ile
 165 170 175
 His Leu Phe Ala Phe Cys Lys Phe Phe Tyr Cys Leu Arg Lys Asp Thr
 180 185 190
 Lys Lys Ile Lys Asp Tyr Leu Gln Ile Leu Arg Pro Asn Ile Ile Lys
 195 200 205
 Asn Lys Trp
 210

<210> 11

<211> 651

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(651)

<400> 11

atg tcc gcc ggg ggc ttc gcg gcg ccg ggg cac gcg gcg ggg ggt ccg
 Met Ser Ala Gly Gly Phe Ala Ala Pro Gly His Ala Ala Gly Gly Pro
 1 5 10 15

48

cct ccg ccg ccc cca cct ctg gga ccc cat tcc aac cgg acc acc cca
 Pro Pro Pro Pro Pro Pro Leu Gly Pro His Ser Asn Arg Thr Thr Pro

96

21

| 20 | 25 | 30 | |
|---|-----|-----|-----|
| cct gag tca gcc ccc cag aac ggt ccg tcc cct atg gcc gct ctc atg | | | 144 |
| Pro Glu Ser Ala Pro Gln Asn Gly Pro Ser Pro Met Ala Ala Leu Met | | | |
| 35 | 40 | 45 | |
| tcg gtg gca gat act ctg ggc aca gcg cac tcg ccc aag gat ggc agt | | | 192 |
| Ser Val Ala Asp Thr Leu Gly Thr Ala His Ser Pro Lys Asp Gly Ser | | | |
| 50 | 55 | 60 | |
| tcc gtg cac tct acc act gcg tcg gcg cgg cga aac agc agc agc cca | | | 240 |
| Ser Val His Ser Thr Thr Ala Ser Ala Arg Arg Asn Ser Ser Ser Pro | | | |
| 65 | 70 | 75 | 80 |
| gtc tcg ccg gcc tcc gtg ccg ggg cag cgc cgc ttg gca tca cgt aac | | | 288 |
| Val Ser Pro Ala Ser Val Pro Gly Gln Arg Arg Leu Ala Ser Arg Asn | | | |
| 85 | 90 | 95 | |
| ggg gac ctg aat tta cag gtg gcg ccc ccg ccg cct agc gcc cac ccg | | | 336 |
| Gly Asp Leu Asn Leu Gln Val Ala Pro Pro Pro Pro Ser Ala His Pro | | | |
| 100 | 105 | 110 | |
| ggc atg gac caa gtg cac ccc caa aac att ccg gat tcc ccc atg gcc | | | 384 |
| Gly Met Asp Gln Val His Pro Gln Asn Ile Pro Asp Ser Pro Met Ala | | | |
| 115 | 120 | 125 | |
| aac agc gga ccc ctc tgc tgc acc att tgc cac gaa cgt ttg gag gat | | | 432 |
| Asn Ser Gly Pro Leu Cys Cys Thr Ile Cys His Glu Arg Leu Glu Asp | | | |
| 130 | 135 | 140 | |
| acg cat ttc gtt cag tgc cct tcc gtc ccc agc cac aaa ttt tgc ttc | | | 480 |
| Thr His Phe Val Gln Cys Pro Ser Val Pro Ser His Lys Phe Cys Phe | | | |
| 145 | 150 | 155 | 160 |
| cct tgc tct aga gag agt atc aag gcc cag ggg gcc acc ggc gag gtg | | | 528 |
| Pro Cys Ser Arg Glu Ser Ile Lys Ala Gln Gly Ala Thr Gly Glu Val | | | |
| 165 | 170 | 175 | |
| tat tgc ccc agc gga gag aaa tgc ccc cta gtc ggg tcg aat gta cct | | | 576 |
| Tyr Cys Pro Ser Gly Glu Lys Cys Pro Leu Val Gly Ser Asn Val Pro | | | |
| 180 | 185 | 190 | |
| tgg gcc ttc atg cag ggc gaa atc gcg act atc tta gct ggg gat gtt | | | 624 |
| Trp Ala Phe Met Gln Gly Glu Ile Ala Thr Ile Leu Ala Gly Asp Val | | | |

22

195

200

205

aaa gtg aaa aag gag aga gac cct tga
 Lys Val Lys Lys Glu Arg Asp Pro *
 210 215

651

<210> 12

<211> 216

<212> PRT

<213> Homo sapiens

<400> 12

Met Ser Ala Gly Gly Phe Ala Ala Pro Gly His Ala Ala Gly Gly Pro
 1 5 10 15
 Pro Pro Pro Pro Pro Pro Leu Gly Pro His Ser Asn Arg Thr Thr Pro
 20 25 30
 Pro Glu Ser Ala Pro Gln Asn Gly Pro Ser Pro Met Ala Ala Leu Met
 35 40 45
 Ser Val Ala Asp Thr Leu Gly Thr Ala His Ser Pro Lys Asp Gly Ser
 50 55 60
 Ser Val His Ser Thr Thr Ala Ser Ala Arg Arg Asn Ser Ser Ser Pro
 65 70 75 80
 Val Ser Pro Ala Ser Val Pro Gly Gln Arg Arg Leu Ala Ser Arg Asn
 85 90 95
 Gly Asp Leu Asn Leu Gln Val Ala Pro Pro Pro Pro Ser Ala His Pro
 100 105 110
 Gly Met Asp Gln Val His Pro Gln Asn Ile Pro Asp Ser Pro Met Ala
 115 120 125
 Asn Ser Gly Pro Leu Cys Cys Thr Ile Cys His Glu Arg Leu Glu Asp
 130 135 140
 Thr His Phe Val Gln Cys Pro Ser Val Pro Ser His Lys Phe Cys Phe
 145 150 155 160
 Pro Cys Ser Arg Glu Ser Ile Lys Ala Gln Gly Ala Thr Gly Glu Val
 165 170 175
 Tyr Cys Pro Ser Gly Glu Lys Cys Pro Leu Val Gly Ser Asn Val Pro
 180 185 190
 Trp Ala Phe Met Gln Gly Glu Ile Ala Thr Ile Leu Ala Gly Asp Val
 195 200 205
 Lys Val Lys Lys Glu Arg Asp Pro
 210 215

<210> 13

<211> 468

23

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(468)

<400> 13

| | |
|---|-----|
| atg gcc tta att att cgt cca tcc aca gat ttc acg ttt ctg ttt cta | 48 |
| Met Ala Leu Ile Ile Arg Pro Ser Thr Asp Phe Thr Phe Leu Phe Leu | |
| 1 5 10 15 | |
| ccc tgt acg tca gtt gga tta ttt aat ttt ctg tgt agt aga ttc tac | 96 |
| Pro Cys Thr Ser Val Gly Leu Phe Asn Phe Leu Cys Ser Arg Phe Tyr | |
| 20 25 30 | |
| ctg acc aag ttc aat aaa gaa aat aat tgt gta tta cct cat tca aaa | 144 |
| Leu Thr Lys Phe Asn Lys Glu Asn Asn Cys Val Leu Pro His Ser Lys | |
| 35 40 45 | |
| gtt tca ttc cag ggc ttt ata tta caa gtt ggc agt gga gca gct gca | 192 |
| Val Ser Phe Gln Gly Phe Ile Leu Gln Val Gly Ser Gly Ala Ala Ala | |
| 50 55 60 | |
| gag cca tcc cga ggc aca gga agc tct ggg ccc tcc tct caa cat cca | 240 |
| Glu Pro Ser Arg Gly Thr Gly Ser Ser Gly Pro Ser Ser Gln His Pro | |
| 65 70 75 80 | |
| tta tct caa gct cat cga cag gga aac ttc gtg gac att gtt gat gcc | 288 |
| Leu Ser Gln Ala His Arg Gln Gly Asn Phe Val Asp Ile Val Asp Ala | |
| 85 90 95 | |
| aag ttg aag att cct gtc tct gga tcc aaa tca gag ggc ctt ctc tac | 336 |
| Lys Leu Lys Ile Pro Val Ser Gly Ser Lys Ser Glu Gly Leu Leu Tyr | |
| 100 105 110 | |
| gtc cac tca tcc aga ggt ggc ccc ttt cag agg tgg cac ctt gac gag | 384 |
| Val His Ser Ser Arg Gly Gly Pro Phe Gln Arg Trp His Leu Asp Glu | |
| 115 120 125 | |
| gtc ttt tta gag ctc aag gat ggt cag cag att cct gtg ttc aag ctc | 432 |
| Val Phe Leu Glu Leu Lys Asp Gly Gln Gln Ile Pro Val Phe Lys Leu | |
| 130 135 140 | |

24

agt ggg gaa aac ggt gat gaa gtg aaa aag gag tag 468
 Ser Gly Glu Asn Gly Asp Glu Val Lys Lys Glu *
 145 150 155

<210> 14
 <211> 155
 <212> PRT
 <213> Homo sapiens

<400> 14
 Met Ala Leu Ile Ile Arg Pro Ser Thr Asp Phe Thr Phe Leu Phe Leu
 1 5 10 15
 Pro Cys Thr Ser Val Gly Leu Phe Asn Phe Leu Cys Ser Arg Phe Tyr
 20 25 30
 Leu Thr Lys Phe Asn Lys Glu Asn Asn Cys Val Leu Pro His Ser Lys
 35 40 45
 Val Ser Phe Gln Gly Phe Ile Leu Gln Val Gly Ser Gly Ala Ala Ala
 50 55 60
 Glu Pro Ser Arg Gly Thr Gly Ser Ser Gly Pro Ser Ser Gln His Pro
 65 70 75 80
 Leu Ser Gln Ala His Arg Gln Gly Asn Phe Val Asp Ile Val Asp Ala
 85 90 95
 Lys Leu Lys Ile Pro Val Ser Gly Ser Lys Ser Glu Gly Leu Leu Tyr
 100 105 110
 Val His Ser Ser Arg Gly Gly Pro Phe Gln Arg Trp His Leu Asp Glu
 115 120 125
 Val Phe Leu Glu Leu Lys Asp Gly Gln Gln Ile Pro Val Phe Lys Leu
 130 135 140
 Ser Gly Glu Asn Gly Asp Glu Val Lys Lys Glu
 145 150 155

<210> 15
 <211> 765
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(765)

<400> 15
 atg gtg tcc tgg atc atc tct cgc ctg gtg gtg ctc atc ttt ggc acc 48
 Met Val Ser Trp Ile Ile Ser Arg Leu Val Val Leu Ile Phe Gly Thr

25

| 1 | 5 | 10 | 15 | |
|---|-----|-----|-----|-----|
| ctg tac cca gcc tat tct tcc tac aag gcc gtg aag aca aaa aac gtg | | | | 96 |
| Leu Tyr Pro Ala Tyr Ser Ser Tyr Lys Ala Val Lys Thr Lys Asn Val | | | | |
| | 20 | 25 | 30 | |
| aag gaa tat gtg aaa tgg atg atg tac tgg atc gtc ttt gcc ttc ttc | | | | 144 |
| Lys Glu Tyr Val Lys Trp Met Met Tyr Trp Ile Val Phe Ala Phe Phe | | | | |
| | 35 | 40 | 45 | |
| acc acg gcc gag acg ctc acg gat ata gtg ctc tcc tgg ttc ccc ttc | | | | 192 |
| Thr Thr Ala Glu Thr Leu Thr Asp Ile Val Leu Ser Trp Phe Pro Phe | | | | |
| | 50 | 55 | 60 | |
| tac ttt gaa ctg aag atc gcc ttc gtg ata tgg ctg ctg tcc cct tac | | | | 240 |
| Tyr Phe Glu Leu Lys Ile Ala Phe Val Ile Trp Leu Leu Ser Pro Tyr | | | | |
| | 65 | 70 | 75 | 80 |
| acc aag ggc tcc agc gtg ctc tac cgc aag ttc gtg cac cca acg ctg | | | | 288 |
| Thr Lys Gly Ser Ser Val Leu Tyr Arg Lys Phe Val His Pro Thr Leu | | | | |
| | 85 | 90 | 95 | |
| tcc aac aag gag aag gag atc gac gag tac atc acg cag gcc cga gac | | | | 336 |
| Ser Asn Lys Glu Lys Glu Ile Asp Glu Tyr Ile Thr Gln Ala Arg Asp | | | | |
| | 100 | 105 | 110 | |
| aag agc tat gag acc atg atg agg gtg ggc aag agg ggc ctg aac ctt | | | | 384 |
| Lys Ser Tyr Glu Thr Met Met Arg Val Gly Lys Arg Gly Leu Asn Leu | | | | |
| | 115 | 120 | 125 | |
| gcc gcc aat gct gca gtc aca gct gcc gcc aag ggc cag ggg gtg ctg | | | | 432 |
| Ala Ala Asn Ala Ala Val Thr Ala Ala Ala Lys Gly Gln Gly Val Leu | | | | |
| | 130 | 135 | 140 | |
| tca gag aag ctc cgc agc ttc agc atg cag gac ctg acc ctg atc cgg | | | | 480 |
| Ser Glu Lys Leu Arg Ser Phe Ser Met Gln Asp Leu Thr Leu Ile Arg | | | | |
| | 145 | 150 | 155 | 160 |
| gac gag gac gca ctg ccc ctg cag agg cct gac ggc cgc ctc cga ccc | | | | 528 |
| Asp Glu Asp Ala Leu Pro Leu Gln Arg Pro Asp Gly Arg Leu Arg Pro | | | | |
| | 165 | 170 | 175 | |
| agc cct ggc agc ctc ctg gac acc atc gag gac tta gga gat gac cct | | | | 576 |
| Ser Pro Gly Ser Leu Leu Asp Thr Ile Glu Asp Leu Gly Asp Asp Pro | | | | |

26

| 180 | 185 | 190 | |
|---|-----|-----|-----|
| gcc ctg agt cta agg tcc agc aca aac ccg gca gat tcc cgg aca gag | | | 624 |
| Ala Leu Ser Leu Arg Ser Ser Thr Asn Pro Ala Asp Ser Arg Thr Glu | | | |
| 195 | 200 | 205 | |
| gct tct gag gat gac atg gga gac aaa gct ccc aag agg gcc aaa ccc | | | 672 |
| Ala Ser Glu Asp Asp Met Gly Asp Lys Ala Pro Lys Arg Ala Lys Pro | | | |
| 210 | 215 | 220 | |
| atc aaa aaa gcg ccc aaa gct gag cca ctg gct tcc aag aca ctg aag | | | 720 |
| Ile Lys Lys Ala Pro Lys Ala Glu Pro Leu Ala Ser Lys Thr Leu Lys | | | |
| 225 | 230 | 235 | 240 |
| acc cgg ccc aag aag aag acc tct ggc ggg ggc gac tca gct tga | | | 765 |
| Thr Arg Pro Lys Lys Lys Thr Ser Gly Gly Gly Asp Ser Ala * | | | |
| 245 | 250 | | |

<210> 16

<211> 254

<212> PRT

<213> Homo sapiens

<400> 16

| | | | |
|---|-----|-----|----|
| Met Val Ser Trp Ile Ile Ser Arg Leu Val Val Leu Ile Phe Gly Thr | | | |
| 1 | 5 | 10 | 15 |
| Leu Tyr Pro Ala Tyr Ser Ser Tyr Lys Ala Val Lys Thr Lys Asn Val | | | |
| 20 | 25 | 30 | |
| Lys Glu Tyr Val Lys Trp Met Met Tyr Trp Ile Val Phe Ala Phe Phe | | | |
| 35 | 40 | 45 | |
| Thr Thr Ala Glu Thr Leu Thr Asp Ile Val Leu Ser Trp Phe Pro Phe | | | |
| 50 | 55 | 60 | |
| Tyr Phe Glu Leu Lys Ile Ala Phe Val Ile Trp Leu Leu Ser Pro Tyr | | | |
| 65 | 70 | 75 | 80 |
| Thr Lys Gly Ser Ser Val Leu Tyr Arg Lys Phe Val His Pro Thr Leu | | | |
| 85 | 90 | 95 | |
| Ser Asn Lys Glu Lys Glu Ile Asp Glu Tyr Ile Thr Gln Ala Arg Asp | | | |
| 100 | 105 | 110 | |
| Lys Ser Tyr Glu Thr Met Met Arg Val Gly Lys Arg Gly Leu Asn Leu | | | |
| 115 | 120 | 125 | |
| Ala Ala Asn Ala Ala Val Thr Ala Ala Ala Lys Gly Gln Gly Val Leu | | | |
| 130 | 135 | 140 | |
| Ser Glu Lys Leu Arg Ser Phe Ser Met Gln Asp Leu Thr Leu Ile Arg | | | |

27

145 150 155 160
 Asp Glu Asp Ala Leu Pro Leu Gln Arg Pro Asp Gly Arg Leu Arg Pro
 165 170 175
 Ser Pro Gly Ser Leu Leu Asp Thr Ile Glu Asp Leu Gly Asp Asp Pro
 180 185 190
 Ala Leu Ser Leu Arg Ser Ser Thr Asn Pro Ala Asp Ser Arg Thr Glu
 195 200 205
 Ala Ser Glu Asp Asp Met Gly Asp Lys Ala Pro Lys Arg Ala Lys Pro
 210 215 220
 Ile Lys Lys Ala Pro Lys Ala Glu Pro Leu Ala Ser Lys Thr Leu Lys
 225 230 235 240
 Thr Arg Pro Lys Lys Lys Thr Ser Gly Gly Gly Asp Ser Ala
 245 250

<210> 17

<211> 408

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(408)

<221> misc_feature

<222> (1)...(408)

<223> n = A,T,C or G

<400> 17

atg gcc cat agg ggc gtg tca gct gtg gtc gtg gga gct gac cgc gtg 48
 Met Ala His Arg Gly Val Ser Ala Val Val Val Gly Ala Asp Arg Val
 1 5 10 15

gtt gcc aac ggn gac aca gcc aac aag gtg ggc acc tac cag ctg gcc 96
 Val Ala Asn Xaa Asp Thr Ala Asn Lys Val Gly Thr Tyr Gln Leu Ala
 20 25 30

att gtc gcc aag cac cat ggc att ccc ttc tac gtg gct gcc ccc agc 144
 Ile Val Ala Lys His His Gly Ile Pro Phe Tyr Val Ala Ala Pro Ser
 35 40 45

tct tca tgt gac ctc cgt ctg gag acc ggc aag gag atc att att gaa 192
 Ser Ser Cys Asp Leu Arg Leu Glu Thr Gly Lys Glu Ile Ile Ile Glu
 50 55 60

28

gag cga ccg ggc cag gag ctg acc gat gtt aat ggg gtc cgg att gca 240
 Glu Arg Pro Gly Gln Glu Leu Thr Asp Val Asn Gly Val Arg Ile Ala
 65 70 75 80

gca cct ggg att gga gtt tgg aat cct gcc ttc gat gtc acc ccc cac 288
 Ala Pro Gly Ile Gly Val Trp Asn Pro Ala Phe Asp Val Thr Pro His
 85 90 95

gac ctc atc act ggt ggc atc atc aca gaa ctg ggg gtc ttt gcc cct 336
 Asp Leu Ile Thr Gly Gly Ile Ile Thr Glu Leu Gly Val Phe Ala Pro
 100 105 110

gag gag ctc cgg aca gcc cta acc acc acc atc tct tcc agg gat gga 384
 Glu Glu Leu Arg Thr Ala Leu Thr Thr Thr Ile Ser Ser Arg Asp Gly
 115 120 125

acc cta gat gga ccc cag atg taa 408
 Thr Leu Asp Gly Pro Gln Met *
 130 135

<210> 18

<211> 135

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(135)

<223> Xaa = Any Amino Acid

<400> 18

Met Ala His Arg Gly Val Ser Ala Val Val Val Gly Ala Asp Arg Val
 1 5 10 15

Val Ala Asn Xaa Asp Thr Ala Asn Lys Val Gly Thr Tyr Gln Leu Ala
 20 25 30

Ile Val Ala Lys His His Gly Ile Pro Phe Tyr Val Ala Ala Pro Ser
 35 40 45

Ser Ser Cys Asp Leu Arg Leu Glu Thr Gly Lys Glu Ile Ile Ile Glu
 50 55 60

Glu Arg Pro Gly Gln Glu Leu Thr Asp Val Asn Gly Val Arg Ile Ala
 65 70 75 80

Ala Pro Gly Ile Gly Val Trp Asn Pro Ala Phe Asp Val Thr Pro His
 85 90 95

29

Asp Leu Ile Thr Gly Gly Ile Ile Thr Glu Leu Gly Val Phe Ala Pro
 100 105 110
 Glu Glu Leu Arg Thr Ala Leu Thr Thr Thr Ile Ser Ser Arg Asp Gly
 115 120 125
 Thr Leu Asp Gly Pro Gln Met
 130 135

<210> 19
 <211> 828
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(828)

<400> 19
 atg ggg aat ttc aga ggt cat gcc ctc cct gga acc ttc ttt ttt att 48
 Met Gly Asn Phe Arg Gly His Ala Leu Pro Gly Thr Phe Phe Phe Ile
 1 5 10 15
 att ggt ctt tgg tgg tgt aca aag agt att ctg aag tat atc tgc aaa 96
 Ile Gly Leu Trp Trp Cys Thr Lys Ser Ile Leu Lys Tyr Ile Cys Lys
 20 25 30
 aag caa aag cga acc tgc tat ctt ggt tcc aaa aca tta ttc tat cga 144
 Lys Gln Lys Arg Thr Cys Tyr Leu Gly Ser Lys Thr Leu Phe Tyr Arg
 35 40 45
 ttg gaa att ttg gag gga att aca ata gtt ggc atg gct tta act ggc 192
 Leu Glu Ile Leu Glu Gly Ile Thr Ile Val Gly Met Ala Leu Thr Gly
 50 55 60
 atg gct ggg gag cag ttt att cct gga ggg ccc cat ctg atg tta tat 240
 Met Ala Gly Glu Gln Phe Ile Pro Gly Gly Pro His Leu Met Leu Tyr
 65 70 75 80
 gac tat aaa caa ggt cac tgg aat caa ctc ctg ggc tgg cat cat ttc 288
 Asp Tyr Lys Gln Gly His Trp Asn Gln Leu Leu Gly Trp His His Phe
 85 90 95
 acc atg tat ttc ttc ttt ggg ctg ttg ggt gtg gca gat atc tta tgt 336
 Thr Met Tyr Phe Phe Phe Gly Leu Leu Gly Val Ala Asp Ile Leu Cys
 100 105 110

| | |
|---|-----|
| ttc acc atc agt tca ctt cct gtg tcc tta acc aag tta atg ttg tca Phe Thr Ile Ser Ser Leu Pro Val Ser Leu Thr Lys Leu Met Leu Ser 115 120 125 | 384 |
| aat gcc tta ttt gtg gag gcc ttt atc ttc tac aac cac act cat ggc Asn Ala Leu Phe Val Glu Ala Phe Ile Phe Tyr Asn His Thr His Gly 130 135 140 | 432 |
| cgg gaa atg ctg gac atc ttt gtg cac cag ctg ctg gtt ttg gtc gtc Arg Glu Met Leu Asp Ile Phe Val His Gln Leu Leu Val Leu Val Val 145 150 155 160 | 480 |
| ttt ctg aca ggc ctc gtt gcc ttc cta gag ttc ctt gtt cgg aac aat Phe Leu Thr Gly Leu Val Ala Phe Leu Glu Phe Leu Val Arg Asn Asn 165 170 175 | 528 |
| gta ctt ctg gag cta ttg cgg tca agt ctc att ctg ctt cag ggg agc Val Leu Leu Glu Leu Leu Arg Ser Ser Leu Ile Leu Leu Gln Gly Ser 180 185 190 | 576 |
| tgg ttc ttt cag att gga ttt gtc ctg tat ccc ccc agt gga ggt cct Trp Phe Phe Gln Ile Gly Phe Val Leu Tyr Pro Pro Ser Gly Gly Pro 195 200 205 | 624 |
| gca tgg gat ctg atg gat cat gaa aat att ttg ttt ctc acc ata tgc Ala Trp Asp Leu Met Asp His Glu Asn Ile Leu Phe Leu Thr Ile Cys 210 215 220 | 672 |
| ttt tgt tgg cat tat gca gta acc att gtc atc gtt gga atg aat tat Phe Cys Trp His Tyr Ala Val Thr Ile Val Ile Val Gly Met Asn Tyr 225 230 235 240 | 720 |
| gct ttc att acc tgg ttg gtt aaa tct aga ctt aag agg ctc tgc tcc Ala Phe Ile Thr Trp Leu Val Lys Ser Arg Leu Lys Arg Leu Cys Ser 245 250 255 | 768 |
| tca gaa gtt gga ctt ctg aaa aat gct gaa cga gaa caa gaa tca gaa Ser Glu Val Gly Leu Leu Lys Asn Ala Glu Arg Glu Gln Glu Ser Glu 260 265 270 | 816 |
| gaa gaa atg tga Glu Glu Met * | 828 |
| 275 | |

<210> 20
 <211> 275
 <212> PRT
 <213> Homo sapiens

<400> 20

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Met Gly Asn Phe Arg Gly His Ala Leu Pro Gly Thr Phe Phe Phe Ile
 1           5           10           15
Ile Gly Leu Trp Trp Cys Thr Lys Ser Ile Leu Lys Tyr Ile Cys Lys
      20           25           30
Lys Gln Lys Arg Thr Cys Tyr Leu Gly Ser Lys Thr Leu Phe Tyr Arg
      35           40           45
Leu Glu Ile Leu Glu Gly Ile Thr Ile Val Gly Met Ala Leu Thr Gly
      50           55           60
Met Ala Gly Glu Gln Phe Ile Pro Gly Gly Pro His Leu Met Leu Tyr
65           70           75           80
Asp Tyr Lys Gln Gly His Trp Asn Gln Leu Leu Gly Trp His His Phe
      85           90           95
Thr Met Tyr Phe Phe Phe Gly Leu Leu Gly Val Ala Asp Ile Leu Cys
      100          105          110
Phe Thr Ile Ser Ser Leu Pro Val Ser Leu Thr Lys Leu Met Leu Ser
      115          120          125
Asn Ala Leu Phe Val Glu Ala Phe Ile Phe Tyr Asn His Thr His Gly
      130          135          140
Arg Glu Met Leu Asp Ile Phe Val His Gln Leu Leu Val Leu Val Val
145          150          155          160
Phe Leu Thr Gly Leu Val Ala Phe Leu Glu Phe Leu Val Arg Asn Asn
      165          170          175
Val Leu Leu Glu Leu Leu Arg Ser Ser Leu Ile Leu Leu Gln Gly Ser
      180          185          190
Trp Phe Phe Gln Ile Gly Phe Val Leu Tyr Pro Pro Ser Gly Gly Pro
      195          200          205
Ala Trp Asp Leu Met Asp His Glu Asn Ile Leu Phe Leu Thr Ile Cys
      210          215          220
Phe Cys Trp His Tyr Ala Val Thr Ile Val Ile Val Gly Met Asn Tyr
225          230          235          240
Ala Phe Ile Thr Trp Leu Val Lys Ser Arg Leu Lys Arg Leu Cys Ser
      245          250          255
Ser Glu Val Gly Leu Leu Lys Asn Ala Glu Arg Glu Gln Glu Ser Glu
      260          265          270
Glu Glu Met
      275

```

<210> 21
 <211> 1623
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1623)

<221> misc_feature
 <222> (1)...(1623)
 <223> n = A.T.C or G

<400> 21
 atg gag cgg gag gcg ttg ccg tgg ggc ctc gag ccc cag gat gtg cag 48
 Met Glu Arg Glu Ala Leu Pro Trp Gly Leu Glu Pro Gln Asp Val Gln
 1 5 10 15
 agt tct gac gaa atg agg agc ccc gaa ggt aac ctc aga ggc aac atg 96
 Ser Ser Asp Glu Met Arg Ser Pro Glu Gly Asn Leu Arg Gly Asn Met
 20 25 30
 agt gag aat gag gaa gag gaa att tct cag caa gaa ggc agt ggg gac 144
 Ser Glu Asn Glu Glu Glu Glu Ile Ser Gln Gln Glu Gly Ser Gly Asp
 35 40 45
 tat gaa gtc gaa gag ata cca ttt ggg ctt gaa ccc cag agc cct ggg 192
 Tyr Glu Val Glu Glu Ile Pro Phe Gly Leu Glu Pro Gln Ser Pro Gly
 50 55 60
 ttt gag cca caa agc cca gag ttt gaa ccc caa agc ccc aga ttt gag 240
 Phe Glu Pro Gln Ser Pro Glu Phe Glu Pro Gln Ser Pro Arg Phe Glu
 65 70 75 80
 cct gaa agc ccg ggg ttt gag tcc cga agc cct ggg ctt gtg ccc cca 288
 Pro Glu Ser Pro Gly Phe Glu Ser Arg Ser Pro Gly Leu Val Pro Pro
 85 90 95
 agc cct gag ttt gca ccc aga agc cct gaa tca gat tct cag agc cct 336
 Ser Pro Glu Phe Ala Pro Arg Ser Pro Glu Ser Asp Ser Gln Ser Pro
 100 105 110
 gag ttt gaa tcc cag agc cct agg tat gaa ccc caa agc cct ggc tat 384

| | |
|---|-----|
| Glu Phe Glu Ser Gln Ser Pro Arg Tyr Glu Pro Gln Ser Pro Gly Tyr | |
| 115 120 125 | |
| gaa cct cgg agc ccc ggg tat gaa ccc cgg agc cct ggc tat gaa tct | 432 |
| Glu Pro Arg Ser Pro Gly Tyr Glu Pro Arg Ser Pro Gly Tyr Glu Ser | |
| 130 135 140 | |
| gag agc tct aga tat gaa tcc cag aac act gag ctc aaa acc caa agc | 480 |
| Glu Ser Ser Arg Tyr Glu Ser Gln Asn Thr Glu Leu Lys Thr Gln Ser | |
| 145 150 155 160 | |
| cca gaa ttt gaa gct caa agt tcc aaa ttc cag gaa ggt gcg gag atg | 528 |
| Pro Glu Phe Glu Ala Gln Ser Ser Lys Phe Gln Glu Gly Ala Glu Met | |
| 165 170 175 | |
| ctt ctg aac ccc gan gaa aag agt cct ttg aat atc tcc gta gga gtt | 576 |
| Leu Leu Asn Pro Xaa Glu Lys Ser Pro Leu Asn Ile Ser Val Gly Val | |
| 180 185 190 | |
| cac ccc ctg gac tcc ttc act cag ggg ttt ggg gag cag ccc aca ggg | 624 |
| His Pro Leu Asp Ser Phe Thr Gln Gly Phe Gly Glu Gln Pro Thr Gly | |
| 195 200 205 | |
| gac ctg ccc ata ggg cca cct ttt gag atg ccc aca ggg gcc ctg ctg | 672 |
| Asp Leu Pro Ile Gly Pro Pro Phe Glu Met Pro Thr Gly Ala Leu Leu | |
| 210 215 220 | |
| tct aca ccg cag ttt gag atg ctt cag aat ccc ctg ggt ctc aca gga | 720 |
| Ser Thr Pro Gln Phe Glu Met Leu Gln Asn Pro Leu Gly Leu Thr Gly | |
| 225 230 235 240 | |
| gcc ctt cga ggt cca ggt cgg cgg ggt ggc cgg gcc agg ggt ggg cag | 768 |
| Ala Leu Arg Gly Pro Gly Arg Arg Gly Gly Arg Ala Arg Gly Gly Gln | |
| 245 250 255 | |
| ggc cct cgg cct aac atc tgt ggc atc tgc ggg aag agc ttc ggg cgg | 816 |
| Gly Pro Arg Pro Asn Ile Cys Gly Ile Cys Gly Lys Ser Phe Gly Arg | |
| 260 265 270 | |
| ggc tcc acc ctg atc cag cac cag cgc atc cac acc ggt gag aag ccc | 864 |
| Gly Ser Thr Leu Ile Gln His Gln Arg Ile His Thr Gly Glu Lys Pro | |
| 275 280 285 | |
| tac aaa tgt gag gtc tgc agc aag gcc ttc tcc cag agc tct gac ctc | 912 |

| | |
|---|------|
| Tyr Lys Cys Glu Val Cys Ser Lys Ala Phe Ser Gln Ser Ser Asp Leu | |
| 290 295 300 | |
| atc aaa cac cag cgc acc cac act ggc gag cgg ccc tac aaa tgt ccc | 960 |
| Ile Lys His Gln Arg Thr His Thr Gly Glu Arg Pro Tyr Lys Cys Pro | |
| 305 310 315 320 | |
| cgt tgc ggc aag gcc ttc gcc gac agc tct tac ctg ctt cgc cac cag | 1008 |
| Arg Cys Gly Lys Ala Phe Ala Asp Ser Ser Tyr Leu Leu Arg His Gln | |
| 325 330 335 | |
| cgc act cac tct ggc cag aag ccc tac aag tgc cca cat tgt ggc aag | 1056 |
| Arg Thr His Ser Gly Gln Lys Pro Tyr Lys Cys Pro His Cys Gly Lys | |
| 340 345 350 | |
| gcc ttc ggc gac agc tcc tac ctc ctg cga cac cag cgc acc cac agc | 1104 |
| Ala Phe Gly Asp Ser Ser Tyr Leu Leu Arg His Gln Arg Thr His Ser | |
| 355 360 365 | |
| cac gag cgg ccc tac agc tgc acc gag tgc ggc aag tgc tat agc cag | 1152 |
| His Glu Arg Pro Tyr Ser Cys Thr Glu Cys Gly Lys Cys Tyr Ser Gln | |
| 370 375 380 | |
| aac tcg tcc ctg cgc agc cat cag agg gtg cac acc ggt cag agg ccc | 1200 |
| Asn Ser Ser Leu Arg Ser His Gln Arg Val His Thr Gly Gln Arg Pro | |
| 385 390 395 400 | |
| ttc agc tgt ggc atc tgc ggc aag agc ttc tcc cag cgg tcg gcc ctt | 1248 |
| Phe Ser Cys Gly Ile Cys Gly Lys Ser Phe Ser Gln Arg Ser Ala Leu | |
| 405 410 415 | |
| atc ccc cat gcc cgc agc cac gcc cgg gag aag ccc ttc aag tgc cct | 1296 |
| Ile Pro His Ala Arg Ser His Ala Arg Glu Lys Pro Phe Lys Cys Pro | |
| 420 425 430 | |
| gag tgc ggc aag cgc ttt ggc cag agc tcg gtg ctg gcc atc cac gcc | 1344 |
| Glu Cys Gly Lys Arg Phe Gly Gln Ser Ser Val Leu Ala Ile His Ala | |
| 435 440 445 | |
| cgc acc cac ctg cca ggc cgc acc tac agc tgc ccc gac tgc ggc aag | 1392 |
| Arg Thr His Leu Pro Gly Arg Thr Tyr Ser Cys Pro Asp Cys Gly Lys | |
| 450 455 460 | |
| acc ttc aat cgc tcc tcc act ctc atc cag cac cag cgc tcc cac acg | 1440 |

35

Thr Phe Asn Arg Ser Ser Thr Leu Ile Gln His Gln Arg Ser His Thr
 465 470 475 480
 ggc gag cgg ccc tac agg tgc gcc gtg tgc ggc aag ggc ttc tgc cgc 1488
 Gly Glu Arg Pro Tyr Arg Cys Ala Val Cys Gly Lys Gly Phe Cys Arg
 485 490 495
 tcc tcc acg ctt ctg cag cat cac cgg gtc cac agt ggc gag cgg cct 1536
 Ser Ser Thr Leu Leu Gln His His Arg Val His Ser Gly Glu Arg Pro
 500 505 510
 tac aag tgc gat gac tgc gga aag gcc ttc tcc cag agc tcc gac ctc 1584
 Tyr Lys Cys Asp Asp Cys Gly Lys Ala Phe Ser Gln Ser Ser Asp Leu
 515 520 525
 atc cgc cac cag cgg acc cac gcg gcg ggc cgg cgc tga 1623
 Ile Arg His Gln Arg Thr His Ala Ala Gly Arg Arg *
 530 535 540

<210> 22

<211> 540

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(540)

<223> Xaa = Any Amino Acid

<400> 22

Met Glu Arg Glu Ala Leu Pro Trp Gly Leu Glu Pro Gln Asp Val Gln
 1 5 10 15
 Ser Ser Asp Glu Met Arg Ser Pro Glu Gly Asn Leu Arg Gly Asn Met
 20 25 30
 Ser Glu Asn Glu Glu Glu Glu Ile Ser Gln Gln Glu Gly Ser Gly Asp
 35 40 45
 Tyr Glu Val Glu Glu Ile Pro Phe Gly Leu Glu Pro Gln Ser Pro Gly
 50 55 60
 Phe Glu Pro Gln Ser Pro Glu Phe Glu Pro Gln Ser Pro Arg Phe Glu
 65 70 75 80
 Pro Glu Ser Pro Gly Phe Glu Ser Arg Ser Pro Gly Leu Val Pro Pro
 85 90 95
 Ser Pro Glu Phe Ala Pro Arg Ser Pro Glu Ser Asp Ser Gln Ser Pro

100 105 110
 Glu Phe Glu Ser Gln Ser Pro Arg Tyr Glu Pro Gln Ser Pro Gly Tyr
 115 120 125
 Glu Pro Arg Ser Pro Gly Tyr Glu Pro Arg Ser Pro Gly Tyr Glu Ser
 130 135 140
 Glu Ser Ser Arg Tyr Glu Ser Gln Asn Thr Glu Leu Lys Thr Gln Ser
 145 150 155 160
 Pro Glu Phe Glu Ala Gln Ser Ser Lys Phe Gln Glu Gly Ala Glu Met
 165 170 175
 Leu Leu Asn Pro Xaa Glu Lys Ser Pro Leu Asn Ile Ser Val Gly Val
 180 185 190
 His Pro Leu Asp Ser Phe Thr Gln Gly Phe Gly Glu Gln Pro Thr Gly
 195 200 205
 Asp Leu Pro Ile Gly Pro Pro Phe Glu Met Pro Thr Gly Ala Leu Leu
 210 215 220
 Ser Thr Pro Gln Phe Glu Met Leu Gln Asn Pro Leu Gly Leu Thr Gly
 225 230 235 240
 Ala Leu Arg Gly Pro Gly Arg Arg Gly Gly Arg Ala Arg Gly Gly Gln
 245 250 255
 Gly Pro Arg Pro Asn Ile Cys Gly Ile Cys Gly Lys Ser Phe Gly Arg
 260 265 270
 Gly Ser Thr Leu Ile Gln His Gln Arg Ile His Thr Gly Glu Lys Pro
 275 280 285
 Tyr Lys Cys Glu Val Cys Ser Lys Ala Phe Ser Gln Ser Ser Asp Leu
 290 295 300
 Ile Lys His Gln Arg Thr His Thr Gly Glu Arg Pro Tyr Lys Cys Pro
 305 310 315 320
 Arg Cys Gly Lys Ala Phe Ala Asp Ser Ser Tyr Leu Leu Arg His Gln
 325 330 335
 Arg Thr His Ser Gly Gln Lys Pro Tyr Lys Cys Pro His Cys Gly Lys
 340 345 350
 Ala Phe Gly Asp Ser Ser Tyr Leu Leu Arg His Gln Arg Thr His Ser
 355 360 365
 His Glu Arg Pro Tyr Ser Cys Thr Glu Cys Gly Lys Cys Tyr Ser Gln
 370 375 380
 Asn Ser Ser Leu Arg Ser His Gln Arg Val His Thr Gly Gln Arg Pro
 385 390 395 400
 Phe Ser Cys Gly Ile Cys Gly Lys Ser Phe Ser Gln Arg Ser Ala Leu
 405 410 415
 Ile Pro His Ala Arg Ser His Ala Arg Glu Lys Pro Phe Lys Cys Pro
 420 425 430
 Glu Cys Gly Lys Arg Phe Gly Gln Ser Ser Val Leu Ala Ile His Ala
 435 440 445
 Arg Thr His Leu Pro Gly Arg Thr Tyr Ser Cys Pro Asp Cys Gly Lys

450 455 460
 Thr Phe Asn Arg Ser Ser Thr Leu Ile Gln His Gln Arg Ser His Thr
 465 470 475 480
 Gly Glu Arg Pro Tyr Arg Cys Ala Val Cys Gly Lys Gly Phe Cys Arg
 485 490 495
 Ser Ser Thr Leu Leu Gln His His Arg Val His Ser Gly Glu Arg Pro
 500 505 510
 Tyr Lys Cys Asp Asp Cys Gly Lys Ala Phe Ser Gln Ser Ser Asp Leu
 515 520 525
 Ile Arg His Gln Arg Thr His Ala Ala Gly Arg Arg
 530 535 540

<210> 23

<211> 432

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(432)

<400> 23

atg gag ccc gcg ctg cgc gct gtg tgc aaa gac gtg cgc atc ggc acc 48
 Met Glu Pro Ala Leu Arg Ala Val Cys Lys Asp Val Arg Ile Gly Thr
 1 5 10 15

atc ctc atc cag acc aac cag ctt acc ggg gag ccc gag ctc cac tac 96
 Ile Leu Ile Gln Thr Asn Gln Leu Thr Gly Glu Pro Glu Leu His Tyr
 20 25 30

ctg agg ctg ccc aag gac atc agc gat gac cac gtg atc ctc atg gac 144
 Leu Arg Leu Pro Lys Asp Ile Ser Asp Asp His Val Ile Leu Met Asp
 35 40 45

tgc acc gtg tcc acg ggc gcg gcg gcc atg atg gca gtg cgc gtg ctc 192
 Cys Thr Val Ser Thr Gly Ala Ala Ala Met Met Ala Val Arg Val Leu
 50 55 60

ctg gac cac gac gtg cct gag gac aag atc ttt ttg ctg tcg ctg ctc 240
 Leu Asp His Asp Val Pro Glu Asp Lys Ile Phe Leu Leu Ser Leu Leu
 65 70 75 80

atg gca gag atg ggc gtg cac tca gtg gcc tat gca ttt ccg cga gtg 288
 Met Ala Glu Met Gly Val His Ser Val Ala Tyr Ala Phe Pro Arg Val

38

85

90

95

aga atc atc acc acg gcg gtg gac aag cgg gtc aat gac ctt ttc cgc 336
 Arg Ile Ile Thr Thr Ala Val Asp Lys Arg Val Asn Asp Leu Phe Arg
 100 105 110

atc atc cca ggc att ggg aac ttt ggc gac cgc tac ttt ggg aca gac 384
 Ile Ile Pro Gly Ile Gly Asn Phe Gly Asp Arg Tyr Phe Gly Thr Asp
 115 120 125

gcg gtc ccc gat ggc agt gac gag gag gaa gtg gcc tac acg ggt tag 432
 Ala Val Pro Asp Gly Ser Asp Glu Glu Glu Val Ala Tyr Thr Gly *
 130 135 140

<210> 24

<211> 143

<212> PRT

<213> Homo sapiens

<400> 24

Met Glu Pro Ala Leu Arg Ala Val Cys Lys Asp Val Arg Ile Gly Thr
 1 5 10 15
 Ile Leu Ile Gln Thr Asn Gln Leu Thr Gly Glu Pro Glu Leu His Tyr
 20 25 30
 Leu Arg Leu Pro Lys Asp Ile Ser Asp Asp His Val Ile Leu Met Asp
 35 40 45
 Cys Thr Val Ser Thr Gly Ala Ala Ala Met Met Ala Val Arg Val Leu
 50 55 60
 Leu Asp His Asp Val Pro Glu Asp Lys Ile Phe Leu Leu Ser Leu Leu
 65 70 75 80
 Met Ala Glu Met Gly Val His Ser Val Ala Tyr Ala Phe Pro Arg Val
 85 90 95
 Arg Ile Ile Thr Thr Ala Val Asp Lys Arg Val Asn Asp Leu Phe Arg
 100 105 110
 Ile Ile Pro Gly Ile Gly Asn Phe Gly Asp Arg Tyr Phe Gly Thr Asp
 115 120 125
 Ala Val Pro Asp Gly Ser Asp Glu Glu Glu Val Ala Tyr Thr Gly
 130 135 140

<210> 25

<211> 912

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(912)

<400> 25

| | |
|---|-----|
| atg ctg gcc ggc cac ggc ggc gtc ttc gcg ctc acg ctg ctg ctc atc | 48 |
| Met Leu Ala Gly His Gly Gly Val Phe Ala Leu Thr Leu Leu Leu Ile | |
| 1 5 10 15 | |
| ctc acc acc acc ggc ctc ttc ttc gtc ttt gac tgt ccc tac ctg gct | 96 |
| Leu Thr Thr Thr Gly Leu Phe Phe Val Phe Asp Cys Pro Tyr Leu Ala | |
| 20 25 30 | |
| cgc aag ctg acc ctt gcc atc ccc atc atc gct gcc atc ctc ttc ttc | 144 |
| Arg Lys Leu Thr Leu Ala Ile Pro Ile Ile Ala Ala Ile Leu Phe Phe | |
| 35 40 45 | |
| ttc gtc atg agc tgc ctg ctg cag aca agc ttc acc gac cct ggg atc | 192 |
| Phe Val Met Ser Cys Leu Leu Gln Thr Ser Phe Thr Asp Pro Gly Ile | |
| 50 55 60 | |
| ctg ccc cgg gcc act gtc tgt gaa gca gcc gcc ctg gag aaa cag atc | 240 |
| Leu Pro Arg Ala Thr Val Cys Glu Ala Ala Ala Leu Glu Lys Gln Ile | |
| 65 70 75 80 | |
| gac aac aca ggc agt tct aca tac cgg cca ccc cct cgg acc cgg gag | 288 |
| Asp Asn Thr Gly Ser Ser Thr Tyr Arg Pro Pro Pro Arg Thr Arg Glu | |
| 85 90 95 | |
| gtg ctg atc aac ggg cag atg gtg aag ctg aag tac tgc ttc acc tgc | 336 |
| Val Leu Ile Asn Gly Gln Met Val Lys Leu Lys Tyr Cys Phe Thr Cys | |
| 100 105 110 | |
| aag atg ttc cgg cca ccc cga acc tca cac tgc agt gtc tgc gac aac | 384 |
| Lys Met Phe Arg Pro Pro Arg Thr Ser His Cys Ser Val Cys Asp Asn | |
| 115 120 125 | |
| tgt gtg gaa cga ttt gac cat cac tgc ccc tgg gtg ggc aac tgt gtg | 432 |
| Cys Val Glu Arg Phe Asp His His Cys Pro Trp Val Gly Asn Cys Val | |
| 130 135 140 | |
| ggg aga cgg aac tat cgc ttc ttc tac gcg ttt att ctc tcc ctc tca | 480 |
| Gly Arg Arg Asn Tyr Arg Phe Phe Tyr Ala Phe Ile Leu Ser Leu Ser | |

40

| | | | | |
|--|-----|-----|-----|--|
| 145 | 150 | 155 | 160 | |
| ttc ctg acg gcc ttc atc ttc gcc tgt gtg gtc acc cac ctg acg ttg. | 528 | | | |
| Phe Leu Thr Ala Phe Ile Phe Ala Cys Val Val Thr His Leu Thr Leu | | | | |
| 165 | 170 | 175 | | |
| cgc gct cag gga agc aac ttc ctc tcc act ctg aag gag aca cca gca | 576 | | | |
| Arg Ala Gln Gly Ser Asn Phe Leu Ser Thr Leu Lys Glu Thr Pro Ala | | | | |
| 180 | 185 | 190 | | |
| agc gtg ctg gag ttg gtg atc tgc ttc ttc tcc atc tgg tcc att ctg | 624 | | | |
| Ser Val Leu Glu Leu Val Ile Cys Phe Phe Ser Ile Trp Ser Ile Leu | | | | |
| 195 | 200 | 205 | | |
| ggc ctc tca ggg ttt cac acg tac ctc gtc gcc tcc aac ctg act act | 672 | | | |
| Gly Leu Ser Gly Phe His Thr Tyr Leu Val Ala Ser Asn Leu Thr Thr | | | | |
| 210 | 215 | 220 | | |
| aat gaa gac atc aaa ggc tcg tgg tcc agc aag agg ggc ggt gag gcc | 720 | | | |
| Asn Glu Asp Ile Lys Gly Ser Trp Ser Ser Lys Arg Gly Gly Glu Ala | | | | |
| 225 | 230 | 235 | 240 | |
| tct gtc aac ccc tac agc cat aaa agt att atc acc aac tgc tgt gct | 768 | | | |
| Ser Val Asn Pro Tyr Ser His Lys Ser Ile Ile Thr Asn Cys Cys Ala | | | | |
| 245 | 250 | 255 | | |
| gtg ctc tgt ggc ccc cta cct ccc agc cta att gac cgg agg gga ttt | 816 | | | |
| Val Leu Cys Gly Pro Leu Pro Pro Ser Leu Ile Asp Arg Arg Gly Phe | | | | |
| 260 | 265 | 270 | | |
| gtg cag tcc gac acc gtg ttg ccc tca ccc atc aga agc gat gag cca | 864 | | | |
| Val Gln Ser Asp Thr Val Leu Pro Ser Pro Ile Arg Ser Asp Glu Pro | | | | |
| 275 | 280 | 285 | | |
| gcc tgc aga gcc aag cct gat gcc agc atg gta gga ggc cac ccc tga | 912 | | | |
| Ala Cys Arg Ala Lys Pro Asp Ala Ser Met Val Gly Gly His Pro * | | | | |
| 290 | 295 | 300 | | |

<210> 26

<211> 303

<212> PRT

<213> Homo sapiens

<400> 26
 Met Leu Ala Gly His Gly Gly Val Phe Ala Leu Thr Leu Leu Ile
 1 5 10 15
 Leu Thr Thr Thr Gly Leu Phe Phe Val Phe Asp Cys Pro Tyr Leu Ala
 20 25 30
 Arg Lys Leu Thr Leu Ala Ile Pro Ile Ile Ala Ala Ile Leu Phe Phe
 35 40 45
 Phe Val Met Ser Cys Leu Leu Gln Thr Ser Phe Thr Asp Pro Gly Ile
 50 55 60
 Leu Pro Arg Ala Thr Val Cys Glu Ala Ala Ala Leu Glu Lys Gln Ile
 65 70 75 80
 Asp Asn Thr Gly Ser Ser Thr Tyr Arg Pro Pro Pro Arg Thr Arg Glu
 85 90 95
 Val Leu Ile Asn Gly Gln Met Val Lys Leu Lys Tyr Cys Phe Thr Cys
 100 105 110
 Lys Met Phe Arg Pro Pro Arg Thr Ser His Cys Ser Val Cys Asp Asn
 115 120 125
 Cys Val Glu Arg Phe Asp His His Cys Pro Trp Val Gly Asn Cys Val
 130 135 140
 Gly Arg Arg Asn Tyr Arg Phe Phe Tyr Ala Phe Ile Leu Ser Leu Ser
 145 150 155 160
 Phe Leu Thr Ala Phe Ile Phe Ala Cys Val Val Thr His Leu Thr Leu
 165 170 175
 Arg Ala Gln Gly Ser Asn Phe Leu Ser Thr Leu Lys Glu Thr Pro Ala
 180 185 190
 Ser Val Leu Glu Leu Val Ile Cys Phe Phe Ser Ile Trp Ser Ile Leu
 195 200 205
 Gly Leu Ser Gly Phe His Thr Tyr Leu Val Ala Ser Asn Leu Thr Thr
 210 215 220
 Asn Glu Asp Ile Lys Gly Ser Trp Ser Ser Lys Arg Gly Gly Glu Ala
 225 230 235 240
 Ser Val Asn Pro Tyr Ser His Lys Ser Ile Ile Thr Asn Cys Cys Ala
 245 250 255
 Val Leu Cys Gly Pro Leu Pro Pro Ser Leu Ile Asp Arg Arg Gly Phe
 260 265 270
 Val Gln Ser Asp Thr Val Leu Pro Ser Pro Ile Arg Ser Asp Glu Pro
 275 280 285
 Ala Cys Arg Ala Lys Pro Asp Ala Ser Met Val Gly Gly His Pro
 290 295 300

<210> 27

<211> 795

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(795)

<221> misc_feature

<222> (1)...(795)

<223> n = A.T.C or G

<400> 27

| | |
|---|-----|
| atg aat tca aag cac act ttt ctg gcc ttg tgt gcc ctt cgc ttt atg | 48 |
| Met Asn Ser Lys His Thr Phe Leu Ala Leu Cys Ala Leu Arg Phe Met | |
| 1 5 10 15 | |
| agg cgg ata att gga ctt aaa gat gaa ttt tat aat cgt tac atc acc | 96 |
| Arg Arg Ile Ile Gly Leu Lys Asp Glu Phe Tyr Asn Arg Tyr Ile Thr | |
| 20 25 30 | |
| aag gga aat ctt ttt gag cca gtt ata aat gca ctt ctg gat aat gga | 144 |
| Lys Gly Asn Leu Phe Glu Pro Val Ile Asn Ala Leu Leu Asp Asn Gly | |
| 35 40 45 | |
| act cgg tat aat ctg ttg aat tca gct gtt att gag ttg ttt gaa ttt | 192 |
| Thr Arg Tyr Asn Leu Leu Asn Ser Ala Val Ile Glu Leu Phe Glu Phe | |
| 50 55 60 | |
| ata aga gtg gaa gat atc aag tct ctt act gcc cat ata gtt gaa aac | 240 |
| Ile Arg Val Glu Asp Ile Lys Ser Leu Thr Ala His Ile Val Glu Asn | |
| 65 70 75 80 | |
| ttt tat aaa gca ctt gaa tcg att gaa tat gtt cag aca ttc aaa gga | 288 |
| Phe Tyr Lys Ala Leu Glu Ser Ile Glu Tyr Val Gln Thr Phe Lys Gly | |
| 85 90 95 | |
| ttg aag act aaa tat gag cag aaa aag aac agt gta cca tct ata ttg | 336 |
| Leu Lys Thr Lys Tyr Glu Gln Lys Lys Asn Ser Val Pro Ser Ile Leu | |
| 100 105 110 | |
| cgt agt aac aga ttt cgc aga gat gca aaa gcc ttg gaa gag gat gaa | 384 |
| Arg Ser Asn Arg Phe Arg Arg Asp Ala Lys Ala Leu Glu Glu Asp Glu | |
| 115 120 125 | |
| gaa atg tgg ttt aat gaa gat gaa gaa gag gaa gga aaa gca gtt gtg | 432 |
| Glu Met Trp Phe Asn Glu Asp Glu Glu Glu Glu Gly Lys Ala Val Val | |

43

| 130 | 135 | 140 | |
|---|-----|-----|-----|
| gca cca gtg gaa aaa cct aag cca gaa gat gat ttt cca gat aat tat | | | 480 |
| Ala Pro Val Glu Lys Pro Lys Pro Glu Asp Asp Phe Pro Asp Asn Tyr | | | |
| 145 | 150 | 155 | 160 |
| | | | |
| gaa aag ttt atg gag act aaa aaa gca aaa gaa agt gaa gac aag gaa | | | 528 |
| Glu Lys Phe Met Glu Thr Lys Lys Ala Lys Glu Ser Glu Asp Lys Glu | | | |
| | 165 | 170 | 175 |
| | | | |
| aac ctt ccc aaa agg aca tct cct ggt ggc ttc aaa ttt act ttc tcc | | | 576 |
| Asn Leu Pro Lys Arg Thr Ser Pro Gly Gly Phe Lys Phe Thr Phe Ser | | | |
| | 180 | 185 | 190 |
| | | | |
| cac tct gcc agt gct gct aat gga aca aac agt aaa tct gta gtg gct | | | 624 |
| His Ser Ala Ser Ala Ala Asn Gly Thr Asn Ser Lys Ser Val Val Ala | | | |
| | 195 | 200 | 205 |
| | | | |
| cag ata cca cca gca act tct aat gga tcc tct tcc aaa acc aca aac | | | 672 |
| Gln Ile Pro Pro Ala Thr Ser Asn Gly Ser Ser Ser Lys Thr Thr Asn | | | |
| | 210 | 215 | 220 |
| | | | |
| ttg cct acg tca gta aca gcc acc aag gga agt ttg gtt ggc tta gtg | | | 720 |
| Leu Pro Thr Ser Val Thr Ala Thr Lys Gly Ser Leu Val Gly Leu Val | | | |
| | 225 | 230 | 240 |
| | | | |
| gat tat cca gat gat gaa gag gaa gat gaa gaa gaa gnn tcg tcc ccc | | | 768 |
| Asp Tyr Pro Asp Asp Glu Glu Glu Asp Glu Glu Glu Xaa Ser Ser Pro | | | |
| | 245 | 250 | 255 |
| | | | |
| agg aaa aga cct cgt ctt ggc tca taa | | | 795 |
| Arg Lys Arg Pro Arg Leu Gly Ser * | | | |
| | 260 | | |

<210> 28

<211> 264

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(264)

<223> Xaa = Any Amino Acid

<400> 28

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Met Asn Ser Lys His Thr Phe Leu Ala Leu Cys Ala Leu Arg Phe Met
 1           5           10           15
Arg Arg Ile Ile Gly Leu Lys Asp Glu Phe Tyr Asn Arg Tyr Ile Thr
      20           25           30
Lys Gly Asn Leu Phe Glu Pro Val Ile Asn Ala Leu Leu Asp Asn Gly
      35           40           45
Thr Arg Tyr Asn Leu Leu Asn Ser Ala Val Ile Glu Leu Phe Glu Phe
      50           55           60
Ile Arg Val Glu Asp Ile Lys Ser Leu Thr Ala His Ile Val Glu Asn
      65           70           75           80
Phe Tyr Lys Ala Leu Glu Ser Ile Glu Tyr Val Gln Thr Phe Lys Gly
      85           90           95
Leu Lys Thr Lys Tyr Glu Gln Lys Lys Asn Ser Val Pro Ser Ile Leu
      100          105          110
Arg Ser Asn Arg Phe Arg Arg Asp Ala Lys Ala Leu Glu Glu Asp Glu
      115          120          125
Glu Met Trp Phe Asn Glu Asp Glu Glu Glu Gly Lys Ala Val Val
      130          135          140
Ala Pro Val Glu Lys Pro Lys Pro Glu Asp Asp Phe Pro Asp Asn Tyr
      145          150          155          160
Glu Lys Phe Met Glu Thr Lys Lys Ala Lys Glu Ser Glu Asp Lys Glu
      165          170          175
Asn Leu Pro Lys Arg Thr Ser Pro Gly Gly Phe Lys Phe Thr Phe Ser
      180          185          190
His Ser Ala Ser Ala Ala Asn Gly Thr Asn Ser Lys Ser Val Val Ala
      195          200          205
Gln Ile Pro Pro Ala Thr Ser Asn Gly Ser Ser Ser Lys Thr Thr Asn
      210          215          220
Leu Pro Thr Ser Val Thr Ala Thr Lys Gly Ser Leu Val Gly Leu Val
      225          230          235          240
Asp Tyr Pro Asp Asp Glu Glu Glu Asp Glu Glu Glu Xaa Ser Ser Pro
      245          250          255
Arg Lys Arg Pro Arg Leu Gly Ser
      260

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<210> 29

<211> 711

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

45

<222> (1)...(711)

<400> 29

| | |
|---|-----|
| atg ggt ggc ccc cgg ggc gcg ggc tgg gtg gcg gcg ggc ctg ctg ctc | 48 |
| Met Gly Gly Pro Arg Gly Ala Gly Trp Val Ala Ala Gly Leu Leu Leu | |
| 1 5 10 15 | |
| ggc gcg ggc gcc tgc tac tgc att tac agg ctg acc cgg ggt cgg cgg | 96 |
| Gly Ala Gly Ala Cys Tyr Cys Ile Tyr Arg Leu Thr Arg Gly Arg Arg | |
| 20 25 30 | |
| cgg ggc gac cgc gag ctc ggg ata cgc tct tcg aag tcc gca gaa gac | 144 |
| Arg Gly Asp Arg Glu Leu Gly Ile Arg Ser Ser Lys Ser Ala Glu Asp | |
| 35 40 45 | |
| tta act gat ggt tca tat gat gat gtt cta aat gct gaa caa ctt cag | 192 |
| Leu Thr Asp Gly Ser Tyr Asp Asp Val Leu Asn Ala Glu Gln Leu Gln | |
| 50 55 60 | |
| aaa ctc ctt tac ctg ctg gag tca acg gag gat cct gta att att gaa | 240 |
| Lys Leu Leu Tyr Leu Leu Glu Ser Thr Glu Asp Pro Val Ile Ile Glu | |
| 65 70 75 80 | |
| aga gct ttg att act ttg ggt aac aat gca gcc ttt tca gtt aac caa | 288 |
| Arg Ala Leu Ile Thr Leu Gly Asn Asn Ala Ala Phe Ser Val Asn Gln | |
| 85 90 95 | |
| gct att att cgt gaa ttg ggt ggt att cca att gtt gca aac aaa atc | 336 |
| Ala Ile Ile Arg Glu Leu Gly Gly Ile Pro Ile Val Ala Asn Lys Ile | |
| 100 105 110 | |
| aac cat tcc aac cag agt att aaa gag aaa gct tta aat gca cta aat | 384 |
| Asn His Ser Asn Gln Ser Ile Lys Glu Lys Ala Leu Asn Ala Leu Asn | |
| 115 120 125 | |
| aac ctg agt gtg aat gtt gaa aat caa atc aag ata aag ata tac atc | 432 |
| Asn Leu Ser Val Asn Val Glu Asn Gln Ile Lys Ile Lys Ile Tyr Ile | |
| 130 135 140 | |
| agt caa gta tgt gag gat gtc ttc tct ggt cct ctg aac tct gct gtg | 480 |
| Ser Gln Val Cys Glu Asp Val Phe Ser Gly Pro Leu Asn Ser Ala Val | |
| 145 150 155 160 | |
| cag ctg gct gga ctg aca ttg ttg aca aac atg act gtt acc aat gac | 528 |

46

Gln Leu Ala Gly Leu Thr Leu Leu Thr Asn Met Thr Val Thr Asn Asp
 165 170 175

cac cag cac atg ctt cac agt tac att aca gac ctg ttc cag gtg tta 576
 His Gln His Met Leu His Ser Tyr Ile Thr Asp Leu Phe Gln Val Leu
 180 185 190

ctt act gga aat gga aac acg aag gtg caa gtt ttg aaa ctg ctt ttg 624
 Leu Thr Gly Asn Gly Asn Thr Lys Val Gln Val Leu Lys Leu Leu Leu
 195 200 205

aat ttg tct gaa aat cca gcc atg aca gaa gga ctt ctc cgt gcc caa 672
 Asn Leu Ser Glu Asn Pro Ala Met Thr Glu Gly Leu Leu Arg Ala Gln
 210 215 220

gtg gat tca tca ttc ctt tcc ctt atg aca gcc acg tag 711
 Val Asp Ser Ser Phe Leu Ser Leu Met Thr Ala Thr *
 225 230 235

<210> 30
 <211> 236
 <212> PRT
 <213> Homo sapiens

<400> 30
 Met Gly Gly Pro Arg Gly Ala Gly Trp Val Ala Ala Gly Leu Leu Leu
 1 5 10 15
 Gly Ala Gly Ala Cys Tyr Cys Ile Tyr Arg Leu Thr Arg Gly Arg Arg
 20 25 30
 Arg Gly Asp Arg Glu Leu Gly Ile Arg Ser Ser Lys Ser Ala Glu Asp
 35 40 45
 Leu Thr Asp Gly Ser Tyr Asp Asp Val Leu Asn Ala Glu Gln Leu Gln
 50 55 60
 Lys Leu Leu Tyr Leu Leu Glu Ser Thr Glu Asp Pro Val Ile Ile Glu
 65 70 75 80
 Arg Ala Leu Ile Thr Leu Gly Asn Asn Ala Ala Phe Ser Val Asn Gln
 85 90 95
 Ala Ile Ile Arg Glu Leu Gly Gly Ile Pro Ile Val Ala Asn Lys Ile
 100 105 110
 Asn His Ser Asn Gln Ser Ile Lys Glu Lys Ala Leu Asn Ala Leu Asn
 115 120 125
 Asn Leu Ser Val Asn Val Glu Asn Gln Ile Lys Ile Lys Ile Tyr Ile
 130 135 140

47

Ser Gln Val Cys Glu Asp Val Phe Ser Gly Pro Leu Asn Ser Ala Val
 145 150 155 160
 Gln Leu Ala Gly Leu Thr Leu Leu Thr Asn Met Thr Val Thr Asn Asp
 165 170 175
 His Gln His Met Leu His Ser Tyr Ile Thr Asp Leu Phe Gln Val Leu
 180 185 190
 Leu Thr Gly Asn Gly Asn Thr Lys Val Gln Val Leu Lys Leu Leu Leu
 195 200 205
 Asn Leu Ser Glu Asn Pro Ala Met Thr Glu Gly Leu Leu Arg Ala Gln
 210 215 220
 Val Asp Ser Ser Phe Leu Ser Leu Met Thr Ala Thr
 225 230 235

<210> 31
 <211> 1737
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1737)

<400> 31

| | |
|---|-----|
| atg cgc gct gcc cgc gcc gcg ccg ctg ctc cag ctg ctg ctc ctg ctg | 48 |
| Met Arg Ala Ala Arg Ala Ala Pro Leu Leu Gln Leu Leu Leu Leu | |
| 1 5 10 15 | |
| ggg ccg tgg ctg gag gct gcg ggc gtt gcg gag tcg ccg ctg ccc gcc | 96 |
| Gly Pro Trp Leu Glu Ala Ala Gly Val Ala Glu Ser Pro Leu Pro Ala | |
| 20 25 30 | |
| gtg gtc ctt gcc atc ctg gcc cgc aat gcc gaa cac tcg ctg ccc cac | 144 |
| Val Val Leu Ala Ile Leu Ala Arg Asn Ala Glu His Ser Leu Pro His | |
| 35 40 45 | |
| tac ctg ggc gct ctg gag cgg ctg gac tac ccc cgg gcc agg atg gcc | 192 |
| Tyr Leu Gly Ala Leu Glu Arg Leu Asp Tyr Pro Arg Ala Arg Met Ala | |
| 50 55 60 | |
| ctc tgg tgt gcc acg gac cac aat gtg gac aac acc aca gag atg ctg | 240 |
| Leu Trp Cys Ala Thr Asp His Asn Val Asp Asn Thr Thr Glu Met Leu | |
| 65 70 75 80 | |
| cag gag tgg ctg gcg gct gtg ggc gat gac tat gct gct gtg gtc tgg | 288 |

| | | | |
|---|-------------|-------------------------------------|-----|
| Gln Glu Trp Leu | Ala Ala Val | Gly Asp Asp Tyr Ala Ala Val Val Trp | |
| | 85 | 90 | 95 |
| agg cct gag ggc gag ccc agg ttc tac cca gat gaa gag ggt ccc aag | | | 336 |
| Arg Pro Glu Gly Glu Pro Arg Phe Tyr Pro Asp Glu Glu Gly Pro Lys | 100 | 105 | 110 |
| cac tgg acc aaa gaa agg cac cag ttt ctg atg gag ctg aag cag gaa | | | 384 |
| His Trp Thr Lys Glu Arg His Gln Phe Leu Met Glu Leu Lys Gln Glu | 115 | 120 | 125 |
| gcc ctc acc ttt gcc agg aac tgg ggg gcc gac tat atc ctg ttt gca | | | 432 |
| Ala Leu Thr Phe Ala Arg Asn Trp Gly Ala Asp Tyr Ile Leu Phe Ala | 130 | 135 | 140 |
| gac aca gac aac att ctg acc aac aat cag act ctg cgg ctt ctc atg | | | 480 |
| Asp Thr Asp Asn Ile Leu Thr Asn Asn Gln Thr Leu Arg Leu Leu Met | 145 | 150 | 155 |
| ggg cag ggg ctt cca gtg gtg gcc cca atg ctg gac tcc cag acc tac | | | 528 |
| Gly Gln Gly Leu Pro Val Val Ala Pro Met Leu Asp Ser Gln Thr Tyr | 165 | 170 | 175 |
| tac tcc aac ttc tgg tgt ggg atc acc ccc cag ggc tac tac cgc cgc | | | 576 |
| Tyr Ser Asn Phe Trp Cys Gly Ile Thr Pro Gln Gly Tyr Tyr Arg Arg | 180 | 185 | 190 |
| aca gcc gag tac ttc ccc acc aag aac cgc cag cgc cgg ggc tgc ttc | | | 624 |
| Thr Ala Glu Tyr Phe Pro Thr Lys Asn Arg Gln Arg Arg Gly Cys Phe | 195 | 200 | 205 |
| cgt gtc ccc atg gtc cac tcc acc ttc ctt gca tcc ctg cgg gct gaa | | | 672 |
| Arg Val Pro Met Val His Ser Thr Phe Leu Ala Ser Leu Arg Ala Glu | 210 | 215 | 220 |
| ggg gca gac cag ctt gct ttc tac ccg cca cat ccc aac tac act tgg | | | 720 |
| Gly Ala Asp Gln Leu Ala Phe Tyr Pro Pro His Pro Asn Tyr Thr Trp | 225 | 230 | 235 |
| cct ttc gac gac atc atc gtc ttc gcc tat gcc tgc cag gct gct ggg | | | 768 |
| Pro Phe Asp Asp Ile Ile Val Phe Ala Tyr Ala Cys Gln Ala Ala Gly | 245 | 250 | 255 |
| gtc tcc gtc cac gtg tgc aat gag cac cgt tat ggg tac atg aat gtg | | | 816 |

| | |
|---|------|
| Val Ser Val His Val Cys Asn Glu His Arg Tyr Gly Tyr Met Asn Val | |
| 260 265 270 | |
| ccg gtg aaa tcc cac cag ggg ctg gaa gac gag agg gtc aac ttc atc | 864 |
| Pro Val Lys Ser His Gln Gly Leu Glu Asp Glu Arg Val Asn Phe Ile | |
| 275 280 285 | |
| cac ctg atc tta gaa gca cta gtg gac ggc ccc cgc atg cag gcc tca | 912 |
| His Leu Ile Leu Glu Ala Leu Val Asp Gly Pro Arg Met Gln Ala Ser | |
| 290 295 300 | |
| gct cat gtg act cgg ccc tct aag agg ccc agc aag ata ggg ttt gac | 960 |
| Ala His Val Thr Arg Pro Ser Lys Arg Pro Ser Lys Ile Gly Phe Asp | |
| 305 310 315 320 | |
| gag gtc ttt gtc atc agc ctg gct cgc agg cct gac cgt cgg gaa cgc | 1008 |
| Glu Val Phe Val Ile Ser Leu Ala Arg Arg Pro Asp Arg Arg Glu Arg | |
| 325 330 335 | |
| atg ctc gcc tcg ctc tgg gag atg gag atc tct ggg agg gtg gtg gac | 1056 |
| Met Leu Ala Ser Leu Trp Glu Met Glu Ile Ser Gly Arg Val Val Asp | |
| 340 345 350 | |
| gct gtg gat ggc tgg atg ctc aac agc agt gcc atc agg aac ctc ggc | 1104 |
| Ala Val Asp Gly Trp Met Leu Asn Ser Ser Ala Ile Arg Asn Leu Gly | |
| 355 360 365 | |
| gta gac ctg ctc ccg ggc tac cag gac cct tac tcg ggc cgc act ctg | 1152 |
| Val Asp Leu Leu Pro Gly Tyr Gln Asp Pro Tyr Ser Gly Arg Thr Leu | |
| 370 375 380 | |
| acc aag ggc gag gtg ggc tgc ttc ctc agc cat tac tcc atc tgg gaa | 1200 |
| Thr Lys Gly Glu Val Gly Cys Phe Leu Ser His Tyr Ser Ile Trp Glu | |
| 385 390 395 400 | |
| gag gtg gtt gcc agg ggc ctg gcc cgg gtc ctg gtg ttt gag gat gac | 1248 |
| Glu Val Val Ala Arg Gly Leu Ala Arg Val Leu Val Phe Glu Asp Asp | |
| 405 410 415 | |
| gtg cgc ttt gag agc aac ttc agg ggg cgg ctg gag cgg ctg atg gag | 1296 |
| Val Arg Phe Glu Ser Asn Phe Arg Gly Arg Leu Glu Arg Leu Met Glu | |
| 420 425 430 | |
| gat gtg gag gca gag aaa ctg tct tgg gac ctg atc tac ctc gga cgg | 1344 |

- 50

| | |
|---|------|
| Asp Val Glu Ala Glu Lys Leu Ser Trp Asp Leu Ile Tyr Leu Gly Arg | |
| 435 440 445 | |
| aag cag gtg aac cct gag aag gag acg gcc gtg gag ggg ctg ccg ggc | 1392 |
| Lys Gln Val Asn Pro Glu Lys Glu Thr Ala Val Glu Gly Leu Pro Gly | |
| 450 455 460 | |
| ctg gtg gtg gct ggg tac tcc tac tgg acg ctg gcc tat gcc ctg cgt | 1440 |
| Leu Val Val Ala Gly Tyr Ser Tyr Trp Thr Leu Ala Tyr Ala Leu Arg | |
| 465 470 475 480 | |
| ctg gcg ggt gcc cgc aag ctg ctg gcc tca cag cct ctg cgc cgc atg | 1488 |
| Leu Ala Gly Ala Arg Lys Leu Leu Ala Ser Gln Pro Leu Arg Arg Met | |
| 485 490 495 | |
| ctg ccc gtg gac gag ttc ctg ccc atc atg ttc gac cag cac ccc aac | 1536 |
| Leu Pro Val Asp Glu Phe Leu Pro Ile Met Phe Asp Gln His Pro Asn | |
| 500 505 510 | |
| gag cag tac aag gca cac ttc tgg cca cgg gac ctg gtg gcc ttc tcc | 1584 |
| Glu Gln Tyr Lys Ala His Phe Trp Pro Arg Asp Leu Val Ala Phe Ser | |
| 515 520 525 | |
| gcc cag ccc ctg ctc gct gcc cct acc cac tat gcc ggg gac gcc gag | 1632 |
| Ala Gln Pro Leu Leu Ala Ala Pro Thr His Tyr Ala Gly Asp Ala Glu | |
| 530 535 540 | |
| tgg ctc agt gac acg gag aca tcc tct cca tgg gat gat gac agc ggc | 1680 |
| Trp Leu Ser Asp Thr Glu Thr Ser Ser Pro Trp Asp Asp Asp Ser Gly | |
| 545 550 555 560 | |
| cgc ctc atc agc tgg agc ggc tcc caa aag acc ctg cgc agc ccc gcc | 1728 |
| Arg Leu Ile Ser Trp Ser Gly Ser Gln Lys Thr Leu Arg Ser Pro Ala | |
| 565 570 575 | |
| tgg acc tga | 1737 |
| Trp Thr * | |

<210> 32
 <211> 578
 <212> PRT
 <213> Homo sapiens

<400> 32

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Met Arg Ala Ala Arg Ala Ala Pro Leu Leu Gln Leu Leu Leu Leu
 1          5          10          15
Gly Pro Trp Leu Glu Ala Ala Gly Val Ala Glu Ser Pro Leu Pro Ala
          20          25          30
Val Val Leu Ala Ile Leu Ala Arg Asn Ala Glu His Ser Leu Pro His
          35          40          45
Tyr Leu Gly Ala Leu Glu Arg Leu Asp Tyr Pro Arg Ala Arg Met Ala
          50          55          60
Leu Trp Cys Ala Thr Asp His Asn Val Asp Asn Thr Thr Glu Met Leu
65          70          75          80
Gln Glu Trp Leu Ala Ala Val Gly Asp Asp Tyr Ala Ala Val Val Trp
          85          90          95
Arg Pro Glu Gly Glu Pro Arg Phe Tyr Pro Asp Glu Glu Gly Pro Lys
          100          105          110
His Trp Thr Lys Glu Arg His Gln Phe Leu Met Glu Leu Lys Gln Glu
          115          120          125
Ala Leu Thr Phe Ala Arg Asn Trp Gly Ala Asp Tyr Ile Leu Phe Ala
          130          135          140
Asp Thr Asp Asn Ile Leu Thr Asn Asn Gln Thr Leu Arg Leu Leu Met
          145          150          155          160
Gly Gln Gly Leu Pro Val Val Ala Pro Met Leu Asp Ser Gln Thr Tyr
          165          170          175
Tyr Ser Asn Phe Trp Cys Gly Ile Thr Pro Gln Gly Tyr Tyr Arg Arg
          180          185          190
Thr Ala Glu Tyr Phe Pro Thr Lys Asn Arg Gln Arg Arg Gly Cys Phe
          195          200          205
Arg Val Pro Met Val His Ser Thr Phe Leu Ala Ser Leu Arg Ala Glu
          210          215          220
Gly Ala Asp Gln Leu Ala Phe Tyr Pro Pro His Pro Asn Tyr Thr Trp
          225          230          235          240
Pro Phe Asp Asp Ile Ile Val Phe Ala Tyr Ala Cys Gln Ala Ala Gly
          245          250          255
Val Ser Val His Val Cys Asn Glu His Arg Tyr Gly Tyr Met Asn Val
          260          265          270
Pro Val Lys Ser His Gln Gly Leu Glu Asp Glu Arg Val Asn Phe Ile
          275          280          285
His Leu Ile Leu Glu Ala Leu Val Asp Gly Pro Arg Met Gln Ala Ser
          290          295          300
Ala His Val Thr Arg Pro Ser Lys Arg Pro Ser Lys Ile Gly Phe Asp
          305          310          315          320
Glu Val Phe Val Ile Ser Leu Ala Arg Arg Pro Asp Arg Arg Glu Arg
          325          330          335

```

52

Met Leu Ala Ser Leu Trp Glu Met Glu Ile Ser Gly Arg Val Val Asp
 340 345 350
 Ala Val Asp Gly Trp Met Leu Asn Ser Ser Ala Ile Arg Asn Leu Gly
 355 360 365
 Val Asp Leu Leu Pro Gly Tyr Gln Asp Pro Tyr Ser Gly Arg Thr Leu
 370 375 380
 Thr Lys Gly Glu Val Gly Cys Phe Leu Ser His Tyr Ser Ile Trp Glu
 385 390 395 400
 Glu Val Val Ala Arg Gly Leu Ala Arg Val Leu Val Phe Glu Asp Asp
 405 410 415
 Val Arg Phe Glu Ser Asn Phe Arg Gly Arg Leu Glu Arg Leu Met Glu
 420 425 430
 Asp Val Glu Ala Glu Lys Leu Ser Trp Asp Leu Ile Tyr Leu Gly Arg
 435 440 445
 Lys Gln Val Asn Pro Glu Lys Glu Thr Ala Val Glu Gly Leu Pro Gly
 450 455 460
 Leu Val Val Ala Gly Tyr Ser Tyr Trp Thr Leu Ala Tyr Ala Leu Arg
 465 470 475 480
 Leu Ala Gly Ala Arg Lys Leu Leu Ala Ser Gln Pro Leu Arg Arg Met
 485 490 495
 Leu Pro Val Asp Glu Phe Leu Pro Ile Met Phe Asp Gln His Pro Asn
 500 505 510
 Glu Gln Tyr Lys Ala His Phe Trp Pro Arg Asp Leu Val Ala Phe Ser
 515 520 525
 Ala Gln Pro Leu Leu Ala Ala Pro Thr His Tyr Ala Gly Asp Ala Glu
 530 535 540
 Trp Leu Ser Asp Thr Glu Thr Ser Ser Pro Trp Asp Asp Asp Ser Gly
 545 550 555 560
 Arg Leu Ile Ser Trp Ser Gly Ser Gln Lys Thr Leu Arg Ser Pro Ala
 565 570 575
 Trp Thr

<210> 33

<211> 1152

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1152)

<400> 33

atg tta ccc aac acc ggg agg ctg gca gga tgt aca gtt ttt atc aca

48

53

| | | | | | | | | | | | | | | | | | |
|--------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|
| Met | Leu | Pro | Asn | Thr | Gly | Arg | Leu | Ala | Gly | Cys | Thr | Val | Phe | Ile | Thr | | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | | |
| ggt | gca | agc | cgt | ggc | att | ggc | aaa | gct | att | gca | ttg | aaa | gca | gca | aag | | 96 |
| Gly | Ala | Ser | Arg | Gly | Ile | Gly | Lys | Ala | Ile | Ala | Leu | Lys | Ala | Ala | Lys | | |
| | | | 20 | | | | | 25 | | | | | 30 | | | | |
| gat | gga | gca | aat | att | gtt | att | gct | gca | aag | acc | gcc | cag | cca | cat | cca | | 144 |
| Asp | Gly | Ala | Asn | Ile | Val | Ile | Ala | Ala | Lys | Thr | Ala | Gln | Pro | His | Pro | | |
| | | | 35 | | | | | 40 | | | | 45 | | | | | |
| aaa | ctt | cta | ggc | aca | atc | tat | act | gct | gct | gaa | gaa | att | gaa | gca | gtt | | 192 |
| Lys | Leu | Leu | Gly | Thr | Ile | Tyr | Thr | Ala | Ala | Glu | Glu | Ile | Glu | Ala | Val | | |
| | 50 | | | | | 55 | | | | 60 | | | | | | | |
| gga | gga | aag | gcc | ttg | cca | tgt | att | gtt | gat | gtg | aga | gat | gaa | cag | cag | | 240 |
| Gly | Gly | Lys | Ala | Leu | Pro | Cys | Ile | Val | Asp | Val | Arg | Asp | Glu | Gln | Gln | | |
| 65 | | | | | 70 | | | | 75 | | | | | 80 | | | |
| atc | agt | gct | gca | gtg | gag | aaa | gcc | atc | aag | aaa | ttt | gga | gga | att | gat | | 288 |
| Ile | Ser | Ala | Ala | Val | Glu | Lys | Ala | Ile | Lys | Lys | Phe | Gly | Gly | Ile | Asp | | |
| | | | | 85 | | | | | 90 | | | | | 95 | | | |
| att | ctg | gta | aat | aat | gcc | agt | gcc | att | agt | ttg | acc | aat | aca | ttg | gac | | 336 |
| Ile | Leu | Val | Asn | Asn | Ala | Ser | Ala | Ile | Ser | Leu | Thr | Asn | Thr | Leu | Asp | | |
| | | | 100 | | | | | 105 | | | | | 110 | | | | |
| aca | cct | acc | aag | aga | ttg | gat | ctg | atg | atg | aac | gtg | aac | acc | aga | ggc | | 384 |
| Thr | Pro | Thr | Lys | Arg | Leu | Asp | Leu | Met | Met | Asn | Val | Asn | Thr | Arg | Gly | | |
| | | | 115 | | | | | 120 | | | | 125 | | | | | |
| acc | tac | ctt | gca | tct | aaa | gca | tgt | att | cct | tat | ttg | aaa | aag | agc | aaa | | 432 |
| Thr | Tyr | Leu | Ala | Ser | Lys | Ala | Cys | Ile | Pro | Tyr | Leu | Lys | Lys | Ser | Lys | | |
| | | | 130 | | | | 135 | | | | 140 | | | | | | |
| gtt | gct | cat | atc | ctc | aat | atc | agt | cca | cca | ctg | aac | cta | aat | cca | gtt | | 480 |
| Val | Ala | His | Ile | Leu | Asn | Ile | Ser | Pro | Pro | Leu | Asn | Leu | Asn | Pro | Val | | |
| 145 | | | | | 150 | | | | | 155 | | | | 160 | | | |
| tggttc | aaa | cag | cac | tgt | gct | tat | acc | att | gct | aag | tat | ggt | atg | tct | | | 528 |
| Trp | Phe | Lys | Gln | His | Cys | Ala | Tyr | Thr | Ile | Ala | Lys | Tyr | Gly | Met | Ser | | |
| | | | 165 | | | | | 170 | | | | | 175 | | | | |
| atg | tat | gtg | ctt | gga | atg | gca | gaa | gaa | ttt | aaa | ggt | gaa | att | gca | gtc | | 576 |

| | |
|---|------|
| Met Tyr Val Leu Gly Met Ala Glu Glu Phe Lys Gly Glu Ile Ala Val | |
| 180 185 190 | |
| aat gca tta tgg cct aaa aca gcc ata cac act gct gct atg gat atg | 624 |
| Asn Ala Leu Trp Pro Lys Thr Ala Ile His Thr Ala Ala Met Asp Met | |
| 195 200 205 | |
| ctg gga gga cct ggt atc gaa agc cag tgt aga aaa gtt gat atc att | 672 |
| Leu Gly Gly Pro Gly Ile Glu Ser Gln Cys Arg Lys Val Asp Ile Ile | |
| 210 215 220 | |
| gca gat gca gca tat tcc att ttc caa aag cca aaa agt ttt act ggc | 720 |
| Ala Asp Ala Ala Tyr Ser Ile Phe Gln Lys Pro Lys Ser Phe Thr Gly | |
| 225 230 235 240 | |
| aac ttt gtc att gat gaa aat atc tta aaa gaa gaa gga ata gaa aat | 768 |
| Asn Phe Val Ile Asp Glu Asn Ile Leu Lys Glu Glu Gly Ile Glu Asn | |
| 245 250 255 | |
| ttt gac gtt tat gca att aaa cca ggt cat cct ttg caa cca gat ttc | 816 |
| Phe Asp Val Tyr Ala Ile Lys Pro Gly His Pro Leu Gln Pro Asp Phe | |
| 260 265 270 | |
| ttc tta gat gaa tac cca gaa gca gtt agc aag aaa gtg gaa tca act | 864 |
| Phe Leu Asp Glu Tyr Pro Glu Ala Val Ser Lys Lys Val Glu Ser Thr | |
| 275 280 285 | |
| ggg gct gtt cca gaa ttc aaa gaa gag aaa ctg cag ctg caa cca aaa | 912 |
| Gly Ala Val Pro Glu Phe Lys Glu Glu Lys Leu Gln Leu Gln Pro Lys | |
| 290 295 300 | |
| cca cgt tct gga gct gtg gaa gaa aca ttt aga att gtt aag gac tct | 960 |
| Pro Arg Ser Gly Ala Val Glu Glu Thr Phe Arg Ile Val Lys Asp Ser | |
| 305 310 315 320 | |
| ctc agt gat gat gtt gtt aaa gcc act caa gca atc tat ctg ttt gaa | 1008 |
| Leu Ser Asp Asp Val Val Lys Ala Thr Gln Ala Ile Tyr Leu Phe Glu | |
| 325 330 335 | |
| ctc tcc ggt gaa gat ggt ggc acg tgg ttt ctt gat ctg aaa agc aag | 1056 |
| Leu Ser Gly Glu Asp Gly Gly Thr Trp Phe Leu Asp Leu Lys Ser Lys | |
| 340 345 350 | |
| ggg ggg aat gtc gga tat gga gag cct tct gat cag gca gat gtg gtg | 1104 |

55

Gly Gly Asn Val Gly Tyr Gly Glu Pro Ser Asp Gln Ala Asp Val Val
 355 360 365

atg agt atg act act gat gac ttt gta aaa atg ttt tca ggg aac taa 1152
 Met Ser Met Thr Thr Asp Asp Phe Val Lys Met Phe Ser Gly Asn *
 370 375 380

<210> 34
 <211> 383
 <212> PRT
 <213> Homo sapiens

<400> 34
 Met Leu Pro Asn Thr Gly Arg Leu Ala Gly Cys Thr Val Phe Ile Thr
 1 5 10 15
 Gly Ala Ser Arg Gly Ile Gly Lys Ala Ile Ala Leu Lys Ala Ala Lys
 20 25 30
 Asp Gly Ala Asn Ile Val Ile Ala Ala Lys Thr Ala Gln Pro His Pro
 35 40 45
 Lys Leu Leu Gly Thr Ile Tyr Thr Ala Ala Glu Glu Ile Glu Ala Val
 50 55 60
 Gly Gly Lys Ala Leu Pro Cys Ile Val Asp Val Arg Asp Glu Gln Gln
 65 70 75 80
 Ile Ser Ala Ala Val Glu Lys Ala Ile Lys Lys Phe Gly Gly Ile Asp
 85 90 95
 Ile Leu Val Asn Asn Ala Ser Ala Ile Ser Leu Thr Asn Thr Leu Asp
 100 105 110
 Thr Pro Thr Lys Arg Leu Asp Leu Met Met Asn Val Asn Thr Arg Gly
 115 120 125
 Thr Tyr Leu Ala Ser Lys Ala Cys Ile Pro Tyr Leu Lys Lys Ser Lys
 130 135 140
 Val Ala His Ile Leu Asn Ile Ser Pro Pro Leu Asn Leu Asn Pro Val
 145 150 155 160
 Trp Phe Lys Gln His Cys Ala Tyr Thr Ile Ala Lys Tyr Gly Met Ser
 165 170 175
 Met Tyr Val Leu Gly Met Ala Glu Glu Phe Lys Gly Glu Ile Ala Val
 180 185 190
 Asn Ala Leu Trp Pro Lys Thr Ala Ile His Thr Ala Ala Met Asp Met
 195 200 205
 Leu Gly Gly Pro Gly Ile Glu Ser Gln Cys Arg Lys Val Asp Ile Ile
 210 215 220
 Ala Asp Ala Ala Tyr Ser Ile Phe Gln Lys Pro Lys Ser Phe Thr Gly
 225 230 235 240

<213> Homo sapiens

<222> (1)...(1371)

$\langle 223 \rangle$ n = A, T, C or G

atg ggg gcc tgc ctg gga gcc tgc tcc ctg ctc agc tgc gcg tcc tgc
Met Gly Ala Cys Leu Gly Ala Cys Ser Leu Leu Ser Cys Ala Ser Cys
1 5 10 15

ctc tgc ggc tct gcc ccc tgc atc ctg tgc agc tgc tgc ccc gcc agc
Leu Cys Gly Ser Ala Pro Cys Ile Leu Cys Ser Cys Cys Pro Ala Ser
20 25 30

cgc aac tcc acc gtg agc cgc ctc atc ttc acg ttc ttc ctc ttc ctg
 Arg Asn Ser Thr Val Ser Arg Leu Ile Phe Thr Phe Phe Leu Phe Leu
 35 40 45

144

| | |
|---|-----|
| ggg gtg ctg gtg tcc atc att atg ctg agc ccg ggc gtg gag agt cag Gly Val Leu Val Ser Ile Ile Met Leu Ser Pro Gly Val Glu Ser Gln 50 55 60 | 192 |
| ctc tac aag ctg ccc tgg gtg tgt gag gag ggg gcc ggg atc ccc acc Leu Tyr Lys Leu Pro Trp Val Cys Glu Glu Gly Ala Gly Ile Pro Thr 65 70 75 80 | 240 |
| gtc ctg cag ggc cac atc gac tgt ggc tcc ctg ctt ggc tac cgc gct Val Leu Gln Gly His Ile Asp Cys Gly Ser Leu Leu Gly Tyr Arg Ala 85 90 95 | 288 |
| gtc tac cgc atg tgc ttc gcc acg gcg gcc ttc ttc ttc ttt ttc acc Val Tyr Arg Met Cys Phe Ala Thr Ala Ala Phe Phe Phe Phe Thr 100 105 110 | 336 |
| ctg ctc atg ctc tgc gtg agc agc agc cgg gac ccc cgg gct gcc atc Leu Leu Met Leu Cys Val Ser Ser Ser Arg Asp Pro Arg Ala Ala Ile 115 120 125 | 384 |
| cag aat ggg ttt tgg ttc ttt aag ttc ctg atc ctg gtg ggc ctc acc Gln Asn Gly Phe Trp Phe Phe Lys Phe Leu Ile Leu Val Gly Leu Thr 130 135 140 | 432 |
| gtg ggt gcc ttc tac atc cct gac ggc tcc ttc acc aac atc tgg ttc Val Gly Ala Phe Tyr Ile Pro Asp Gly Ser Phe Thr Asn Ile Trp Phe 145 150 155 160 | 480 |
| tac ttc ggc gtc gtg ggc tcc ttc ctc ttc atc ctc atc cag ctg gtg Tyr Phe Gly Val Val Gly Ser Phe Leu Phe Ile Leu Ile Gln Leu Val 165 170 175 | 528 |
| ctg ctc atc gac ttt gcg cac tcc tgg aac cag cgg tgg ctg ggc aag Leu Leu Ile Asp Phe Ala His Ser Trp Asn Gln Arg Trp Leu Gly Lys 180 185 190 | 576 |
| gcc gag gag tgc gat tcc cgt gcc tgg tac gca ggc ctc ttc ttc ttc Ala Glu Glu Cys Asp Ser Arg Ala Trp Tyr Ala Gly Leu Phe Phe Phe 195 200 205 | 624 |
| act ctc ctc ttc tac ttg ctg tgc atc gcg gcc gtg gcg ctg atg ttc Thr Leu Leu Phe Tyr Leu Leu Ser Ile Ala Ala Val Ala Leu Met Phe 210 215 220 | 672 |


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ctg cac gtc atg atg acg ctc acc aac tgg tac aag ccc ggt gag acc      1248
Leu His Val Met Met Thr Leu Thr Asn Trp Tyr Lys Pro Gly Glu Thr
                405                410                415

cgg aag atg atc agc acg tgg acc gcc gtg tgg gtg aag atc tgt gcc      1296
Arg Lys Met Ile Ser Thr Trp Thr Ala Val Trp Val Lys Ile Cys Ala
                420                425                430

agc tgg gca ggg ctg ctc ctc tac ctg tgg acc ctg gta gcc cca ctc      1344
Ser Trp Ala Gly Leu Leu Leu Tyr Leu Trp Thr Leu Val Ala Pro Leu
                435                440                445

ctc ctg cgc aac cgc gac ttc agc tga                                  1371
Leu Leu Arg Asn Arg Asp Phe Ser *
                450                455

```

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<210> 36
<211> 456
<212> PRT
<213> Homo sapiens

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<220>
<221> VARIANT
<222> (1)...(456)
<223> Xaa = Any Amino Acid

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<400> 36
Met Gly Ala Cys Leu Gly Ala Cys Ser Leu Leu Ser Cys Ala Ser Cys
 1          5          10          15
Leu Cys Gly Ser Ala Pro Cys Ile Leu Cys Ser Cys Cys Pro Ala Ser
 20          25          30
Arg Asn Ser Thr Val Ser Arg Leu Ile Phe Thr Phe Phe Leu Phe Leu
 35          40          45
Gly Val Leu Val Ser Ile Ile Met Leu Ser Pro Gly Val Glu Ser Gln
 50          55          60
Leu Tyr Lys Leu Pro Trp Val Cys Glu Glu Gly Ala Gly Ile Pro Thr
 65          70          75          80
Val Leu Gln Gly His Ile Asp Cys Gly Ser Leu Leu Gly Tyr Arg Ala
 85          90          95
Val Tyr Arg Met Cys Phe Ala Thr Ala Ala Phe Phe Phe Phe Phe Thr
100         105         110
Leu Leu Met Leu Cys Val Ser Ser Ser Arg Asp Pro Arg Ala Ala Ile

```

| | | |
|---|-----|-----|
| 115 | 120 | 125 |
| Gln Asn Gly Phe Trp Phe Phe Lys Phe Leu Ile Leu Val Gly Leu Thr | | |
| 130 | 135 | 140 |
| Val Gly Ala Phe Tyr Ile Pro Asp Gly Ser Phe Thr Asn Ile Trp Phe | | |
| 145 | 150 | 155 |
| Tyr Phe Gly Val Val Gly Ser Phe Leu Phe Ile Leu Ile Gln Leu Val | | |
| 165 | 170 | 175 |
| Leu Leu Ile Asp Phe Ala His Ser Trp Asn Gln Arg Trp Leu Gly Lys | | |
| 180 | 185 | 190 |
| Ala Glu Glu Cys Asp Ser Arg Ala Trp Tyr Ala Gly Leu Phe Phe Phe | | |
| 195 | 200 | 205 |
| Thr Leu Leu Phe Tyr Leu Leu Ser Ile Ala Ala Val Ala Leu Met Phe | | |
| 210 | 215 | 220 |
| Met Tyr Tyr Thr Glu Pro Ser Gly Cys His Glu Gly Lys Val Phe Ile | | |
| 225 | 230 | 235 |
| Ser Leu Asn Leu Thr Phe Cys Val Cys Val Ser Ile Ala Ala Val Leu | | |
| 245 | 250 | 255 |
| Pro Lys Val Gln Asp Ala Gln Pro Asn Ser Gly Leu Leu Gln Ala Ser | | |
| 260 | 265 | 270 |
| Val Ile Thr Leu Tyr Thr Met Phe Val Thr Trp Ser Ala Leu Ser Ser | | |
| 275 | 280 | 285 |
| Ile Pro Glu Gln Lys Cys Asn Pro His Leu Pro Thr Gln Leu Gly Asn | | |
| 290 | 295 | 300 |
| Glu Thr Val Val Ala Gly Pro Glu Gly Tyr Glu Thr Gln Trp Trp Asp | | |
| 305 | 310 | 315 |
| Ala Pro Ser Ile Val Gly Leu Ile Ile Phe Leu Leu Cys Thr Leu Phe | | |
| 325 | 330 | 335 |
| Ile Ser Leu Arg Ser Ser Asp His Arg Gln Val Asn Ser Leu Met Gln | | |
| 340 | 345 | 350 |
| Thr Glu Glu Cys Pro Pro Met Leu Asp Ala Thr Xaa Gln Gln Gln Gln | | |
| 355 | 360 | 365 |
| Gln Val Ala Ala Cys Glu Gly Arg Ala Phe Asp Asn Glu Gln Asp Gly | | |
| 370 | 375 | 380 |
| Val Thr Tyr Ser Tyr Ser Phe Phe His Phe Cys Leu Val Leu Ala Ser | | |
| 385 | 390 | 395 |
| Leu His Val Met Met Thr Leu Thr Asn Trp Tyr Lys Pro Gly Glu Thr | | |
| 405 | 410 | 415 |
| Arg Lys Met Ile Ser Thr Trp Thr Ala Val Trp Val Lys Ile Cys Ala | | |
| 420 | 425 | 430 |
| Ser Trp Ala Gly Leu Leu Leu Tyr Leu Trp Thr Leu Val Ala Pro Leu | | |
| 435 | 440 | 445 |
| Leu Leu Arg Asn Arg Asp Phe Ser | | |
| 450 | 455 | |

61

<210> 37
 <211> 1257
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1257)

<400> 37

| | |
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| atg tta ccc aac acc ggg agg ctg gca gga tgt aca gtt ttt atc aca | 48 |
| Met Leu Pro Asn Thr Gly Arg Leu Ala Gly Cys Thr Val Phe Ile Thr | |
| 1 5 10 15 | |
| ggt gca agc cgt ggc att ggc aaa gct att gca ttg aaa gca gca aag | 96 |
| Gly Ala Ser Arg Gly Ile Gly Lys Ala Ile Ala Leu Lys Ala Ala Lys | |
| 20 25 30 | |
| gat gga gca aat att gtt att gct gca aag acc gcc cag cca cat cca | 144 |
| Asp Gly Ala Asn Ile Val Ile Ala Ala Lys Thr Ala Gln Pro His Pro | |
| 35 40 45 | |
| aaa ctt cta ggc aca atc tat act gct gct gaa gaa att gaa gca gtt | 192 |
| Lys Leu Leu Gly Thr Ile Tyr Thr Ala Ala Glu Glu Ile Glu Ala Val | |
| 50 55 60 | |
| gga gga aag gcc ttg cca tgt att gtt gat gtg aga gat gaa cag cag | 240 |
| Gly Gly Lys Ala Leu Pro Cys Ile Val Asp Val Arg Asp Glu Gln Gln | |
| 65 70 75 80 | |
| atc agt gct gca gtg gag aaa gcc atc aag aaa ttt gga gga att gat | 288 |
| Ile Ser Ala Ala Val Glu Lys Ala Ile Lys Lys Phe Gly Gly Ile Asp | |
| 85 90 95 | |
| att ctg gta aat aat gcc agt gcc att agt ttg acc aat aca ttg gac | 336 |
| Ile Leu Val Asn Asn Ala Ser Ala Ile Ser Leu Thr Asn Thr Leu Asp | |
| 100 105 110 | |
| aca cct acc aag aga ttg gat ctg atg atg aac gtg aac acc aga ggc | 384 |
| Thr Pro Thr Lys Arg Leu Asp Leu Met Met Asn Val Asn Thr Arg Gly | |
| 115 120 125 | |
| acc tac ctt gca tct aaa gca tgt att cct tat ttg aaa aag agc aaa | 432 |
| Thr Tyr Leu Ala Ser Lys Ala Cys Ile Pro Tyr Leu Lys Lys Ser Lys | |

| 130 | 135 | 140 | |
|---|-----|-----|-----|
| gtt gct cat atc ctc aat atc agt cca cca ctg aac cta aat cca gtt | | | 480 |
| Val Ala His Ile Leu Asn Ile Ser Pro Pro Leu Asn Leu Asn Pro Val | | | |
| 145 | 150 | 155 | 160 |
| tgg ttc aaa cag cac tgt gct tat acc att gct aag tat ggt atg tct | | | 528 |
| Trp Phe Lys Gln His Cys Ala Tyr Thr Ile Ala Lys Tyr Gly Met Ser | | | |
| | 165 | 170 | 175 |
| atg tat gtg ctt gga atg gca gaa gaa ttt aaa ggt gaa att gca gtc | | | 576 |
| Met Tyr Val Leu Gly Met Ala Glu Glu Phe Lys Gly Glu Ile Ala Val | | | |
| | 180 | 185 | 190 |
| aat gca tta tgg cct aaa aca gcc ata cac act gct gct atg gat atg | | | 624 |
| Asn Ala Leu Trp Pro Lys Thr Ala Ile His Thr Ala Ala Met Asp Met | | | |
| | 195 | 200 | 205 |
| ctg gga gga cct ggt atc gaa agc cag tgt aga aaa gtt gat atc att | | | 672 |
| Leu Gly Gly Pro Gly Ile Glu Ser Gln Cys Arg Lys Val Asp Ile Ile | | | |
| | 210 | 215 | 220 |
| gca gat gca gca tat tcc att ttc caa aag cca aaa agt ttt act ggc | | | 720 |
| Ala Asp Ala Ala Tyr Ser Ile Phe Gln Lys Pro Lys Ser Phe Thr Gly | | | |
| | 225 | 230 | 235 |
| aac ttt gtc att gat gaa aat atc tta aaa gaa gaa gga ata gaa aat | | | 768 |
| Asn Phe Val Ile Asp Glu Asn Ile Leu Lys Glu Glu Gly Ile Glu Asn | | | |
| | 245 | 250 | 255 |
| ttt gac gtt tat gca att aaa cca ggt cat cct ttg caa cca gat ttc | | | 816 |
| Phe Asp Val Tyr Ala Ile Lys Pro Gly His Pro Leu Gln Pro Asp Phe | | | |
| | 260 | 265 | 270 |
| ttc tta gat gaa tac cca gaa gca gtt agc aag aaa gtg gaa tca act | | | 864 |
| Phe Leu Asp Glu Tyr Pro Glu Ala Val Ser Lys Lys Val Glu Ser Thr | | | |
| | 275 | 280 | 285 |
| ggt gct gtt cca gaa ttc aaa gaa gag aaa ctg cag ctg caa cca aaa | | | 912 |
| Gly Ala Val Pro Glu Phe Lys Glu Glu Lys Leu Gln Leu Gln Pro Lys | | | |
| | 290 | 295 | 300 |
| cca cgt tct gga gct gtg gaa gaa aca ttt aga att gtt aag gac tct | | | 960 |
| Pro Arg Ser Gly Ala Val Glu Glu Thr Phe Arg Ile Val Lys Asp Ser | | | |

63

| | | | | |
|---|------|-----|------|--|
| 305 | 310 | 315 | 320 | |
| ctc agt gat gat gtt gtt aaa gcc act caa gca atc tat ctg ttt gaa | 1008 | | | |
| Leu Ser Asp Asp Val Val Lys Ala Thr Gln Ala Ile Tyr Leu Phe Glu | | | | |
| 325 | 330 | 335 | | |
| ctc tcc ggt gaa gat ggt ggc acg tgg ttt ctt gat ctg aaa agc aag | 1056 | | | |
| Leu Ser Gly Glu Asp Gly Gly Thr Trp Phe Leu Asp Leu Lys Ser Lys | | | | |
| 340 | 345 | 350 | | |
| ggt ggg aat gtc gga tat gga gag cct tct gat cag gca gat gtg gtg | 1104 | | | |
| Gly Gly Asn Val Gly Tyr Gly Glu Pro Ser Asp Gln Ala Asp Val Val | | | | |
| 355 | 360 | 365 | | |
| atg agt atg act act gat gac ttt gta aaa atg ttt tca ggg aaa cta | 1152 | | | |
| Met Ser Met Thr Thr Asp Asp Phe Val Lys Met Phe Ser Gly Lys Leu | | | | |
| 370 | 375 | 380 | | |
| aaa cca aca atg gca ttc atg tca ggg aaa ttg aag att aaa ggt aac | 1200 | | | |
| Lys Pro Thr Met Ala Phe Met Ser Gly Lys Leu Lys Ile Lys Gly Asn | | | | |
| 385 | 390 | 395 | 400 | |
| atg gcc cta gca atc aaa ttg gag aag cta atg aat cag atg aat gcc | 1248 | | | |
| Met Ala Leu Ala Ile Lys Leu Glu Lys Leu Met Asn Gln Met Asn Ala | | | | |
| 405 | 410 | 415 | | |
| aga ctg tga | | | 1257 | |
| Arg Leu * | | | | |

<210> 38

<211> 418

<212> PRT

<213> Homo sapiens

<400> 38

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Pro | Asn | Thr | Gly | Arg | Leu | Ala | Gly | Cys | Thr | Val | Phe | Ile | Thr |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Gly | Ala | Ser | Arg | Gly | Ile | Gly | Lys | Ala | Ile | Ala | Leu | Lys | Ala | Ala | Lys |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Asp | Gly | Ala | Asn | Ile | Val | Ile | Ala | Ala | Lys | Thr | Ala | Gln | Pro | His | Pro |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Lys | Leu | Leu | Gly | Thr | Ile | Tyr | Thr | Ala | Ala | Glu | Glu | Ile | Glu | Ala | Val |

| | | | | |
|---|-----|----|-----|-----|
| 50 | | 55 | | 60 |
| Gly Gly Lys Ala Leu Pro Cys Ile Val Asp Val Arg Asp Glu Gln Gln | | | | |
| 65 | | 70 | | 75 |
| Ile Ser Ala Ala Val Glu Lys Ala Ile Lys Lys Phe Gly Gly Ile Asp | | | | 80 |
| | 85 | | 90 | 95 |
| Ile Leu Val Asn Asn Ala Ser Ala Ile Ser Leu Thr Asn Thr Leu Asp | | | | |
| | 100 | | 105 | 110 |
| Thr Pro Thr Lys Arg Leu Asp Leu Met Met Asn Val Asn Thr Arg Gly | | | | |
| | 115 | | 120 | 125 |
| Thr Tyr Leu Ala Ser Lys Ala Cys Ile Pro Tyr Leu Lys Lys Ser Lys | | | | |
| | 130 | | 135 | 140 |
| Val Ala His Ile Leu Asn Ile Ser Pro Pro Leu Asn Leu Asn Pro Val | | | | |
| | 145 | | 150 | 155 |
| Trp Phe Lys Gln His Cys Ala Tyr Thr Ile Ala Lys Tyr Gly Met Ser | | | | |
| | 165 | | 170 | 175 |
| Met Tyr Val Leu Gly Met Ala Glu Glu Phe Lys Gly Glu Ile Ala Val | | | | |
| | 180 | | 185 | 190 |
| Asn Ala Leu Trp Pro Lys Thr Ala Ile His Thr Ala Ala Met Asp Met | | | | |
| | 195 | | 200 | 205 |
| Leu Gly Gly Pro Gly Ile Glu Ser Gln Cys Arg Lys Val Asp Ile Ile | | | | |
| | 210 | | 215 | 220 |
| Ala Asp Ala Ala Tyr Ser Ile Phe Gln Lys Pro Lys Ser Phe Thr Gly | | | | |
| | 225 | | 230 | 235 |
| Asn Phe Val Ile Asp Glu Asn Ile Leu Lys Glu Glu Gly Ile Glu Asn | | | | |
| | 245 | | 250 | 255 |
| Phe Asp Val Tyr Ala Ile Lys Pro Gly His Pro Leu Gln Pro Asp Phe | | | | |
| | 260 | | 265 | 270 |
| Phe Leu Asp Glu Tyr Pro Glu Ala Val Ser Lys Lys Val Glu Ser Thr | | | | |
| | 275 | | 280 | 285 |
| Gly Ala Val Pro Glu Phe Lys Glu Glu Lys Leu Gln Leu Gln Pro Lys | | | | |
| | 290 | | 295 | 300 |
| Pro Arg Ser Gly Ala Val Glu Glu Thr Phe Arg Ile Val Lys Asp Ser | | | | |
| | 305 | | 310 | 315 |
| Leu Ser Asp Asp Val Val Lys Ala Thr Gln Ala Ile Tyr Leu Phe Glu | | | | |
| | 325 | | 330 | 335 |
| Leu Ser Gly Glu Asp Gly Gly Thr Trp Phe Leu Asp Leu Lys Ser Lys | | | | |
| | 340 | | 345 | 350 |
| Gly Gly Asn Val Gly Tyr Gly Glu Pro Ser Asp Gln Ala Asp Val Val | | | | |
| | 355 | | 360 | 365 |
| Met Ser Met Thr Thr Asp Asp Phe Val Lys Met Phe Ser Gly Lys Leu | | | | |
| | 370 | | 375 | 380 |
| Lys Pro Thr Met Ala Phe Met Ser Gly Lys Leu Lys Ile Lys Gly Asn | | | | |
| | 385 | | 390 | 395 |
| Met Ala Leu Ala Ile Lys Leu Glu Lys Leu Met Asn Gln Met Asn Ala | | | | 400 |

65

405 410 415
 Arg Leu

 <210> 39
 <211> 627
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (1)...(627)

 <400> 39
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 Met Val Phe Tyr Phe Thr Ser Ser Ser Val Asn Ser Ser Ala Tyr Thr
 1 5 10 15

 att tac atg gga aaa gat aaa tat gaa aat gaa gat ctg atc aag cat 96
 Ile Tyr Met Gly Lys Asp Lys Tyr Glu Asn Glu Asp Leu Ile Lys His
 20 25 30

 ggc tgg cct gaa gat atc tgg ttt cat gtg gac aaa ctg tct tcg gct 144
 Gly Trp Pro Glu Asp Ile Trp Phe His Val Asp Lys Leu Ser Ser Ala
 35 40 45

 cat gta tac ctt cga tta cat aag gga gag aat ata gaa gac atc cca 192
 His Val Tyr Leu Arg Leu His Lys Gly Glu Asn Ile Glu Asp Ile Pro
 50 55 60

 aag gaa gtg ctg atg gac tgt gcc cac ctt gtg aag gcc aat agc att 240
 Lys Glu Val Leu Met Asp Cys Ala His Leu Val Lys Ala Asn Ser Ile
 65 70 75 80

 caa ggc tgc aag atg aac aac gtt aat gtg gta tat acg ccg tgg tct 288
 Gln Gly Cys Lys Met Asn Asn Val Asn Val Val Tyr Thr Pro Trp Ser
 85 90 95

 aac ctg aag aaa aca gct gac atg gat gtg ggg cag ata ggc ttt cac 336
 Asn Leu Lys Lys Thr Ala Asp Met Asp Val Gly Gln Ile Gly Phe His
 100 105 110

 agg cag aag gat gta aaa att gtg aca gtg gag aag aaa gta aat gag 384
 Arg Gln Lys Asp Val Lys Ile Val Thr Val Glu Lys Lys Val Asn Glu

66

| 115 | 120 | 125 | |
|---|-----|-----|-----|
| atc ctg aac cga tta gaa aag acc aaa gtc gag cgg ttc cca gac cta | | | 432 |
| Ile Leu Asn Arg Leu Glu Lys Thr Lys Val Glu Arg Phe Pro Asp Leu | | | |
| 130 | 135 | 140 | |
| gca gca gag aaa gaa tgc aga gat cgt gaa gag agg aat gag aaa aaa | | | 480 |
| Ala Ala Glu Lys Glu Cys Arg Asp Arg Glu Glu Arg Asn Glu Lys Lys | | | |
| 145 | 150 | 155 | 160 |
| gcc caa att cag gaa atg aaa aag aga gaa aaa gaa gaa atg aag aag | | | 528 |
| Ala Gln Ile Gln Glu Met Lys Lys Arg Glu Lys Glu Glu Met Lys Lys | | | |
| | 165 | 170 | 175 |
| aag agg gaa atg gat gaa ctt agg agc tat tca tca cta atg aaa gtt | | | 576 |
| Lys Arg Glu Met Asp Glu Leu Arg Ser Tyr Ser Ser Leu Met Lys Val | | | |
| | 180 | 185 | 190 |
| gaa aat atg tct tca aat cag gat ggc aat gat tca gat gaa ttc atg | | | 624 |
| Glu Asn Met Ser Ser Asn Gln Asp Gly Asn Asp Ser Asp Glu Phe Met | | | |
| 195 | 200 | 205 | |
| taa | | | 627 |
| * | | | |

<210> 40
 <211> 208
 <212> PRT
 <213> Homo sapiens

<400> 40
 Met Val Phe Tyr Phe Thr Ser Ser Ser Val Asn Ser Ser Ala Tyr Thr
 1 5 10 15
 Ile Tyr Met Gly Lys Asp Lys Tyr Glu Asn Glu Asp Leu Ile Lys His
 20 25 30
 Gly Trp Pro Glu Asp Ile Trp Phe His Val Asp Lys Leu Ser Ser Ala
 35 40 45
 His Val Tyr Leu Arg Leu His Lys Gly Glu Asn Ile Glu Asp Ile Pro
 50 55 60
 Lys Glu Val Leu Met Asp Cys Ala His Leu Val Lys Ala Asn Ser Ile
 65 70 75 80
 Gln Gly Cys Lys Met Asn Asn Val Asn Val Val Tyr Thr Pro Trp Ser

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| | | | | | | | | | | 85 | | | 90 | | | 95 | | |
| Asn | Leu | Lys | Lys | Thr | Ala | Asp | Met | Asp | Val | Gly | Gln | Ile | Gly | Phe | His | | | |
| | | | | | | | 100 | | | 105 | | | 110 | | | | | |
| Arg | Gln | Lys | Asp | Val | Lys | Ile | Val | Thr | Val | Glu | Lys | Lys | Val | Asn | Glu | | | |
| | | | | | | | 115 | | | 120 | | | 125 | | | | | |
| Ile | Leu | Asn | Arg | Leu | Glu | Lys | Thr | Lys | Val | Glu | Arg | Phe | Pro | Asp | Leu | | | |
| | | | | | | | 130 | | | 135 | | | 140 | | | | | |
| Ala | Ala | Glu | Lys | Glu | Cys | Arg | Asp | Arg | Glu | Glu | Arg | Asn | Glu | Lys | Lys | | | |
| | | | | | | | 145 | | | 150 | | | 155 | | | 160 | | |
| Ala | Gln | Ile | Gln | Glu | Met | Lys | Lys | Arg | Glu | Lys | Glu | Glu | Met | Lys | Lys | | | |
| | | | | | | | 165 | | | 170 | | | 175 | | | | | |
| Lys | Arg | Glu | Met | Asp | Glu | Leu | Arg | Ser | Tyr | Ser | Ser | Leu | Met | Lys | Val | | | |
| | | | | | | | 180 | | | 185 | | | 190 | | | | | |
| Glu | Asn | Met | Ser | Ser | Asn | Gln | Asp | Gly | Asn | Asp | Ser | Asp | Glu | Phe | Met | | | |
| | | | | | | | 195 | | | 200 | | | 205 | | | | | |

```
<220>
<221> CDS
<222> (1)...(474)

<221> misc_feature
<222> (1)...(474)
<223> n = A.T.C or G
```

| | | | | | | | | | | | | | | | | |
|----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> 41 | | | | | | | | | | | | | | | | |
| atg | agc | ggg | tcc | ctc | ggc | cga | gct | gct | gcg | gct | ctg | ctc | cgc | tgg | agg | 48 |
| Met | Ser | Gly | Ser | Leu | Gly | Arg | Ala | Ala | Ala | Ala | Leu | Leu | Arg | Trp | Arg | |
| | | | | 5 | 10 | | | | | | 15 | | | | | |
| | | | | | | | | | | | | | | | | |
| ctc | tgc | gcg | ggc | ggc | ggt | ggc | ctt | tgg | ggt | ccg | gtc | gtc | cgg | act | gcg | 96 |
| Leu | Cys | Ala | Gly | Gly | Gly | Gly | Leu | Trp | Gly | Pro | Val | Val | Arg | Thr | Ala | |
| | | | | 20 | 25 | | | | | | 30 | | | | | |
| | | | | | | | | | | | | | | | | |
| gga | tcg | gcc | ccg | ggc | ggc | ggc | ggc | tcg | gcg | gan | nag | ttg | gac | gcg | ctg | 144 |
| Gly | Ser | Ala | Pro | Gly | Gly | Gly | Gly | Ser | Ala | Xaa | Xaa | Leu | Asp | Ala | Leu | |
| | | | | 35 | 40 | | | | | | 45 | | | | | |
| | | | | | | | | | | | | | | | | |
| gtg | aag | aag | gac | aag | gtg | gtg | gtc | ttc | ctc | aag | ggg | acg | ccg | gag | cag | 192 |
| Val | Lys | Lys | Asp | Lys | Val | Val | Val | Phe | Leu | Lys | Gly | Thr | Pro | Glu | Gln | |

68

| | | | |
|---|-----|-----|----|
| 50 | 55 | 60 | |
| ccc cag tgc ggc ttc agc aac gcc gtg gtg cag atc ctg cgg ctg cac | 240 | | |
| Pro Gln Cys Gly Phe Ser Asn Ala Val Val Gln Ile Leu Arg Leu His | | | |
| 65 | 70 | 75 | 80 |
| ggc gtc cgc gat tac gcg gcc tac aac gtg ctg gac gac ccg gag ctc | 288 | | |
| Gly Val Arg Asp Tyr Ala Ala Tyr Asn Val Leu Asp Asp Pro Glu Leu | | | |
| 85 | 90 | 95 | |
| cga caa ggc att aaa gac tat tcc aac tgg ccc acc atc ccg caa gtg | 336 | | |
| Arg Gln Gly Ile Lys Asp Tyr Ser Asn Trp Pro Thr Ile Pro Gln Val | | | |
| 100 | 105 | 110 | |
| tac.ctc aat ggc gag ttt gta ggg ggc tgt gac att ctt ctg cag atg | 384 | | |
| Tyr Leu Asn Gly Glu Phe Val Gly Gly Cys Asp Ile Leu Leu Gln Met | | | |
| 115 | 120 | 125 | |
| cac cag aat ggg gac ttg gtg gaa gaa ctg aaa aag ctg ggg atc cac | 432 | | |
| His Gln Asn Gly Asp Leu Val Glu Glu Leu Lys Lys Leu Gly Ile His | | | |
| 130 | 135 | 140 | |
| tcc gcc ctt tta gat gaa aag aaa gac caa gac tcc aag tga | 474 | | |
| Ser Ala Leu Leu Asp Glu Lys Lys Asp Gln Asp Ser Lys * | | | |
| 145 | 150 | 155 | |

<210> 42

<211> 157

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(157)

<223> Xaa = Any Amino Acid

<400> 42

| | |
|---|----------|
| Met Ser Gly Ser Leu Gly Arg Ala Ala Ala Ala Leu Leu Arg Trp Arg | |
| 1 | 5 10 15 |
| Leu Cys Ala Gly Gly Gly Gly Leu Trp Gly Pro Val Val Arg Thr Ala | |
| | 20 25 30 |
| Gly Ser Ala Pro Gly Gly Gly Gly Ser Ala Xaa Xaa Leu Asp Ala Leu | |
| | 35 40 45 |

69

Val Lys Lys Asp Lys Val Val Val Phe Leu Lys Gly Thr Pro Glu Gln
 50 55 60
 Pro Gln Cys Gly Phe Ser Asn Ala Val Val Gln Ile Leu Arg Leu His
 65 70 75 80
 Gly Val Arg Asp Tyr Ala Ala Tyr Asn Val Leu Asp Asp Pro Glu Leu
 85 90 95
 Arg Gln Gly Ile Lys Asp Tyr Ser Asn Trp Pro Thr Ile Pro Gln Val
 100 105 110
 Tyr Leu Asn Gly Glu Phe Val Gly Gly Cys Asp Ile Leu Leu Gln Met
 115 120 125
 His Gln Asn Gly Asp Leu Val Glu Glu Leu Lys Lys Leu Gly Ile His
 130 135 140
 Ser Ala Leu Leu Asp Glu Lys Lys Asp Gln Asp Ser Lys
 145 150 155

<210> 43

<211> 1032

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1032)

<400> 43

atg ggt ggc ccc cgg ggc gcg ggc tgg gtg gcg gcg ggc ctg ctg ctc 48
 Met Gly Gly Pro Arg Gly Ala Gly Trp Val Ala Ala Gly Leu Leu Leu
 1 5 10 15
 ggc gcg ggc gcc tgc tac tgc att tac agg ctg acc cgg ggt cgg cgg 96
 Gly Ala Gly Ala Cys Tyr Cys Ile Tyr Arg Leu Thr Arg Gly Arg Arg
 20 25 30
 cgg ggc gac cgc gag ctc ggg ata cgc tct tcg aag tcc gca ggt gcc 144
 Arg Gly Asp Arg Glu Leu Gly Ile Arg Ser Ser Lys Ser Ala Gly Ala
 35 40 45
 ctg gaa gaa ggg acg tca gag ggt cag ttg tgc ggg cgc tcg gcc cgg 192
 Leu Glu Glu Gly Thr Ser Glu Gly Gln Leu Cys Gly Arg Ser Ala Arg
 50 55 60
 cct cag acg gga ggt acc tgg gag tca cag tgg tcc aag acc tcg cag 240
 Pro Gln Thr Gly Gly Thr Trp Glu Ser Gln Trp Ser Lys Thr Ser Gln
 65 70 75 80

| | |
|--|-----|
| cct gaa gac tta act gat ggt tca tat gat gat gtt cta aat gct gaa Pro Glu Asp Leu Thr Asp Gly Ser Tyr Asp Asp Val Leu Asn Ala Glu | 288 |
| 85 90 95 | |
| caa ctt cag aaa ctc ctt tac ctg ctg gag tca acg gag gat cct gta Gln Leu Gln Lys Leu Leu Tyr Leu Leu Glu Ser Thr Glu Asp Pro Val | 336 |
| 100 105 110 | |
| att att gaa aga gct ttg att act ttg ggt aac aat gca gcc ttt tca Ile Ile Glu Arg Ala Leu Ile Thr Leu Gly Asn Asn Ala Ala Phe Ser | 384 |
| 115 120 125 | |
| gtt aac caa gct att att cgt gaa ttg ggt ggt att cca att gtt gca Val Asn Gln Ala Ile Ile Arg Glu Leu Gly Gly Ile Pro Ile Val Ala | 432 |
| 130 135 140 | |
| aac aaa atc aac cat tcc aac cag agt att aaa gag aaa gct tta aat Asn Lys Ile Asn His Ser Asn Gln Ser Ile Lys Glu Lys Ala Leu Asn | 480 |
| 145 150 155 160 | |
| gca cta aat aac ctg agt gtg aat gtt gaa aat caa atc aag ata aag Ala Leu Asn Asn Leu Ser Val Asn Val Glu Asn Gln Ile Lys Ile Lys | 528 |
| 165 170 175 | |
| ata tac atc agt caa gta tgt gag gat gtc ttc tct ggt cct ctg aac Ile Tyr Ile Ser Gln Val Cys Glu Asp Val Phe Ser Gly Pro Leu Asn | 576 |
| 180 185 190 | |
| tct gct gtg cag ctg gct gga ctg aca ttg ttg aca aac atg act gtt Ser Ala Val Gln Leu Ala Gly Leu Thr Leu Leu Thr Asn Met Thr Val | 624 |
| 195 200 205 | |
| acc aat gac cac cag cac atg ctt cac agt tac att aca gac ctg ttc Thr Asn Asp His Gln His Met Leu His Ser Tyr Ile Thr Asp Leu Phe | 672 |
| 210 215 220 | |
| cag gtg tta ctt act gga aat gga aac acg aag gtg caa gtt ttg aaa Gln Val Leu Leu Thr Gly Asn Gly Asn Thr Lys Val Gln Val Leu Lys | 720 |
| 225 230 235 240 | |
| ctg ctt ttg aat ttg tct gaa aat cca gcc atg aca gaa gga ctt ctc Leu Leu Leu Asn Leu Ser Glu Asn Pro Ala Met Thr Glu Gly Leu Leu | 768 |
| 245 250 255 | |

cgt gcc caa gtg gat tca tca ttc ctt tcc ctt tat gac agc cac gta 816
 Arg Ala Gln Val Asp Ser Ser Phe Leu Ser Leu Tyr Asp Ser His Val
 260 265 270

gca aag gag att ctt ctt cga gta ctt acg cta ttt cag aat ata aag 864
 Ala Lys Glu Ile Leu Leu Arg Val Leu Thr Leu Phe Gln Asn Ile Lys
 275 280 285

aac tgc ctc aaa ata gaa ggc cat tta gct gtg cag cct act ttc act 912
 Asn Cys Leu Lys Ile Glu Gly His Leu Ala Val Gln Pro Thr Phe Thr
 290 295 300

gaa ggt tca ttg ttt ttc ctg tta cat gga gaa gaa tgt gcc cag aaa 960
 Glu Gly Ser Leu Phe Phe Leu Leu His Gly Glu Glu Cys Ala Gln Lys
 305 310 315 320

ata aga gct tta gtt gat cac cat gat gca gag gtg aag gaa aag gtt 1008
 Ile Arg Ala Leu Val Asp His His Asp Ala Glu Val Lys Glu Lys Val
 325 330 335

gta aca ata ata ccc aaa atc tga 1032
 Val Thr Ile Ile Pro Lys Ile *
 340

<210> 44
 <211> 343
 <212> PRT
 <213> Homo sapiens

<400> 44
 Met Gly Gly Pro Arg Gly Ala Gly Trp Val Ala Ala Gly Leu Leu Leu
 1 5 10 15
 Gly Ala Gly Ala Cys Tyr Cys Ile Tyr Arg Leu Thr Arg Gly Arg Arg
 20 25 30
 Arg Gly Asp Arg Glu Leu Gly Ile Arg Ser Ser Lys Ser Ala Gly Ala
 35 40 45
 Leu Glu Glu Gly Thr Ser Glu Gly Gln Leu Cys Gly Arg Ser Ala Arg
 50 55 60
 Pro Gln Thr Gly Gly Thr Trp Glu Ser Gln Trp Ser Lys Thr Ser Gln
 65 70 75 80
 Pro Glu Asp Leu Thr Asp Gly Ser Tyr Asp Asp Val Leu Asn Ala Glu
 85 90 95

Gln Leu Gln Lys Leu Leu Tyr Leu Leu Glu Ser Thr Glu Asp Pro Val
 100 105 110
 Ile Ile Glu Arg Ala Leu Ile Thr Leu Gly Asn Asn Ala Ala Phe Ser
 115 120 125
 Val Asn Gln Ala Ile Ile Arg Glu Leu Gly Gly Ile Pro Ile Val Ala
 130 135 140
 Asn Lys Ile Asn His Ser Asn Gln Ser Ile Lys Glu Lys Ala Leu Asn
 145 150 155 160
 Ala Leu Asn Asn Leu Ser Val Asn Val Glu Asn Gln Ile Lys Ile Lys
 165 170 175
 Ile Tyr Ile Ser Gln Val Cys Glu Asp Val Phe Ser Gly Pro Leu Asn
 180 185 190
 Ser Ala Val Gln Leu Ala Gly Leu Thr Leu Leu Thr Asn Met Thr Val
 195 200 205
 Thr Asn Asp His Gln His Met Leu His Ser Tyr Ile Thr Asp Leu Phe
 210 215 220
 Gln Val Leu Leu Thr Gly Asn Gly Asn Thr Lys Val Gln Val Leu Lys
 225 230 235 240
 Leu Leu Leu Asn Leu Ser Glu Asn Pro Ala Met Thr Glu Gly Leu Leu
 245 250 255
 Arg Ala Gln Val Asp Ser Ser Phe Leu Ser Leu Tyr Asp Ser His Val
 260 265 270
 Ala Lys Glu Ile Leu Leu Arg Val Leu Thr Leu Phe Gln Asn Ile Lys
 275 280 285
 Asn Cys Leu Lys Ile Glu Gly His Leu Ala Val Gln Pro Thr Phe Thr
 290 295 300
 Glu Gly Ser Leu Phe Phe Leu Leu His Gly Glu Glu Cys Ala Gln Lys
 305 310 315 320
 Ile Arg Ala Leu Val Asp His His Asp Ala Glu Val Lys Glu Lys Val
 325 330 335
 Val Thr Ile Ile Pro Lys Ile
 340

<210> 45

<211> 1335

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1335)

<221> misc_feature

<222> (1)...(1335)

atg tcg gga aga gat aca atc ctt ggc ctg tgt atc ctc gca tta gcc 48
Met Ser Gly Arg Asp Thr Ile Leu Gly Leu Cys Ile Leu Ala Leu Ala
1 5 10 15

ttg tct ttg gcc atg atg ttt acc ttc aga ttc atc acc acc ctt ctg 96
Leu Ser Leu Ala Met Met Phe Thr Phe Arg Phe Ile Thr Thr Leu Leu
20 25 30

ggt cac att ttc att tca ttg gtt att ttg gga ttg ttg ttt gtc tgc 144
Val His Ile Phe Ile Ser Leu Val Ile Leu Gly Leu Leu Phe Val Cys
35 40 45

ggt gtt tta tgg tgg ctg tat tat gac tat acc aac gac ctc agc ata 192
Gly Val Leu Trp Trp Leu Tyr Tyr Asp Tyr Thr Asn Asp Leu Ser Ile
50 55 60

gaa ttg gac aca gaa agg gaa aat atg aag tgc gtg ctg ggg ttt gct 240
Glu Leu Asp Thr Glu Arg Glu Asn Met Lys Cys Val Leu Gly Phe Ala
65 70 75 80

atc gta tcc aca ggc atc acg gca gtg ctg ctc gtc ttg att ttt gtt 288
Ile Val Ser Thr Gly Ile Thr Ala Val Leu Leu Val Leu Ile Phe Val
85 90 95

ctc aga aag aga ata aaa ttg aca gtt gag ctt ttc caa atc aca aat 336
Leu Arg Lys Arg Ile Lys Leu Thr Val Glu Leu Phe Gln Ile Thr Asn
100 105 110

aaa gcc atc agc agt gct ccc ttc ctg ctg ttc cag cca ctg tgg aca 384
Lys Ala Ile Ser Ser Ala Pro Phe Leu Leu Phe Gln Pro Leu Trp Thr
115 120 125

ttt gcc atc ctc att ttc ttc tgg gtc ctc tgg gtg gct gtg ctg ctg 432
Phe Ala Ile Leu Ile Phe Phe Trp Val Leu Trp Val Ala Val Leu Leu
130 135 140

agc ctg gga act gca gga gct gcc cag gtt atg gaa ggc ggc caa gtg 480
Ser Leu Gly Thr Ala Gly Ala Ala Gln Val Met Glu Gly Gly Gln Val
145 150 155 160

gaa tat aag ccc ctt tcg ggc att cgg tac atg tgg tcg tac cat tta 528

| | |
|---|------|
| Glu Tyr Lys Pro Leu Ser Gly Ile Arg Tyr Met Trp Ser Tyr His Leu | |
| 165 170 175 | |
| att ggc ctc atc tgg act agt gaa ttc atc ctt gcg tgc cag caa atg | 576 |
| Ile Gly Leu Ile Trp Thr Ser Glu Phe Ile Leu Ala Cys Gln Gln Met | |
| 180 185 190 | |
| act ata gct ggg gca gtg gnt act tgt tat ttc aac aga agt aaa aat | 624 |
| Thr Ile Ala Gly Ala Val Xaa Thr Cys Tyr Phe Asn Arg Ser Lys Asn | |
| 195 200 205 | |
| gat cct cct gat cat ccc atc ctt tcg tct ctc tcc att ctc ttc ttc | 672 |
| Asp Pro Pro Asp His Pro Ile Leu Ser Ser Leu Ser Ile Leu Phe Phe | |
| 210 215 220 | |
| tac cat caa gga acc att gtg aaa ggg tca ttt tta atc tct gtg gtg | 720 |
| Tyr His Gln Gly Thr Ile Val Lys Gly Ser Phe Leu Ile Ser Val Val | |
| 225 230 235 240 | |
| agg att ccg aga atc att gtc atg tac atg caa aac gca ctg aaa gaa | 768 |
| Arg Ile Pro Arg Ile Ile Val Met Tyr Met Gln Asn Ala Leu Lys Glu | |
| 245 250 255 | |
| cag cat ggt gca ttg tcc agg tac ctg ttc cga tgc tgc tac tgc tgt | 816 |
| Gln His Gly Ala Leu Ser Arg Tyr Leu Phe Arg Cys Cys Tyr Cys Cys | |
| 260 265 270 | |
| ttc tgg tgt ctt gac aaa tac ctg ctc cat ctc aac cag aat gca tat | 864 |
| Phe Trp Cys Leu Asp Lys Tyr Leu Leu His Leu Asn Gln Asn Ala Tyr | |
| 275 280 285 | |
| act aca act gct att aat ggg aca gat ttc tgt aca tca gca aaa gat | 912 |
| Thr Thr Thr Ala Ile Asn Gly Thr Asp Phe Cys Thr Ser Ala Lys Asp | |
| 290 295 300 | |
| gca ttc aaa atc ttg tcc aag aac tca agt cac ttt aca tct att aac | 960 |
| Ala Phe Lys Ile Leu Ser Lys Asn Ser Ser His Phe Thr Ser Ile Asn | |
| 305 310 315 320 | |
| tgc ttt gga gac ttc ata att ttt cta gga aag gtg tta gtg gtg tgt | 1008 |
| Cys Phe Gly Asp Phe Ile Ile Phe Leu Gly Lys Val Leu Val Val Cys | |
| 325 330 335 | |
| ttc act gtt ttt gga gga ctc atg gct ttt aac tac aat cgg gca ttc | 1056 |

75

Phe Thr Val Phe Gly Gly Leu Met Ala Phe Asn Tyr Asn Arg Ala Phe
 340 345 350

cag gtg tgg gca gtc cct ctg tta ttg gta gct ttt ttt gcc tac tta 1104
 Gln Val Trp Ala Val Pro Leu Leu Leu Val Ala Phe Phe Ala Tyr Leu
 355 360 365

gta gcc cat agt ttt tta tct gtg ttt gaa act gtg ctg gat gca ctt 1152
 Val Ala His Ser Phe Leu Ser Val Phe Glu Thr Val Leu Asp Ala Leu
 370 375 380

ttc ctg tgt ttt gct gtt gat ctg gaa aca aat gat gga tcg tca gaa 1200
 Phe Leu Cys Phe Ala Val Asp Leu Glu Thr Asn Asp Gly Ser Ser Glu
 385 390 395 400

aag ccc tac ttt atg gat caa gaa ttt ctg agt ttc gta aaa agg agc 1248
 Lys Pro Tyr Phe Met Asp Gln Glu Phe Leu Ser Phe Val Lys Arg Ser
 405 410 415

aac aaa tta aac aat gca agg gca cag cag gac aag cac tca tta agg 1296
 Asn Lys Leu Asn Asn Ala Arg Ala Gln Gln Asp Lys His Ser Leu Arg
 420 425 430

aat gag gag gga aca gaa ctc cag gcc att gtg aga tag 1335
 Asn Glu Glu Gly Thr Glu Leu Gln Ala Ile Val Arg *
 435 440

<210> 46

<211> 444

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(444)

<223> Xaa = Any Amino Acid

<400> 46

Met Ser Gly Arg Asp Thr Ile Leu Gly Leu Cys Ile Leu Ala Leu Ala
 1 5 10 15

Leu Ser Leu Ala Met Met Phe Thr Phe Arg Phe Ile Thr Thr Leu Leu
 20 25 30

Val His Ile Phe Ile Ser Leu Val Ile Leu Gly Leu Leu Phe Val Cys

| | | | | | |
|---|-----|-----|--|--|-----|
| 35 | 40 | 45 | | | |
| Gly Val Leu Trp Trp Leu Tyr Tyr Asp Tyr Thr Asn Asp Leu Ser Ile | | | | | |
| 50 | 55 | 60 | | | |
| Glu Leu Asp Thr Glu Arg Glu Asn Met Lys Cys Val Leu Gly Phe Ala | | | | | |
| 65 | 70 | 75 | | | 80 |
| Ile Val Ser Thr Gly Ile Thr Ala Val Leu Leu Val Leu Ile Phe Val | | | | | |
| 85 | 90 | 95 | | | |
| Leu Arg Lys Arg Ile Lys Leu Thr Val Glu Leu Phe Gln Ile Thr Asn | | | | | |
| 100 | 105 | 110 | | | |
| Lys Ala Ile Ser Ser Ala Pro Phe Leu Leu Phe Gln Pro Leu Trp Thr | | | | | |
| 115 | 120 | 125 | | | |
| Phe Ala Ile Leu Ile Phe Phe Trp Val Leu Trp Val Ala Val Leu Leu | | | | | |
| 130 | 135 | 140 | | | |
| Ser Leu Gly Thr Ala Gly Ala Ala Gln Val Met Glu Gly Gly Gln Val | | | | | |
| 145 | 150 | 155 | | | 160 |
| Glu Tyr Lys Pro Leu Ser Gly Ile Arg Tyr Met Trp Ser Tyr His Leu | | | | | |
| 165 | 170 | 175 | | | |
| Ile Gly Leu Ile Trp Thr Ser Glu Phe Ile Leu Ala Cys Gln Gln Met | | | | | |
| 180 | 185 | 190 | | | |
| Thr Ile Ala Gly Ala Val Xaa Thr Cys Tyr Phe Asn Arg Ser Lys Asn | | | | | |
| 195 | 200 | 205 | | | |
| Asp Pro Pro Asp His Pro Ile Leu Ser Ser Leu Ser Ile Leu Phe Phe | | | | | |
| 210 | 215 | 220 | | | |
| Tyr His Gln Gly Thr Ile Val Lys Gly Ser Phe Leu Ile Ser Val Val | | | | | |
| 225 | 230 | 235 | | | 240 |
| Arg Ile Pro Arg Ile Ile Val Met Tyr Met Gln Asn Ala Leu Lys Glu | | | | | |
| 245 | 250 | 255 | | | |
| Gln His Gly Ala Leu Ser Arg Tyr Leu Phe Arg Cys Cys Tyr Cys Cys | | | | | |
| 260 | 265 | 270 | | | |
| Phe Trp Cys Leu Asp Lys Tyr Leu Leu His Leu Asn Gln Asn Ala Tyr | | | | | |
| 275 | 280 | 285 | | | |
| Thr Thr Thr Ala Ile Asn Gly Thr Asp Phe Cys Thr Ser Ala Lys Asp | | | | | |
| 290 | 295 | 300 | | | |
| Ala Phe Lys Ile Leu Ser Lys Asn Ser Ser His Phe Thr Ser Ile Asn | | | | | |
| 305 | 310 | 315 | | | 320 |
| Cys Phe Gly Asp Phe Ile Ile Phe Leu Gly Lys Val Leu Val Val Cys | | | | | |
| 325 | 330 | 335 | | | |
| Phe Thr Val Phe Gly Gly Leu Met Ala Phe Asn Tyr Asn Arg Ala Phe | | | | | |
| 340 | 345 | 350 | | | |
| Gln Val Trp Ala Val Pro Leu Leu Leu Val Ala Phe Phe Ala Tyr Leu | | | | | |
| 355 | 360 | 365 | | | |
| Val Ala His Ser Phe Leu Ser Val Phe Glu Thr Val Leu Asp Ala Leu | | | | | |
| 370 | 375 | 380 | | | |
| Phe Leu Cys Phe Ala Val Asp Leu Glu Thr Asn Asp Gly Ser Ser Glu | | | | | |

385 390 395 400
Lys Pro Tyr Phe Met Asp Gln Glu Phe Leu Ser Phe Val Lys Arg Ser
 405 410 415
Asn Lys Leu Asn Asn Ala Arg Ala Gln Gln Asp Lys His Ser Leu Arg
 420 425 430
Asn Glu Glu Gly Thr Glu Leu Gln Ala Ile Val Arg
 435 440

```
<210> 47
<211> 351
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (1)...(351)
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<400> 47

atg gcg gat gag gcg ttg ttt ttg ctt ctc cat aac gag atg gtg tct 48
Met Ala Asp Glu Ala Leu Phe Leu Leu Leu His Asn Glu Met Val Ser
1 5 10 15

gga gtg tac aag tcc gcg gag cag ggg gag gtg gaa aac gga cga tgt 96
Gly Val Tyr Lys Ser Ala Glu Gln Gly Glu Val Glu Asn Gly Arg Cys
20 25 30

att act aag ctg gaa aac atg ggg ttt cga gtg gga caa gga ttg ata 144
Ile Thr Lys Leu Glu Asn Met Gly Phe Arg Val Gly Gln Gly Leu Ile
35 40 45

gaa agg ttt aca aaa gat act gca agg ttc aag gat gag tta gat atc 192
Glu Arg Phe Thr Lys Asp Thr Ala Arg Phe Lys Asp Glu Leu Asp Ile
50 55 60

atg aag ttc att tgt aaa gat ttt tgg act acg gta ttc aag aaa caa 240
Met Lys Phe Ile Cys Lys Asp Phe Trp Thr Thr Val Phe Lys Lys Gln
65 70 75 80

atc gac aat cta agg aca aat cat cag ggc atc tat gta ctt cag gac 288
Ile Asp Asn Leu Arg Thr Asn His Gln Gly Ile Tyr Val Leu Gln Asp
85 90 95

aac aaa ttt cgc ctg ctt act cag atg tct gca gga aaa cag tat tta 336
Asn Lys Phe Arg Leu Leu Thr Gln Met Ser Ala Gly Lys Gln Tyr Leu

78

100

105

110

gaa cat gca tcc taa

Glu His Ala Ser *

351

115

<210> 48

<211> 116

<212> PRT

<213> Homo sapiens

<400> 48

Met Ala Asp Glu Ala Leu Phe Leu Leu Leu His Asn Glu Met Val Ser
 1 5 10 15
 Gly Val Tyr Lys Ser Ala Glu Gln Gly Glu Val Glu Asn Gly Arg Cys
 20 25 30
 Ile Thr Lys Leu Glu Asn Met Gly Phe Arg Val Gly Gln Gly Leu Ile
 35 40 45
 Glu Arg Phe Thr Lys Asp Thr Ala Arg Phe Lys Asp Glu Leu Asp Ile
 50 55 60
 Met Lys Phe Ile Cys Lys Asp Phe Trp Thr Thr Val Phe Lys Lys Gln
 65 70 75 80
 Ile Asp Asn Leu Arg Thr Asn His Gln Gly Ile Tyr Val Leu Gln Asp
 85 90 95
 Asn Lys Phe Arg Leu Leu Thr Gln Met Ser Ala Gly Lys Gln Tyr Leu
 100 105 110
 Glu His Ala Ser
 115

<210> 49

<211> 516

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(516)

<400> 49

atg aag aaa tgt ctt ttg ccc gtt ttg att acg tgc atg caa aca gcg
 Met Lys Lys Cys Leu Leu Pro Val Leu Ile Thr Cys Met Gln Thr Ala
 1 5 10 15

48

79

| | |
|---|-----|
| att tgc aaa gac cgt atg atg atg atc atg atc tta ctg gtg aat tac | 96 |
| Ile Cys Lys Asp Arg Met Met Met Ile Met Ile Leu Leu Val Asn Tyr | |
| 20 25 30 | |
| cta cct gat gaa ttt ata gaa tgt gaa gac cca gtg gat cat gtt gga | 144 |
| Leu Pro Asp Glu Phe Ile Glu Cys Glu Asp Pro Val Asp His Val Gly | |
| 35 40 45 | |
| aat gca act gca tcc cag gaa ctt ggt tat ggt tgt ctc aag ttc ggc | 192 |
| Asn Ala Thr Ala Ser Gln Glu Leu Gly Tyr Gly Cys Leu Lys Phe Gly | |
| 50 55 60 | |
| ggt cag gcc tac agc gac gtg gaa cac act tca gtc cag tgc cat gcc | 240 |
| Gly Gln Ala Tyr Ser Asp Val Glu His Thr Ser Val Gln Cys His Ala | |
| 65 70 75 80 | |
| tta gat gga att gag tgt gcc agt cct agg acc ttt cta cga gaa aat | 288 |
| Leu Asp Gly Ile Glu Cys Ala Ser Pro Arg Thr Phe Leu Arg Glu Asn | |
| 85 90 95 | |
| aaa cct tgt ata aag tat acc gga cac tac ttc ata acc act tta ctc | 336 |
| Lys Pro Cys Ile Lys Tyr Thr Gly His Tyr Phe Ile Thr Thr Leu Leu | |
| 100 105 110 | |
| tac tcc ttc ttc ctg gga tgt ttt ggt gtg gat cga ttc tgt ttg gga | 384 |
| Tyr Ser Phe Phe Leu Gly Cys Phe Gly Val Asp Arg Phe Cys Leu Gly | |
| 115 120 125 | |
| cac act ggc act gca gta ggg aag ctg ttg acg ctt gga gga ctt ggg | 432 |
| His Thr Gly Thr Ala Val Gly Lys Leu Leu Thr Leu Gly Gly Leu Gly | |
| 130 135 140 | |
| att tgg tgg ttt gtt gac ctt att ttg cta att act gga ggg ctg atg | 480 |
| Ile Trp Trp Phe Val Asp Leu Ile Leu Leu Ile Thr Gly Gly Leu Met | |
| 145 150 155 160 | |
| cca agt gat ggc agc aac tgg tgc act gtt tac taa | 516 |
| Pro Ser Asp Gly Ser Asn Trp Cys Thr Val Tyr * | |
| 165 170 | |

<210> 50

<211> 171

<212> PRT

<213> Homo sapiens

<400> 50

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Met Lys Lys Cys Leu Leu Pro Val Leu Ile Thr Cys Met Gln Thr Ala
 1           5           10           15
Ile Cys Lys Asp Arg Met Met Met Ile Met Ile Leu Leu Val Asn Tyr
      20           25           30
Leu Pro Asp Glu Phe Ile Glu Cys Glu Asp Pro Val Asp His Val Gly
      35           40           45
Asn Ala Thr Ala Ser Gln Glu Leu Gly Tyr Gly Cys Leu Lys Phe Gly
      50           55           60
Gly Gln Ala Tyr Ser Asp Val Glu His Thr Ser Val Gln Cys His Ala
65           70           75           80
Leu Asp Gly Ile Glu Cys Ala Ser Pro Arg Thr Phe Leu Arg Glu Asn
      85           90           95
Lys Pro Cys Ile Lys Tyr Thr Gly His Tyr Phe Ile Thr Thr Leu Leu
      100          105          110
Tyr Ser Phe Phe Leu Gly Cys Phe Gly Val Asp Arg Phe Cys Leu Gly
      115          120          125
His Thr Gly Thr Ala Val Gly Lys Leu Leu Thr Leu Gly Gly Leu Gly
      130          135          140
Ile Trp Trp Phe Val Asp Leu Ile Leu Leu Ile Thr Gly Gly Leu Met
145          150          155          160
Pro Ser Asp Gly Ser Asn Trp Cys Thr Val Tyr
      165          170

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<210> 51

<211> 870

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(870)

<400> 51

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atg ccc cta tta aaa ctt gta cat ggc tcc cca ttg gtt ttt gga gaa      48
Met Pro Leu Leu Lys Leu Val His Gly Ser Pro Leu Val Phe Gly Glu
 1           5           10           15

aag ttc aag ctt ttt acc ttg gtg tct gcc tgt atc cca gtg ttc agg      96
Lys Phe Lys Leu Phe Thr Leu Val Ser Ala Cys Ile Pro Val Phe Arg
      20           25           30

```

| | |
|---|-----|
| ctg gct aga cgg cgg aag aag atc cta ttt tac tgt cac ttc cca gat Leu Ala Arg Arg Arg Lys Lys Ile Leu Phe Tyr Cys His Phe Pro Asp 35 40 45 | 144 |
| ctg ctt ctc acc aag aga gat tct ttt ctt aaa cga cta tac agg gcc Leu Leu Leu Thr Lys Arg Asp Ser Phe Leu Lys Arg Leu Tyr Arg Ala 50 55 60 | 192 |
| cca att gac tgg ata gag gaa tac acc aca ggc atg gca gac tgc atc Pro Ile Asp Trp Ile Glu Glu Tyr Thr Thr Gly Met Ala Asp Cys Ile 65 70 75 80 | 240 |
| tta gtc aac agc cag ttc aca gct gct gtt ttt aag gaa aca ttc aag Leu Val Asn Ser Gln Phe Thr Ala Ala Val Phe Lys Glu Thr Phe Lys 85 90 95 | 288 |
| tcc ctg tct cac ata gac cct gat gtc ctc tat cca tct cta aat gtc Ser Leu Ser His Ile Asp Pro Asp Val Leu Tyr Pro Ser Leu Asn Val 100 105 110 | 336 |
| acc agc ttt gac tca gtt gtt cct gaa aag ctg gat gac cta gtc ccc Thr Ser Phe Asp Ser Val Val Pro Glu Lys Leu Asp Asp Leu Val Pro 115 120 125 | 384 |
| aag ggg aaa aaa ttc ctg ctg ctc tcc atc aac aga tac gaa agg aag Lys Gly Lys Lys Phe Leu Leu Leu Ser Ile Asn Arg Tyr Glu Arg Lys 130 135 140 | 432 |
| aaa aat ctg act ttg gca ctg gaa gcc cta gta cag ctg cgt gga aga Lys Asn Leu Thr Leu Ala Leu Glu Ala Leu Val Gln Leu Arg Gly Arg 145 150 155 160 | 480 |
| ttg aca tcc caa gat tgg gag agg gtt cat ctg atc gtg gca ggt ggt Leu Thr Ser Gln Asp Trp Glu Arg Val His Leu Ile Val Ala Gly Gly 165 170 175 | 528 |
| tat gac gag aga gtc ctg gag aat gtg gaa cat tat cag gaa ttg aag Tyr Asp Glu Arg Val Leu Glu Asn Val Glu His Tyr Gln Glu Leu Lys 180 185 190 | 576 |
| aaa atg gtc caa cag tcc gac ctt ggc cag tat gtg acc ttc ttg agg Lys Met Val Gln Gln Ser Asp Leu Gly Gln Tyr Val Thr Phe Leu Arg 195 200 205 | 624 |

82

| | |
|---|-----|
| tct ttc tca gac aaa cag aaa atc tcc ctc ctc cac agc tgc acg tgt | 672 |
| Ser Phe Ser Asp Lys Gln Lys Ile Ser Leu Leu His Ser Cys Thr Cys | |
| 210 215 220 | |
| gtg ctt tac aca cca agc aat gag cac ttt ggc att gtc cct ctg gaa | 720 |
| Val Leu Tyr Thr Pro Ser Asn Glu His Phe Gly Ile Val Pro Leu Glu | |
| 225 230 235 240 | |
| gcc atg tac atg cag tgc cca gtc att gct gtt aat tcg ggt gga ccc | 768 |
| Ala Met Tyr Met Gln Cys Pro Val Ile Ala Val Asn Ser Gly Gly Pro | |
| 245 250 255 | |
| ttg gag tcc att gac cac agt gtc aca ggg ttt ctg tgt gag cct gac | 816 |
| Leu Glu Ser Ile Asp His Ser Val Thr Gly Phe Leu Cys Glu Pro Asp | |
| 260 265 270 | |
| ccg gtg cac ttc tca gaa gca ata gaa aag ttc atc cag aaa agt cat | 864 |
| Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Gln Lys Ser His | |
| 275 280 285 | |
| ccg tga | 870 |
| Pro * | |

<210> 52
 <211> 289
 <212> PRT
 <213> Homo sapiens

<400> 52
 Met Pro Leu Leu Lys Leu Val His Gly Ser Pro Leu Val Phe Gly Glu
 1 5 10 15
 Lys Phe Lys Leu Phe Thr Leu Val Ser Ala Cys Ile Pro Val Phe Arg
 20 25 30
 Leu Ala Arg Arg Arg Lys Lys Ile Leu Phe Tyr Cys His Phe Pro Asp
 35 40 45
 Leu Leu Leu Thr Lys Arg Asp Ser Phe Leu Lys Arg Leu Tyr Arg Ala
 50 55 60
 Pro Ile Asp Trp Ile Glu Glu Tyr Thr Thr Gly Met Ala Asp Cys Ile
 65 70 75 80
 Leu Val Asn Ser Gln Phe Thr Ala Ala Val Phe Lys Glu Thr Phe Lys
 85 90 95
 Ser Leu Ser His Ile Asp Pro Asp Val Leu Tyr Pro Ser Leu Asn Val

83

```

      100              105              110
Thr Ser Phe Asp Ser Val Val Pro Glu Lys Leu Asp Asp Leu Val Pro
      115              120              125
Lys Gly Lys Lys Phe Leu Leu Leu Ser Ile Asn Arg Tyr Glu Arg Lys
      130              135              140
Lys Asn Leu Thr Leu Ala Leu Glu Ala Leu Val Gln Leu Arg Gly Arg
      145              150              155              160
Leu Thr Ser Gln Asp Trp Glu Arg Val His Leu Ile Val Ala Gly Gly
      165              170              175
Tyr Asp Glu Arg Val Leu Glu Asn Val Glu His Tyr Gln Glu Leu Lys
      180              185              190
Lys Met Val Gln Gln Ser Asp Leu Gly Gln Tyr Val Thr Phe Leu Arg
      195              200              205
Ser Phe Ser Asp Lys Gln Lys Ile Ser Leu Leu His Ser Cys Thr Cys
      210              215              220
Val Leu Tyr Thr Pro Ser Asn Glu His Phe Gly Ile Val Pro Leu Glu
      225              230              235              240
Ala Met Tyr Met Gln Cys Pro Val Ile Ala Val Asn Ser Gly Gly Pro
      245              250              255
Leu Glu Ser Ile Asp His Ser Val Thr Gly Phe Leu Cys Glu Pro Asp
      260              265              270
Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Gln Lys Ser His
      275              280              285
Pro

```

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<210> 53
<211> 1041
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (1)...(1041)

```

```

<221> misc_feature
<222> (1)...(1041)
<223> n = A,T,C or G

```

```

<400> 53

```

```

atg cca cgg gtg ttt gtg ttt cgt gcc ctt ttg ttg gtc ctc atc ttt
Met Pro Arg Val Phe Val Phe Arg Ala Leu Leu Leu Val Leu Ile Phe
  1              5              10              15

```

48

| | |
|---|-----|
| ctc tnt gtg gtt tcc tat tgg ctt ttt tac ggg gtc cgc att ttg gac Leu Xaa Val Val Ser Tyr Trp Leu Phe Tyr Gly Val Arg Ile Leu Asp 20 25 30 | 96 |
| tct cgg gac cgg aat tac cag ggc att gtg caa tat gca gtc tcc ctt Ser Arg Asp Arg Asn Tyr Gln Gly Ile Val Gln Tyr Ala Val Ser Leu 35 40 45 | 144 |
| gtg gat gcc ctc ctc ttc atc cat tac ctg gcc atc gtc ctg ctg gag Val Asp Ala Leu Leu Phe Ile His Tyr Leu Ala Ile Val Leu Leu Glu 50 55 60 | 192 |
| ctc agg cag ctg cag ccc atg ttc acg ctg cag gtg gtc cgc tcc acc Leu Arg Gln Leu Gln Pro Met Phe Thr Leu Gln Val Val Arg Ser Thr 65 70 75 80 | 240 |
| gat ggc gag tcc cgc ttc tac agc ctg gga cac ctg agt atc cag cga Asp Gly Glu Ser Arg Phe Tyr Ser Leu Gly His Leu Ser Ile Gln Arg 85 90 95 | 288 |
| gca gca ttg gtg gtc cta gaa aat tac tac aaa gat ttc acc atc tat Ala Ala Leu Val Val Leu Glu Asn Tyr Tyr Lys Asp Phe Thr Ile Tyr 100 105 110 | 336 |
| aac cca aac ctc cta aca gcc tcc aaa ttc cga gca gcc aag cat atg Asn Pro Asn Leu Leu Thr Ala Ser Lys Phe Arg Ala Ala Lys His Met 115 120 125 | 384 |
| gcc ggg ctg aaa gtc tac aat gta gat ggc ccc agt aac aat gcc act Ala Gly Leu Lys Val Tyr Asn Val Asp Gly Pro Ser Asn Asn Ala Thr 130 135 140 | 432 |
| ggc cag tcc cgg gcc atg att gct gca gct gct cgg cgc agg gac tca Gly Gln Ser Arg Ala Met Ile Ala Ala Ala Arg Arg Arg Asp Ser 145 150 155 160 | 480 |
| agc cac aac gag ttg tat tat gaa gag gcc gaa cat gaa cgg cga gta Ser His Asn Glu Leu Tyr Tyr Glu Glu Ala Glu His Glu Arg Arg Val 165 170 175 | 528 |
| aag aag cgg aaa gca agg ctg gtg gtt gca gtg gaa gag gcc ttc atc Lys Lys Arg Lys Ala Arg Leu Val Val Ala Val Glu Glu Ala Phe Ile 180 185 190 | 576 |

85

| | |
|---|------|
| cac att cag cgt ctc cag gct gag gag cag cag aaa gcc cca ggg gag His Ile Gln Arg Leu Gln Ala Glu Glu Gln Gln Lys Ala Pro Gly Glu 195 200 205 | 624 |
| gtg atg gac cct agg gag gcc gcc cag gcg att ttc ccc tcc atg gcc Val Met Asp Pro Arg Glu Ala Ala Gln Xaa Ile Phe Pro Ser Met Ala 210 215 220 | 672 |
| agg gct ctc cag aag tac ctg cgc atc acc cgg cag cag aac tac cac Arg Ala Leu Gln Lys Tyr Leu Arg Ile Thr Arg Gln Gln Asn Tyr His 225 230 235 240 | 720 |
| agc atg gag agc atc ctg cag cac ctg gcc ttc tgc atc acc aac ggc Ser Met Glu Ser Ile Leu Gln His Leu Ala Phe Cys Ile Thr Asn Gly 245 250 255 | 768 |
| atg acc ccc aag gcc ttc cta gaa cgg tac ctc agt gcg ggc ccc acc Met Thr Pro Lys Ala Phe Leu Glu Arg Tyr Leu Ser Ala Gly Pro Thr 260 265 270 | 816 |
| ctg caa tat gac aag gac cgc tgg ctc tct aca cag tgg agg ctt gtc Leu Gln Tyr Asp Lys Asp Arg Trp Leu Ser Thr Gln Trp Arg Leu Val 275 280 285 | 864 |
| agt gat gag gct gtg act aat gga tta cgg gat gga att gtg ttc gtc Ser Asp Glu Ala Val Thr Asn Gly Leu Arg Asp Gly Ile Val Phe Val 290 295 300 | 912 |
| ctt aag tgc ttg gac ttc agc ctc gta gtc aat gtg aag aaa att cca Leu Lys Cys Leu Asp Phe Ser Leu Val Val Asn Val Lys Lys Ile Pro 305 310 315 320 | 960 |
| ttc atc ata ctc tct gaa gag ttc ata gac ccc aaa tct cac aaa ttt Phe Ile Ile Leu Ser Glu Glu Phe Ile Asp Pro Lys Ser His Lys Phe 325 330 335 | 1008 |
| gtc ctt cgc tta cag tct gag aca tcc gtt taa Val Leu Arg Leu Gln Ser Glu Thr Ser Val * | 1041 |
| 340 345 | |

<210> 54

<211> 346

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(346)

<223> Xaa = Any Amino Acid

<400> 54

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Met Pro Arg Val Phe Val Phe Arg Ala Leu Leu Leu Val Leu Ile Phe
 1           5           10           15
Leu Xaa Val Val Ser Tyr Trp Leu Phe Tyr Gly Val Arg Ile Leu Asp
          20           25           30
Ser Arg Asp Arg Asn Tyr Gln Gly Ile Val Gln Tyr Ala Val Ser Leu
          35           40           45
Val Asp Ala Leu Leu Phe Ile His Tyr Leu Ala Ile Val Leu Leu Glu
          50           55           60
Leu Arg Gln Leu Gln Pro Met Phe Thr Leu Gln Val Val Arg Ser Thr
          65           70           75           80
Asp Gly Glu Ser Arg Phe Tyr Ser Leu Gly His Leu Ser Ile Gln Arg
          85           90           95
Ala Ala Leu Val Val Leu Glu Asn Tyr Tyr Lys Asp Phe Thr Ile Tyr
          100          105          110
Asn Pro Asn Leu Leu Thr Ala Ser Lys Phe Arg Ala Ala Lys His Met
          115          120          125
Ala Gly Leu Lys Val Tyr Asn Val Asp Gly Pro Ser Asn Asn Ala Thr
          130          135          140
Gly Gln Ser Arg Ala Met Ile Ala Ala Ala Arg Arg Arg Asp Ser
          145          150          155          160
Ser His Asn Glu Leu Tyr Tyr Glu Glu Ala Glu His Glu Arg Arg Val
          165          170          175
Lys Lys Arg Lys Ala Arg Leu Val Val Ala Val Glu Glu Ala Phe Ile
          180          185          190
His Ile Gln Arg Leu Gln Ala Glu Glu Gln Gln Lys Ala Pro Gly Glu
          195          200          205
Val Met Asp Pro Arg Glu Ala Ala Gln Xaa Ile Phe Pro Ser Met Ala
          210          215          220
Arg Ala Leu Gln Lys Tyr Leu Arg Ile Thr Arg Gln Gln Asn Tyr His
          225          230          235          240
Ser Met Glu Ser Ile Leu Gln His Leu Ala Phe Cys Ile Thr Asn Gly
          245          250          255
Met Thr Pro Lys Ala Phe Leu Glu Arg Tyr Leu Ser Ala Gly Pro Thr
          260          265          270
Leu Gln Tyr Asp Lys Asp Arg Trp Leu Ser Thr Gln Trp Arg Leu Val
          275          280          285

```

87

Ser Asp Glu Ala Val Thr Asn Gly Leu Arg Asp Gly Ile Val Phe Val
 290 295 300
 Leu Lys Cys Leu Asp Phe Ser Leu Val Val Asn Val Lys Lys Ile Pro
 305 310 315 320
 Phe Ile Ile Leu Ser Glu Glu Phe Ile Asp Pro Lys Ser His Lys Phe
 325 330 335
 Val Leu Arg Leu Gln Ser Glu Thr Ser Val
 340 345

<210> 55

<211> 195

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(195)

<400> 55

atg gcc ttt ctc gcc aag aaa ggg tac cgg cat gac agc tca aca gca 48
 Met Ala Phe Leu Ala Lys Lys Gly Tyr Arg His Asp Ser Ser Thr Ala
 1 5 10 15

gtg gcc ggc agc ccc cga ggc cat ggg cag agc cgc gag aca acc cag 96
 Val Ala Gly Ser Pro Arg Gly His Gly Gln Ser Arg Glu Thr Thr Gln
 20 25 30

gaa cgc agg aag aag gaa gcc aac aag gcg aca aga gcc aac cac aac 144
 Glu Arg Arg Lys Lys Glu Ala Asn Lys Ala Thr Arg Ala Asn His Asn
 35 40 45

cgg aga acc atg gcc gac cgc aag agg agc aaa ggc atg atc cca tcc 192
 Arg Arg Thr Met Ala Asp Arg Lys Arg Ser Lys Gly Met Ile Pro Ser
 50 55 60

tga 195
 *

<210> 56

<211> 64

<212> PRT

<213> Homo sapiens

<400> 56

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Phe | Leu | Ala | Lys | Lys | Gly | Tyr | Arg | His | Asp | Ser | Ser | Thr | Ala |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Val | Ala | Gly | Ser | Pro | Arg | Gly | His | Gly | Gln | Ser | Arg | Glu | Thr | Thr | Gln |
| | | | 20 | | | | 25 | | | | | | 30 | | |
| Glu | Arg | Arg | Lys | Lys | Glu | Ala | Asn | Lys | Ala | Thr | Arg | Ala | Asn | His | Asn |
| | | 35 | | | | 40 | | | | | 45 | | | | |
| Arg | Arg | Thr | Met | Ala | Asp | Arg | Lys | Arg | Ser | Lys | Gly | Met | Ile | Pro | Ser |
| 50 | | | | | | 55 | | | | | 60 | | | | |

<210> 57

<211> 1011

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1011)

<400> 57

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| atg | ggt | aca | tct | gat | tcc | cac | cac | gcg | ggg | ctc | agc | tta | gtt | agc | agg | 48 |
| Met | Gly | Thr | Ser | Asp | Ser | His | His | Ala | Gly | Leu | Ser | Leu | Val | Ser | Arg | |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | | |
| aga | cct | tca | ggt | ggt | gct | gct | ggg | gaa | cgg | gag | ctg | gat | gag | gtt | gat | 96 |
| Arg | Pro | Ser | Gly | Gly | Ala | Ala | Gly | Glu | Arg | Glu | Leu | Asp | Glu | Val | Asp | |
| | | | 20 | | | | 25 | | | | | 30 | | | | |
| atg | tca | gat | ctc | tct | cca | gaa | gag | caa | tgg | agg | gtc | gag | cac | gca | cgc | 144 |
| Met | Ser | Asp | Leu | Ser | Pro | Glu | Glu | Gln | Trp | Arg | Val | Glu | His | Ala | Arg | |
| | | 35 | | | | 40 | | | | | 45 | | | | | |
| atg | cat | gcc | aag | cac | cgt | ggc | cat | gaa | gct | atg | cat | gct | gaa | atg | gtc | 192 |
| Met | His | Ala | Lys | His | Arg | Gly | His | Glu | Ala | Met | His | Ala | Glu | Met | Val | |
| | 50 | | | | | 55 | | | | 60 | | | | | | |
| ctc | atc | ctc | atc | gca | acc | ttg | gtg | gtg | gcc | cag | ctg | ctc | ctg | gtg | cag | 240 |
| Leu | Ile | Leu | Ile | Ala | Thr | Leu | Val | Val | Ala | Gln | Leu | Leu | Leu | Val | Gln | |
| 65 | | | | 70 | | | | 75 | | | | | | 80 | | |
| tgg | aag | cag | agg | cac | cca | cgc | tcc | tac | aat | atg | gtg | acc | ctc | ttt | cag | 288 |
| Trp | Lys | Gln | Arg | His | Pro | Arg | Ser | Tyr | Asn | Met | Val | Thr | Leu | Phe | Gln | |
| | | | | 85 | | | | 90 | | | | | | 95 | | |

| | |
|---|-----|
| atg tgg gtt gtt ccc ctc tat ttc aca gtg aag ctg cac tgg tgg agg Met Trp Val Val Pro Leu Tyr Phe Thr Val Lys Leu His Trp Trp Arg 100 105 110 | 336 |
| ttc cta gtg atc tgg atc ttg ttc tct gct gtc aca gcc ttt gtt acc Phe Leu Val Ile Trp Ile Leu Phe Ser Ala Val Thr Ala Phe Val Thr 115 120 125 | 384 |
| ttc cga gcc acc cga aaa cct cta gta cag aca acc cca agg ttg gtt Phe Arg Ala Thr Arg Lys Pro Leu Val Gln Thr Thr Pro Arg Leu Val 130 135 140 | 432 |
| tat aag tgg ttc ctg cta atc tat aaa atc agc tat gcc act ggc att Tyr Lys Trp Phe Leu Leu Ile Tyr Lys Ile Ser Tyr Ala Thr Gly Ile 145 150 155 160 | 480 |
| gtt ggc tac atg gct gtc atg ttt acc ctc ttt ggt ctt aac tta tta Val Gly Tyr Met Ala Val Met Phe Thr Leu Phe Gly Leu Asn Leu Leu 165 170 175 | 528 |
| ttc aag atc aaa cca gaa gat gcc atg gac ttt ggc atc tcc ctt ctc Phe Lys Ile Lys Pro Glu Asp Ala Met Asp Phe Gly Ile Ser Leu Leu 180 185 190 | 576 |
| ttc tat ggc ctc tac tat gga gtt ctg gaa cgg gac ttt gca gaa atg Phe Tyr Gly Leu Tyr Tyr Gly Val Leu Glu Arg Asp Phe Ala Glu Met 195 200 205 | 624 |
| tgt gca gac tac atg gca tct acc ata ggg ttc tac agc gag tcg ggc Cys Ala Asp Tyr Met Ala Ser Thr Ile Gly Phe Tyr Ser Glu Ser Gly 210 215 220 | 672 |
| atg cct acc aaa cat ctt tca gac agt gtg tgt gct gtg tgt ggg cag Met Pro Thr Lys His Leu Ser Asp Ser Val Cys Ala Val Cys Gly Gln 225 230 235 240 | 720 |
| cag atc ttt gtg gac gtc agt gaa gag ggg atc att gag aac acg tat Gln Ile Phe Val Asp Val Ser Glu Glu Gly Ile Ile Glu Asn Thr Tyr 245 250 255 | 768 |
| agg ctg tcc tgc aat cat gtc ttc cac gag ttc tgc atc cgt ggc tgg Arg Leu Ser Cys Asn His Val Phe His Glu Phe Cys Ile Arg Gly Trp 260 265 270 | 816 |

| | |
|---|------|
| tgc atc gtg gga aag aag caa acg tgt ccc tac tgc aaa gag aag gta | 864 |
| Cys Ile Val Gly Lys Lys Gln Thr Cys Pro Tyr Cys Lys Glu Lys Val | |
| 275 280 285 | |
| gac ctc aag agg atg ttc agc aat ccc tgg gag agg cct cac gtc atg | 912 |
| Asp Leu Lys Arg Met Phe Ser Asn Pro Trp Glu Arg Pro His Val Met | |
| 290 295 300 | |
| tat ggg caa ctg ctg gac tgg ctt cga tac ttg gta gcc tgg cag cct | 960 |
| Tyr Gly Gln Leu Leu Asp Trp Leu Arg Tyr Leu Val Ala Trp Gln Pro | |
| 305 310 315 320 | |
| gtc atc att ggt gta gtc caa ggc atc aac tac atc ctg ggc ctg gaa | 1008 |
| Val Ile Ile Gly Val Val Gln Gly Ile Asn Tyr Ile Leu Gly Leu Glu | |
| 325 330 335 | |
| tag | 1011 |
| * | |

<210> 58
 <211> 336
 <212> PRT
 <213> Homo sapiens

<400> 58

| | |
|---|--|
| Met Gly Thr Ser Asp Ser His His Ala Gly Leu Ser Leu Val Ser Arg | |
| 1 5 10 15 | |
| Arg Pro Ser Gly Gly Ala Ala Gly Glu Arg Glu Leu Asp Glu Val Asp | |
| 20 25 30 | |
| Met Ser Asp Leu Ser Pro Glu Glu Gln Trp Arg Val Glu His Ala Arg | |
| 35 40 45 | |
| Met His Ala Lys His Arg Gly His Glu Ala Met His Ala Glu Met Val | |
| 50 55 60 | |
| Leu Ile Leu Ile Ala Thr Leu Val Val Ala Gln Leu Leu Leu Val Gln | |
| 65 70 75 80 | |
| Trp Lys Gln Arg His Pro Arg Ser Tyr Asn Met Val Thr Leu Phe Gln | |
| 85 90 95 | |
| Met Trp Val Val Pro Leu Tyr Phe Thr Val Lys Leu His Trp Trp Arg | |
| 100 105 110 | |
| Phe Leu Val Ile Trp Ile Leu Phe Ser Ala Val Thr Ala Phe Val Thr | |
| 115 120 125 | |

91

Phe Arg Ala Thr Arg Lys Pro Leu Val Gln Thr Thr Pro Arg Leu Val
 130 135 140
 Tyr Lys Trp Phe Leu Leu Ile Tyr Lys Ile Ser Tyr Ala Thr Gly Ile
 145 150 155 160
 Val Gly Tyr Met Ala Val Met Phe Thr Leu Phe Gly Leu Asn Leu Leu
 165 170 175
 Phe Lys Ile Lys Pro Glu Asp Ala Met Asp Phe Gly Ile Ser Leu Leu
 180 185 190
 Phe Tyr Gly Leu Tyr Tyr Gly Val Leu Glu Arg Asp Phe Ala Glu Met
 195 200 205
 Cys Ala Asp Tyr Met Ala Ser Thr Ile Gly Phe Tyr Ser Glu Ser Gly
 210 215 220
 Met Pro Thr Lys His Leu Ser Asp Ser Val Cys Ala Val Cys Gly Gln
 225 230 235 240
 Gln Ile Phe Val Asp Val Ser Glu Glu Gly Ile Ile Glu Asn Thr Tyr
 245 250 255
 Arg Leu Ser Cys Asn His Val Phe His Glu Phe Cys Ile Arg Gly Trp
 260 265 270
 Cys Ile Val Gly Lys Lys Gln Thr Cys Pro Tyr Cys Lys Glu Lys Val
 275 280 285
 Asp Leu Lys Arg Met Phe Ser Asn Pro Trp Glu Arg Pro His Val Met
 290 295 300
 Tyr Gly Gln Leu Leu Asp Trp Leu Arg Tyr Leu Val Ala Trp Gln Pro
 305 310 315 320
 Val Ile Ile Gly Val Val Gln Gly Ile Asn Tyr Ile Leu Gly Leu Glu
 325 330 335

<210> 59
 <211> 393
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(393)

<221> misc_feature
 <222> (1)...(393)
 <223> n = A,T,C or G

<400> 59

atg ctg gac ttg cag aag cag ctg ggc aga tnc cag ggn gcc ana ttt
 Met Leu Asp Leu Gln Lys Gln Leu Gly Arg Xaa Gln Xaa Ala Xaa Phe
 1 5 10 15

48

```

ccc ggc acc ttc gtg ggc acc aca gag ccc gcc tcc cca ccc ctg agc      96
Pro Gly Thr Phe Val Gly Thr Thr Glu Pro Ala Ser Pro Pro Leu Ser
          20                25                30

agc acc tca ccc acc act gct gcg gcc act atg cct gtg gtg ccc tct      144
Ser Thr Ser Pro Thr Thr Ala Ala Ala Thr Met Pro Val Val Pro Ser
          35                40                45

gtg gcc agc ctg gcc cct ccg ggg gag gcc tcg ctc tgc ctg gaa gag      192
Val Ala Ser Leu Ala Pro Pro Gly Glu Ala Ser Leu Cys Leu Glu Glu
          50                55                60

gtg gcc ccc cct gcc agt ggg acc cgc aaa gct cgg gtg ctc tat gac      240
Val Ala Pro Pro Ala Ser Gly Thr Arg Lys Ala Arg Val Leu Tyr Asp
          65                70                75                80

tac gag gca gcc gac agc agt gag ctg gcc ctg ctg gct gat gag ctc      288
Tyr Glu Ala Ala Asp Ser Ser Glu Leu Ala Leu Leu Ala Asp Glu Leu
          85                90                95

atc act gtc tac agc ctg cct ggc atg gac cct gac tgg ctc att ggc      336
Ile Thr Val Tyr Ser Leu Pro Gly Met Asp Pro Asp Trp Leu Ile Gly
          100                105                110

gag aga ggc aac aag aag ggc aag gtc cct gtc acc tac ttg gaa ctg      384
Glu Arg Gly Asn Lys Lys Gly Lys Val Pro Val Thr Tyr Leu Glu Leu
          115                120                125

ctc agc tag      393
Leu Ser *
          130

```

<210> 60

<211> 130

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(130)

<223> Xaa = Any Amino Acid

<400> 60

```

Met Leu Asp Leu Gln Lys Gln Leu Gly Arg Xaa Gln Xaa Ala Xaa Phe
 1           5           10           15
Pro Gly Thr Phe Val Gly Thr Thr Glu Pro Ala Ser Pro Pro Leu Ser
 20           25           30
Ser Thr Ser Pro Thr Thr Ala Ala Thr Met Pro Val Val Pro Ser
 35           40           45
Val Ala Ser Leu Ala Pro Pro Gly Glu Ala Ser Leu Cys Leu Glu Glu
 50           55           60
Val Ala Pro Pro Ala Ser Gly Thr Arg Lys Ala Arg Val Leu Tyr Asp
 65           70           75           80
Tyr Glu Ala Ala Asp Ser Ser Glu Leu Ala Leu Leu Ala Asp Glu Leu
 85           90           95
Ile Thr Val Tyr Ser Leu Pro Gly Met Asp Pro Asp Trp Leu Ile Gly
 100          105          110
Glu Arg Gly Asn Lys Lys Gly Lys Val Pro Val Thr Tyr Leu Glu Leu
 115          120          125
Leu Ser
 130

```

<210> 61

<211> 1383

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1383)

<221> misc_feature

<222> (1)...(1383)

<223> n = A,T,C or G

<400> 61

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atg gcc ccg ggt cgc gcg gtg gcc ggg ctc ctg ttg ctg gcg gcc gcc      48
Met Ala Pro Gly Arg Ala Val Ala Gly Leu Leu Leu Leu Ala Ala Ala
 1           5           10           15

gnc ctc gga gga gtg gcg gag ggg cca ggg cta gcc ttc agc gag gat      96
Xaa Leu Gly Gly Val Ala Glu Gly Pro Gly Leu Ala Phe Ser Glu Asp
 20           25           30

gtg ctg agc gtg ttc ggc gcg aat ctg agc ctg tcg gcg gcg cag ctc      144
Val Leu Ser Val Phe Gly Ala Asn Leu Ser Leu Ser Ala Ala Gln Leu

```

94

| | | | |
|---|-----------------|-----|-----|
| 35 | 40 | 45 | |
| cag cac ttg ctg gag cag atg gga gcc gcc tcc cgc | gtg ggc gtc ccg | 192 | |
| Gln His Leu Leu Glu Gln Met Gly Ala Ala Ser Arg Val Gly Val Pro | | | |
| 50 | 55 | 60 | |
| gag cct ggc cag ctg cac ttc aac cag tgt tta act gct gaa gag atc | 240 | | |
| Glu Pro Gly Gln Leu His Phe Asn Gln Cys Leu Thr Ala Glu Glu Ile | | | |
| 65 | 70 | 75 | 80 |
| ttt tcc ctt cat ggc ttt tca aat gct acc caa ata acc agc tcc aaa | 288 | | |
| Phe Ser Leu His Gly Phe Ser Asn Ala Thr Gln Ile Thr Ser Ser Lys | | | |
| 85 | 90 | 95 | |
| ttc tct gtc atc tgt cca gca gtc tta cag caa ttg aac ttt cac cca | 336 | | |
| Phe Ser Val Ile Cys Pro Ala Val Leu Gln Gln Leu Asn Phe His Pro | | | |
| 100 | 105 | 110 | |
| tgt gag gat cgg ccc aag cac aaa aca aga cca agt cat tca gaa gtt | 384 | | |
| Cys Glu Asp Arg Pro Lys His Lys Thr Arg Pro Ser His Ser Glu Val | | | |
| 115 | 120 | 125 | |
| tgg gga tat gga ttc ctg tca gtg acg att att aat ctg gca tct ctc | 432 | | |
| Trp Gly Tyr Gly Phe Leu Ser Val Thr Ile Ile Asn Leu Ala Ser Leu | | | |
| 130 | 135 | 140 | |
| ctc gga ttg att ttg act cca ctg ata aag aaa tct tat ttc cca aag | 480 | | |
| Leu Gly Leu Ile Leu Thr Pro Leu Ile Lys Lys Ser Tyr Phe Pro Lys | | | |
| 145 | 150 | 155 | 160 |
| att ttg acc ttt ttt gtg ggg ctg gct att ggg act ctt ttt tca aat | 528 | | |
| Ile Leu Thr Phe Phe Val Gly Leu Ala Ile Gly Thr Leu Phe Ser Asn | | | |
| 165 | 170 | 175 | |
| gca att ttc caa ctt att cca gag gca ttt gga ttt gat ccc aaa gtc | 576 | | |
| Ala Ile Phe Gln Leu Ile Pro Glu Ala Phe Gly Phe Asp Pro Lys Val | | | |
| 180 | 185 | 190 | |
| gac agt tat gtt gag aag gca gtt gct gtg ttt ggt gga ttt tac cta | 624 | | |
| Asp Ser Tyr Val Glu Lys Ala Val Ala Val Phe Gly Gly Phe Tyr Leu | | | |
| 195 | 200 | 205 | |
| ctt ttc ttt ttt gaa aga atg cta aag atg tta tta aag aca tat ggt | 672 | | |
| Leu Phe Phe Phe Glu Arg Met Leu Lys Met Leu Leu Lys Thr Tyr Gly | | | |

| 210 | 215 | 220 | |
|---|-----|-----|------|
| cag aat ggt cat acc cac ttt gga aat gat aac ttt ggt cct caa gaa | | | 720 |
| Gln Asn Gly His Thr His Phe Gly Asn Asp Asn Phe Gly Pro Gln Glu | | | |
| 225 | 230 | 235 | 240 |
| aaa act cat caa cct aaa gca tta cct gcc atc aat ggt gtg aca tgc | | | 768 |
| Lys Thr His Gln Pro Lys Ala Leu Pro Ala Ile Asn Gly Val Thr Cys | | | |
| | 245 | 250 | 255 |
| tat gca aat cct gct gtc aca gaa gct aat gga cat atc cat ttt gat | | | 816 |
| Tyr Ala Asn Pro Ala Val Thr Glu Ala Asn Gly His Ile His Phe Asp | | | |
| | 260 | 265 | 270 |
| aat gtc agt gtg gta tct cta cag gat gga aaa aaa gag cca agt tca | | | 864 |
| Asn Val Ser Val Val Ser Leu Gln Asp Gly Lys Lys Glu Pro Ser Ser | | | |
| | 275 | 280 | 285 |
| tgt acc tgt ttg aag ggg ccc aaa ctg tca gaa ata ggg acg att gcc | | | 912 |
| Cys Thr Cys Leu Lys Gly Pro Lys Leu Ser Glu Ile Gly Thr Ile Ala | | | |
| | 290 | 295 | 300 |
| tgg atg ata acg ctc tgc gat gcc ctc cac aat ttc atc gat ggc ctg | | | 960 |
| Trp Met Ile Thr Leu Cys Asp Ala Leu His Asn Phe Ile Asp Gly Leu | | | |
| | 305 | 310 | 315 |
| gcg att ggg gct tcc tgc acc ttg tct ctc ctt cag gga ctc agt act | | | 1008 |
| Ala Ile Gly Ala Ser Cys Thr Leu Ser Leu Leu Gln Gly Leu Ser Thr | | | |
| | 325 | 330 | 335 |
| tcc ata gca atc cta tgt gag gag ttt ccc cac gag tta gga gac ttt | | | 1056 |
| Ser Ile Ala Ile Leu Cys Glu Glu Phe Pro His Glu Leu Gly Asp Phe | | | |
| | 340 | 345 | 350 |
| gtg atc cta ctc aat gca ggg atg agc act cga caa gcc ttg cta ttc | | | 1104 |
| Val Ile Leu Leu Asn Ala Gly Met Ser Thr Arg Gln Ala Leu Leu Phe | | | |
| | 355 | 360 | 365 |
| aac ttc ctt tct gca tgt tcc tgc tat gtt ggg cta gct ttt ggc att | | | 1152 |
| Asn Phe Leu Ser Ala Cys Ser Cys Tyr Val Gly Leu Ala Phe Gly Ile | | | |
| | 370 | 375 | 380 |
| ttg gtg ggc aac aat ttc gct cca aat att ata ttt gca ctt gct gga | | | 1200 |
| Leu Val Gly Asn Asn Phe Ala Pro Asn Ile Ile Phe Ala Leu Ala Gly | | | |

96

| | | | | |
|---|-----|-----|-----|------|
| 385 | 390 | 395 | 400 | |
| ggc atg ttc ctc tat att tct ctg gca gat atg ttt cca gag atg aat | | | | 1248 |
| Gly Met Phe Leu Tyr Ile Ser Leu Ala Asp Met Phe Pro Glu Met Asn | | | | |
| | 405 | 410 | 415 | |
| gat atg ctg aga gaa aag gta act gga aga aaa acc gat ttc acc ttc | | | | 1296 |
| Asp Met Leu Arg Glu Lys Val Thr Gly Arg Lys Thr Asp Phe Thr Phe | | | | |
| | 420 | 425 | 430 | |
| ttc atg att cag aat gct gga atg tta act gga ttc aca gcc att cta | | | | 1344 |
| Phe Met Ile Gln Asn Ala Gly Met Leu Thr Gly Phe Thr Ala Ile Leu | | | | |
| | 435 | 440 | 445 | |
| ctc att acc ttg tat gca gga gaa atc gaa ttg gag taa | | | | 1383 |
| Leu Ile Thr Leu Tyr Ala Gly Glu Ile Glu Leu Glu * | | | | |
| | 450 | 455 | 460 | |

<210> 62

<211> 460

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(460)

<223> Xaa = Any Amino Acid

<400> 62

| | | | | |
|---|-----|-----|-----|--|
| Met Ala Pro Gly Arg Ala Val Ala Gly Leu Leu Leu Leu Ala Ala Ala | | | | |
| 1 | 5 | 10 | 15 | |
| Xaa Leu Gly Gly Val Ala Glu Gly Pro Gly Leu Ala Phe Ser Glu Asp | | | | |
| | 20 | 25 | 30 | |
| Val Leu Ser Val Phe Gly Ala Asn Leu Ser Leu Ser Ala Ala Gln Leu | | | | |
| | 35 | 40 | 45 | |
| Gln His Leu Leu Glu Gln Met Gly Ala Ala Ser Arg Val Gly Val Pro | | | | |
| | 50 | 55 | 60 | |
| Glu Pro Gly Gln Leu His Phe Asn Gln Cys Leu Thr Ala Glu Glu Ile | | | | |
| 65 | 70 | 75 | 80 | |
| Phe Ser Leu His Gly Phe Ser Asn Ala Thr Gln Ile Thr Ser Ser Lys | | | | |
| | 85 | 90 | 95 | |
| Phe Ser Val Ile Cys Pro Ala Val Leu Gln Gln Leu Asn Phe His Pro | | | | |
| | 100 | 105 | 110 | |

Cys Glu Asp Arg Pro Lys His Lys Thr Arg Pro Ser His Ser Glu Val
 115 120 125
 Trp Gly Tyr Gly Phe Leu Ser Val Thr Ile Ile Asn Leu Ala Ser Leu
 130 135 140
 Leu Gly Leu Ile Leu Thr Pro Leu Ile Lys Lys Ser Tyr Phe Pro Lys
 145 150 155 160
 Ile Leu Thr Phe Phe Val Gly Leu Ala Ile Gly Thr Leu Phe Ser Asn
 165 170 175
 Ala Ile Phe Gln Leu Ile Pro Glu Ala Phe Gly Phe Asp Pro Lys Val
 180 185 190
 Asp Ser Tyr Val Glu Lys Ala Val Ala Val Phe Gly Gly Phe Tyr Leu
 195 200 205
 Leu Phe Phe Phe Glu Arg Met Leu Lys Met Leu Leu Lys Thr Tyr Gly
 210 215 220
 Gln Asn Gly His Thr His Phe Gly Asn Asp Asn Phe Gly Pro Gln Glu
 225 230 235 240
 Lys Thr His Gln Pro Lys Ala Leu Pro Ala Ile Asn Gly Val Thr Cys
 245 250 255
 Tyr Ala Asn Pro Ala Val Thr Glu Ala Asn Gly His Ile His Phe Asp
 260 265 270
 Asn Val Ser Val Val Ser Leu Gln Asp Gly Lys Lys Glu Pro Ser Ser
 275 280 285
 Cys Thr Cys Leu Lys Gly Pro Lys Leu Ser Glu Ile Gly Thr Ile Ala
 290 295 300
 Trp Met Ile Thr Leu Cys Asp Ala Leu His Asn Phe Ile Asp Gly Leu
 305 310 315 320
 Ala Ile Gly Ala Ser Cys Thr Leu Ser Leu Leu Gln Gly Leu Ser Thr
 325 330 335
 Ser Ile Ala Ile Leu Cys Glu Glu Phe Pro His Glu Leu Gly Asp Phe
 340 345 350
 Val Ile Leu Leu Asn Ala Gly Met Ser Thr Arg Gln Ala Leu Leu Phe
 355 360 365
 Asn Phe Leu Ser Ala Cys Ser Cys Tyr Val Gly Leu Ala Phe Gly Ile
 370 375 380
 Leu Val Gly Asn Asn Phe Ala Pro Asn Ile Ile Phe Ala Leu Ala Gly
 385 390 395 400
 Gly Met Phe Leu Tyr Ile Ser Leu Ala Asp Met Phe Pro Glu Met Asn
 405 410 415
 Asp Met Leu Arg Glu Lys Val Thr Gly Arg Lys Thr Asp Phe Thr Phe
 420 425 430
 Phe Met Ile Gln Asn Ala Gly Met Leu Thr Gly Phe Thr Ala Ile Leu
 435 440 445
 Leu Ile Thr Leu Tyr Ala Gly Glu Ile Glu Leu Glu
 450 455 460

<210> 63
 <211> 378
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(378)

<400> 63

| | |
|---|-----|
| atg ctg aca gaa gtc atg gag gtc tgg cat ggc tta gtg atc gcg gtg | 48 |
| Met Leu Thr Glu Val Met Glu Val Trp His Gly Leu Val Ile Ala Val | |
| 1 5 10 15 | |
| gtg tcc ctc ttc ctg cag gcc tgc ttc ctc acc gcc atc aac tac ctg | 96 |
| Val Ser Leu Phe Leu Gln Ala Cys Phe Leu Thr Ala Ile Asn Tyr Leu | |
| 20 25 30 | |
| ctc agc agg cac atg gcc cac aag agt gaa cag ata ctg aaa gcg gcc | 144 |
| Leu Ser Arg His Met Ala His Lys Ser Glu Gln Ile Leu Lys Ala Ala | |
| 35 40 45 | |
| agt ctc cag gtt ccc agg ccc agc cct ggc cac cat cat cca cct gct | 192 |
| Ser Leu Gln Val Pro Arg Pro Ser Pro Gly His His His Pro Pro Ala | |
| 50 55 60 | |
| gtc aaa gag atg aag gag act cag aca gag aga gac atc cca atg tct | 240 |
| Val Lys Glu Met Lys Glu Thr Gln Thr Glu Arg Asp Ile Pro Met Ser | |
| 65 70 75 80 | |
| gat tcc ctt tac agg cat gac agc gac aca ccc tca gat agc ttg gat | 288 |
| Asp Ser Leu Tyr Arg His Asp Ser Asp Thr Pro Ser Asp Ser Leu Asp | |
| 85 90 95 | |
| agc tcc tgc agt tcg cct cct gcc tgc cag gcc aca gag gat gtg gat | 336 |
| Ser Ser Cys Ser Ser Pro Pro Ala Cys Gln Ala Thr Glu Asp Val Asp | |
| 100 105 110 | |
| tac aca caa gtc gtc ttt tct gac cct gga gaa cta aaa tga | 378 |
| Tyr Thr Gln Val Val Phe Ser Asp Pro Gly Glu Leu Lys * | |
| 115 120 125 | |

<210> 64
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 64
 Met Leu Thr Glu Val Met Glu Val Trp His Gly Leu Val Ile Ala Val
 1 5 10 15
 Val Ser Leu Phe Leu Gln Ala Cys Phe Leu Thr Ala Ile Asn Tyr Leu
 20 25 30
 Leu Ser Arg His Met Ala His Lys Ser Glu Gln Ile Leu Lys Ala Ala
 35 40 45
 Ser Leu Gln Val Pro Arg Pro Ser Pro Gly His His His Pro Pro Ala
 50 55 60
 Val Lys Glu Met Lys Glu Thr Gln Thr Glu Arg Asp Ile Pro Met Ser
 65 70 75 80
 Asp Ser Leu Tyr Arg His Asp Ser Asp Thr Pro Ser Asp Ser Leu Asp
 85 90 95
 Ser Ser Cys Ser Ser Pro Pro Ala Cys Gln Ala Thr Glu Asp Val Asp
 100 105 110
 Tyr Thr Gln Val Val Phe Ser Asp Pro Gly Glu Leu Lys
 115 120 125

<210> 65
 <211> 519
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(519)

<400> 65
 atg ctg aca gaa gtc atg gag gtc tgg cat ggc tta gtg atc gcg gtg 48
 Met Leu Thr Glu Val Met Glu Val Trp His Gly Leu Val Ile Ala Val
 1 5 10 15
 gtg tcc ctc ttc ctg cag gcc tgc ttc ctc acc gcc atc aac tac ctg 96
 Val Ser Leu Phe Leu Gln Ala Cys Phe Leu Thr Ala Ile Asn Tyr Leu
 20 25 30
 ctc agc agg cac atg gcc cac aag agt gaa cag ata ctg aaa gcg gcc 144
 Leu Ser Arg His Met Ala His Lys Ser Glu Gln Ile Leu Lys Ala Ala
 35 40 45

100

```

agt ctc cag gtt ccc agg ccc agc cct ggc cac cat cat cca cct gct      192
Ser Leu Gln Val Pro Arg Pro Ser Pro Gly His His His Pro Pro Ala
      50              55              60

gtc aaa gag atg aag gag act cag aca gag aga gac atc cca atg tct      240
Val Lys Glu Met Lys Glu Thr Gln Thr Glu Arg Asp Ile Pro Met Ser
      65              70              75              80

gat tcc ctt tac agg cat gac agc gac aca ccc tca gat agc ttg gat      288
Asp Ser Leu Tyr Arg His Asp Ser Asp Thr Pro Ser Asp Ser Leu Asp
              85              90              95

agc tcc tgc agt tgc cct cct gcc tgc cag gcc aca gag gat gtg gat      336
Ser Ser Cys Ser Ser Pro Pro Ala Cys Gln Ala Thr Glu Asp Val Asp
              100              105              110

tac aca caa gtc gtc ttt tct gac cct gga gaa cta aaa aat gac tcc      384
Tyr Thr Gln Val Val Phe Ser Asp Pro Gly Glu Leu Lys Asn Asp Ser
              115              120              125

ccg ctg gac tat gag aac ata aag gaa atc aca gat tat gtc aat gtc      432
Pro Leu Asp Tyr Glu Asn Ile Lys Glu Ile Thr Asp Tyr Val Asn Val
              130              135              140

aat cca gaa aga cac aag ccc agt ttc tgg tat ttt gtc aac cct gct      480
Asn Pro Glu Arg His Lys Pro Ser Phe Trp Tyr Phe Val Asn Pro Ala
      145              150              155              160

ctg tct gag cca gcg gaa tat gat caa gtg gcc atg tga      519
Leu Ser Glu Pro Ala Glu Tyr Asp Gln Val Ala Met *
              165              170

```

<210> 66
 <211> 172
 <212> PRT
 <213> Homo sapiens

<400> 66
 Met Leu Thr Glu Val Met Glu Val Trp His Gly Leu Val Ile Ala Val
 1 5 10 15
 Val Ser Leu Phe Leu Gln Ala Cys Phe Leu Thr Ala Ile Asn Tyr Leu
 20 25 30

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ser | Arg | His | Met | Ala | His | Lys | Ser | Glu | Gln | Ile | Leu | Lys | Ala | Ala |
| | 35 | | | | | | 40 | | | | | 45 | | | |
| Ser | Leu | Gln | Val | Pro | Arg | Pro | Ser | Pro | Gly | His | His | Pro | Pro | Ala | |
| | 50 | | | | | 55 | | | | 60 | | | | | |
| Val | Lys | Glu | Met | Lys | Glu | Thr | Gln | Thr | Glu | Arg | Asp | Ile | Pro | Met | Ser |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Asp | Ser | Leu | Tyr | Arg | His | Asp | Ser | Asp | Thr | Pro | Ser | Asp | Ser | Leu | Asp |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Ser | Ser | Cys | Ser | Ser | Pro | Pro | Ala | Cys | Gln | Ala | Thr | Glu | Asp | Val | Asp |
| | | | | 100 | | | | 105 | | | | | 110 | | |
| Tyr | Thr | Gln | Val | Val | Phe | Ser | Asp | Pro | Gly | Glu | Leu | Lys | Asn | Asp | Ser |
| | | | | 115 | | | 120 | | | | | 125 | | | |
| Pro | Leu | Asp | Tyr | Glu | Asn | Ile | Lys | Glu | Ile | Thr | Asp | Tyr | Val | Asn | Val |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Asn | Pro | Glu | Arg | His | Lys | Pro | Ser | Phe | Trp | Tyr | Phe | Val | Asn | Pro | Ala |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Leu | Ser | Glu | Pro | Ala | Glu | Tyr | Asp | Gln | Val | Ala | Met | | | | |
| | | | | 165 | | | | 170 | | | | | | | |

```
<210> 67.  
<211> 393  
<212> DNA  
<213> Homo sapiens
```

<220>
<221> CDS
<222> (1)...(393)

| | | | | | | | | | | | | | | | | |
|----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> 67 | | | | | | | | | | | | | | | | |
| atg | caa | gca | gag | gct | ggg | gac | ctc | agc | aca | gcc | ctg | gag | agg | ttt | ggc | 48 |
| Met | Gln | Ala | Glu | Ala | Gly | Asp | Leu | Ser | Thr | Ala | Leu | Glu | Arg | Phe | Gly | |
| 1 | | 5 | | | 10 | | | | | 15 | | | | | | |
| | | | | | | | | | | | | | | | | |
| caa | gcc | atc | tgc | ctg | ctg | cct | gag | agg | gct | tca | gcc | tac | aac | aac | cgt | 96 |
| Gln | Ala | Ile | Cys | Leu | Leu | Pro | Glu | Arg | Ala | Ser | Ala | Tyr | Asn | Asn | Arg | |
| 20 | | | 25 | | | | | 30 | | | | | | | | |
| | | | | | | | | | | | | | | | | |
| gcc | cag | gcc | cgg | cga | ctc | cag | gga | gac | gtg | gca | ggc | gcc | ctg | gag | gat | 144 |
| Ala | Gln | Ala | Arg | Arg | Leu | Gln | Gly | Asp | Val | Ala | Gly | Ala | Leu | Glu | Asp | |
| 35 | | | 40 | | | | | 45 | | | | | | | | |
| | | | | | | | | | | | | | | | | |
| ctg | gaa | cgc | gcg | gtg | gag | ctg | agc | ggc | ggc | cgg | ggc | cgc | gcc | gcc | cgc | 192 |
| Leu | Glu | Arg | Ala | Val | Glu | Leu | Ser | Gly | Gly | Arg | Gly | Arg | Ala | Ala | Arg | |
| 50 | | 55 | | | | | 60 | | | | | | | | | |

102

cag agc ttt gtg cag cgc gga ctc ctg gcg cgg ctg cag ggc cga gac 240
 Gln Ser Phe Val Gln Arg Gly Leu Leu Ala Arg Leu Gln Gly Arg Asp
 65 70 75 80
 gac gac gcc cgc agg gac ttc gag agg gcg gca cgg ctg ggc agc ccc 288
 Asp Asp Ala Arg Arg Asp Phe Glu Arg Ala Ala Arg Leu Gly Ser Pro
 85 90 95
 ttc gcg cgg cgc cag ctg gtg ctg ctc aac ccc tac gcc gcg ctg tgc 336
 Phe Ala Arg Arg Gln Leu Val Leu Leu Asn Pro Tyr Ala Ala Leu Cys
 100 105 110
 aac cgc atg ctg gcc gac atg atg ggg cag ctg cgc cgc ccc cgt gac 384
 Asn Arg Met Leu Ala Asp Met Met Gly Gln Leu Arg Arg Pro Arg Asp
 115 120 125
 agc cgc tga 393
 Ser Arg *
 130

<210> 68
 <211> 130
 <212> PRT
 <213> Homo sapiens

<400> 68
 Met Gln Ala Glu Ala Gly Asp Leu Ser Thr Ala Leu Glu Arg Phe Gly
 1 5 10 15
 Gln Ala Ile Cys Leu Leu Pro Glu Arg Ala Ser Ala Tyr Asn Asn Arg
 20 25 30
 Ala Gln Ala Arg Arg Leu Gln Gly Asp Val Ala Gly Ala Leu Glu Asp
 35 40 45
 Leu Glu Arg Ala Val Glu Leu Ser Gly Gly Arg Gly Arg Ala Ala Arg
 50 55 60
 Gln Ser Phe Val Gln Arg Gly Leu Leu Ala Arg Leu Gln Gly Arg Asp
 65 70 75 80
 Asp Asp Ala Arg Arg Asp Phe Glu Arg Ala Ala Arg Leu Gly Ser Pro
 85 90 95
 Phe Ala Arg Arg Gln Leu Val Leu Leu Asn Pro Tyr Ala Ala Leu Cys
 100 105 110
 Asn Arg Met Leu Ala Asp Met Met Gly Gln Leu Arg Arg Pro Arg Asp
 115 120 125

103

Ser Arg
130

<210> 69

<211> 378

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(378)

<400> 69

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| atg | agg | cca | cga | tgc | tgc | atc | ttg | gct | ctt | gtc | tgc | tgg | ata | aca | gtc | 48 |
| Met | Arg | Pro | Arg | Cys | Cys | Ile | Leu | Ala | Leu | Val | Cys | Trp | Ile | Thr | Val | |
| 1 | | | 5 | | | | | 10 | | | | 15 | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| ttc | ctc | ctc | cag | tgt | tca | aaa | gga | act | aca | gac | gct | cct | gtt | ggc | tca | 96 |
| Phe | Leu | Leu | Gln | Cys | Ser | Lys | Gly | Thr | Thr | Asp | Ala | Pro | Val | Gly | Ser | |
| | | | 20 | | | | | 25 | | | | 30 | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gga | ctg | tgg | ctg | tgc | cag | ccg | aca | ccc | agg | tgt | ggg | aac | aag | atc | tac | 144 |
| Gly | Leu | Trp | Leu | Cys | Gln | Pro | Thr | Pro | Arg | Cys | Gly | Asn | Lys | Ile | Tyr | |
| | | 35 | | | | 40 | | | | | 45 | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| aac | cct | tca | gag | cag | tgc | tgt | tat | gat | gat | gcc | atc | tta | tcc | tta | aag | 192 |
| Asn | Pro | Ser | Glu | Gln | Cys | Cys | Tyr | Asp | Asp | Ala | Ile | Leu | Ser | Leu | Lys | |
| | 50 | | | | 55 | | | | | 60 | | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gag | acc | cgc | cgc | tgt | ggc | tcc | acc | tgc | acc | ttc | tgg | ccc | tgc | ttt | gag | 240 |
| Glu | Thr | Arg | Arg | Cys | Gly | Ser | Thr | Cys | Thr | Phe | Trp | Pro | Cys | Phe | Glu | |
| 65 | | | | 70 | | | | 75 | | | | 80 | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ctc | tgc | tgt | ccc | gag | tct | ttt | ggc | ccc | cag | cag | aag | ttt | ctt | gtg | aag | 288 |
| Leu | Cys | Cys | Pro | Glu | Ser | Phe | Gly | Pro | Gln | Gln | Lys | Phe | Leu | Val | Lys | |
| | | | 85 | | | | 90 | | | | | 95 | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ttg | agg | gtt | ctg | ggt | atg | aag | tct | cag | tgt | cac | tta | tct | ccc | atc | tcc | 336 |
| Leu | Arg | Val | Leu | Gly | Met | Lys | Ser | Gln | Cys | His | Leu | Ser | Pro | Ile | Ser | |
| | | 100 | | | | 105 | | | | | 110 | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|-----|
| cgg | agc | tgt | acc | agg | aac | agg | agg | cac | gtc | ctg | tac | cca | taa | | | 378 |
| Arg | Ser | Cys | Thr | Arg | Asn | Arg | Arg | His | Val | Leu | Tyr | Pro | * | | | |
| | | 115 | | | | 120 | | | | | 125 | | | | | |

104

<210> 70
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 70
 Met Arg Pro Arg Cys Cys Ile Leu Ala Leu Val Cys Trp Ile Thr Val
 1 5 10 15
 Phe Leu Leu Gln Cys Ser Lys Gly Thr Thr Asp Ala Pro Val Gly Ser
 20 25 30
 Gly Leu Trp Leu Cys Gln Pro Thr Pro Arg Cys Gly Asn Lys Ile Tyr
 35 40 45
 Asn Pro Ser Glu Gln Cys Cys Tyr Asp Asp Ala Ile Leu Ser Leu Lys
 50 55 60
 Glu Thr Arg Arg Cys Gly Ser Thr Cys Thr Phe Trp Pro Cys Phe Glu
 65 70 75 80
 Leu Cys Cys Pro Glu Ser Phe Gly Pro Gln Gln Lys Phe Leu Val Lys
 85 90 95
 Leu Arg Val Leu Gly Met Lys Ser Gln Cys His Leu Ser Pro Ile Ser
 100 105 110
 Arg Ser Cys Thr Arg Asn Arg Arg His Val Leu Tyr Pro
 115 120 125

<210> 71
 <211> 657
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(657)

<400> 71
 atg gct caa gag aaa gat tgc caa gga atc atc gag gac gtc atc ctg 48
 Met Ala Gln Glu Lys Asp Cys Gln Gly Ile Ile Glu Asp Val Ile Leu
 1 5 10 15
 ctg ggt gcg cct gtg gag gga gaa gcc aag cat tgg gag cct ttc cgg 96
 Leu Gly Ala Pro Val Glu Gly Glu Ala Lys His Trp Glu Pro Phe Arg
 20 25 30
 aag gtg gtg tcc ggg agg atc atc aac ggc tac tgc agg gga gac tgg 144

105

| | |
|---|-----|
| Lys Val Val Ser Gly Arg Ile Ile Asn Gly Tyr Cys Arg Gly Asp Trp | |
| 35 40 45 | |
| ctg ctg agt ttc gtg tac cgc aca tcc tcg gtg cag ctc cac gtc gcc | 192 |
| Leu Leu Ser Phe Val Tyr Arg Thr Ser Ser Val Gln Leu His Val Ala | |
| 50 55 60 | |
| ggc cta cag ccc gtg ctg ctg cag gac agg agg gtg gag aac gtg gac | 240 |
| Gly Leu Gln Pro Val Leu Leu Gln Asp Arg Arg Val Glu Asn Val Asp | |
| 65 70 75 80 | |
| ctg acc tct gtg gtc agc ggc cac ctg gac tat gcc aag cag atg gat | 288 |
| Leu Thr Ser Val Val Ser Gly His Leu Asp Tyr Ala Lys Gln Met Asp | |
| 85 90 95 | |
| gcc atc ctg aag gcc gtg ggc atc cgc acc aag cca ggc tgg gac gag | 336 |
| Ala Ile Leu Lys Ala Val Gly Ile Arg Thr Lys Pro Gly Trp Asp Glu | |
| 100 105 110 | |
| aag ggg ctc ttg ctg gcc cca ggc tgc ctg ccc tcc gag gag cct cgc | 384 |
| Lys Gly Leu Leu Leu Ala Pro Gly Cys Leu Pro Ser Glu Glu Pro Arg | |
| 115 120 125 | |
| cag gca gca gct gcc gcc tca tca ggc gag acc ccc cac cag gtt ggg | 432 |
| Gln Ala Ala Ala Ala Ala Ser Ser Gly Glu Thr Pro His Gln Val Gly | |
| 130 135 140 | |
| caa acc cag ggt ccc ata tcc gga gac acc tcc aaa ttg gcc atg tcc | 480 |
| Gln Thr Gln Gly Pro Ile Ser Gly Asp Thr Ser Lys Leu Ala Met Ser | |
| 145 150 155 160 | |
| aca gac ccc agc caa gcc cag gtg cca gta ggg ctg gac cag tct gaa | 528 |
| Thr Asp Pro Ser Gln Ala Gln Val Pro Val Gly Leu Asp Gln Ser Glu | |
| 165 170 175 | |
| ggg gcc tcc ctt cct gct gct gcc agc cct gaa agg ccc ccc atc tgc | 576 |
| Gly Ala Ser Leu Pro Ala Ala Ala Ser Pro Glu Arg Pro Pro Ile Cys | |
| 180 185 190 | |
| agc cat ggc atg gac ccc aac cca ctg ggc tgc ccc gat tgt gcc tgc | 624 |
| Ser His Gly Met Asp Pro Asn Pro Leu Gly Cys Pro Asp Cys Ala Cys | |
| 195 200 205 | |
| aag acc cag ggc ccc agc acg ggg ctg gac tga | 657 |

106

Lys Thr Gln Gly Pro Ser Thr Gly Leu Asp *
 210 215

<210> 72
 <211> 218
 <212> PRT
 <213> Homo sapiens

<400> 72
 Met Ala Gln Glu Lys Asp Cys Gln Gly Ile Ile Glu Asp Val Ile Leu
 1 5 10 15
 Leu Gly Ala Pro Val Glu Gly Glu Ala Lys His Trp Glu Pro Phe Arg
 20 25 30
 Lys Val Val Ser Gly Arg Ile Ile Asn Gly Tyr Cys Arg Gly Asp Trp
 35 40 45
 Leu Leu Ser Phe Val Tyr Arg Thr Ser Ser Val Gln Leu His Val Ala
 50 55 60
 Gly Leu Gln Pro Val Leu Leu Gln Asp Arg Arg Val Glu Asn Val Asp
 65 70 75 80
 Leu Thr Ser Val Val Ser Gly His Leu Asp Tyr Ala Lys Gln Met Asp
 85 90 95
 Ala Ile Leu Lys Ala Val Gly Ile Arg Thr Lys Pro Gly Trp Asp Glu
 100 105 110
 Lys Gly Leu Leu Leu Ala Pro Gly Cys Leu Pro Ser Glu Glu Pro Arg
 115 120 125
 Gln Ala Ala Ala Ala Ala Ser Ser Gly Glu Thr Pro His Gln Val Gly
 130 135 140
 Gln Thr Gln Gly Pro Ile Ser Gly Asp Thr Ser Lys Leu Ala Met Ser
 145 150 155 160
 Thr Asp Pro Ser Gln Ala Gln Val Pro Val Gly Leu Asp Gln Ser Glu
 165 170 175
 Gly Ala Ser Leu Pro Ala Ala Ala Ser Pro Glu Arg Pro Pro Ile Cys
 180 185 190
 Ser His Gly Met Asp Pro Asn Pro Leu Gly Cys Pro Asp Cys Ala Cys
 195 200 205
 Lys Thr Gln Gly Pro Ser Thr Gly Leu Asp
 210 215

<210> 73
 <211> 441
 <212> DNA
 <213> Homo sapiens

107

<220>

<221> CDS

<222> (1)...(441)

<400> 73

| | |
|--|----|
| atg ttg ttg gcc ctg gtc tgt ctg ctc agc tgc ctg cta ccc tcc agt | 48 |
| Met Leu Leu Ala Leu Val Cys Leu Leu Ser Cys Leu Leu Pro Ser Ser | |
| 1 5 10 15 | |

| | |
|---|----|
| gag gcc aag ctc tac ggt cgt tgt gaa ctg gcc aga gtg cta cat gac | 96 |
| Glu Ala Lys Leu Tyr Gly Arg Cys Glu Leu Ala Arg Val Leu His Asp | |
| 20 25 30 | |

| | |
|---|-----|
| ttc ggg ctg gac gga tac cgg gga tac agc ctg gct gac tgg gtc tgc | 144 |
| Phe Gly Leu Asp Gly Tyr Arg Gly Tyr Ser Leu Ala Asp Trp Val Cys | |
| 35 40 45 | |

| | |
|---|-----|
| ctt gct tat ttc aca agc ggt ttc aac gca gct gct ttg gac tac gag | 192 |
| Leu Ala Tyr Phe Thr Ser Gly Phe Asn Ala Ala Ala Leu Asp Tyr Glu | |
| 50 55 60 | |

| | |
|--|-----|
| gct gat ggg agc acc aac aac ggg atc ttc cag atc aac agc cgg agg | 240 |
| Ala Asp Gly Ser Thr Asn Asn Gly Ile Phe Gln Ile Asn Ser Arg Arg | |
| 65 70 75 80 | |

| | |
|---|-----|
| tgg tgc agc aac ctc acc ccg aac gtc ccc aac gtg tgc cgg atg tac | 288 |
| Trp Cys Ser Asn Leu Thr Pro Asn Val Pro Asn Val Cys Arg Met Tyr | |
| 85 90 95 | |

| | |
|---|-----|
| tgc tca gat ttg ttg aat cct aat ctc aag gat acc gtt atc tgt gcc | 336 |
| Cys Ser Asp Leu Leu Asn Pro Asn Leu Lys Asp Thr Val Ile Cys Ala | |
| 100 105 110 | |

| | |
|---|-----|
| atg aag ata acc caa gag cct cag ggt ctg ggt tac tgg gag gcc tgg | 384 |
| Met Lys Ile Thr Gln Glu Pro Gln Gly Leu Gly Tyr Trp Glu Ala Trp | |
| 115 120 125 | |

| | |
|---|-----|
| agg cat cac tgc cag gga aaa gac ctc act gaa tgg gtg gat ggc tgt | 432 |
| Arg His His Cys Gln Gly Lys Asp Leu Thr Glu Trp Val Asp Gly Cys | |
| 130 135 140 | |

| | |
|-------------|-----|
| gac ttc tag | 441 |
| Asp Phe * | |
| 145 | |

108

<210> 74
 <211> 146
 <212> PRT
 <213> Homo sapiens

<400> 74
 Met Leu Leu Ala Leu Val Cys Leu Leu Ser Cys Leu Leu Pro Ser Ser
 1 5 10 15
 Glu Ala Lys Leu Tyr Gly Arg Cys Glu Leu Ala Arg Val Leu His Asp
 20 25 30
 Phe Gly Leu Asp Gly Tyr Arg Gly Tyr Ser Leu Ala Asp Trp Val Cys
 35 40 45
 Leu Ala Tyr Phe Thr Ser Gly Phe Asn Ala Ala Ala Leu Asp Tyr Glu
 50 55 60
 Ala Asp Gly Ser Thr Asn Asn Gly Ile Phe Gln Ile Asn Ser Arg Arg
 65 70 75 80
 Trp Cys Ser Asn Leu Thr Pro Asn Val Pro Asn Val Cys Arg Met Tyr
 85 90 95
 Cys Ser Asp Leu Leu Asn Pro Asn Leu Lys Asp Thr Val Ile Cys Ala
 100 105 110
 Met Lys Ile Thr Gln Glu Pro Gln Gly Leu Gly Tyr Trp Glu Ala Trp
 115 120 125
 Arg His His Cys Gln Gly Lys Asp Leu Thr Glu Trp Val Asp Gly Cys
 130 135 140
 Asp Phe
 145

<210> 75
 <211> 345
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(345)

<400> 75
 atg ctg tgc ttc ctg agg gga atg gct ttc gtc ccc ttc ctc ttg gtg 48
 Met Leu Cys Phe Leu Arg Gly Met Ala Phe Val Pro Phe Leu Leu Val
 1 5 10 15
 acc tgg tcg tca gcc gcc ttc att atc tcc tac gtg gtc gcc gtg ctc 96

109

Thr Trp Ser Ser Ala Ala Phe Ile Ile Ser Tyr Val Val Ala Val Leu
 20 25 30
 tcc ggg cac gtc aac ccc ttc ctc ccg tat atc agt gat acg gga aca 144
 Ser Gly His Val Asn Pro Phe Leu Pro Tyr Ile Ser Asp Thr Gly Thr
 35 40 45
 aca cct cca gag agt ggt att ttt gga ttt atg ata aac ttc tct gca 192
 Thr Pro Pro Glu Ser Gly Ile Phe Gly Phe Met Ile Asn Phe Ser Ala
 50 55 60
 ttt ctt ggt gca gcc acg atg tat aca aga tac aaa ata gta cag aag 240
 Phe Leu Gly Ala Ala Thr Met Tyr Thr Arg Tyr Lys Ile Val Gln Lys
 65 70 75 80
 caa aat caa acc tgc tat ttc agc act cct gtt ttt aac ttg gtg tct 288
 Gln Asn Gln Thr Cys Tyr Phe Ser Thr Pro Val Phe Asn Leu Val Ser
 85 90 95
 tta gtg ctt gga ttg gtg gga tgt ttc gga atg ggc att gtc gcc aat 336
 Leu Val Leu Gly Leu Val Gly Cys Phe Gly Met Gly Ile Val Ala Asn
 100 105 110
 ttt cag tga 345
 Phe Gln *

<210> 76

<211> 114

<212> PRT

<213> Homo sapiens

<400> 76

Met Leu Cys Phe Leu Arg Gly Met Ala Phe Val Pro Phe Leu Leu Val
 1 5 10 15
 Thr Trp Ser Ser Ala Ala Phe Ile Ile Ser Tyr Val Val Ala Val Leu
 20 25 30
 Ser Gly His Val Asn Pro Phe Leu Pro Tyr Ile Ser Asp Thr Gly Thr
 35 40 45
 Thr Pro Pro Glu Ser Gly Ile Phe Gly Phe Met Ile Asn Phe Ser Ala
 50 55 60
 Phe Leu Gly Ala Ala Thr Met Tyr Thr Arg Tyr Lys Ile Val Gln Lys
 65 70 75 80

110

Gln Asn Gln Thr Cys Tyr Phe Ser Thr Pro Val Phe Asn Leu Val Ser
 85 90 95
 Leu Val Leu Gly Leu Val Gly Cys Phe Gly Met Gly Ile Val Ala Asn
 100 105 110
 Phe Gln

<210> 77

<211> 972

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(972)

<400> 77

atg ccc cta tta aaa ctt gta cat ggc tcc cca ttg gtt ttt gga gaa 48
 Met Pro Leu Leu Lys Leu Val His Gly Ser Pro Leu Val Phe Gly Glu
 1 5 10 15

aag ttc aag ctt ttt acc ttg gtg tct gcc tgt atc cca gtg ttc agg 96
 Lys Phe Lys Leu Phe Thr Leu Val Ser Ala Cys Ile Pro Val Phe Arg
 20 25 30

ctg gct aga cgg cgg aag aag atc cta ttt tac tgt cac ttc cca gat 144
 Leu Ala Arg Arg Arg Lys Lys Ile Leu Phe Tyr Cys His Phe Pro Asp
 35 40 45

ctg ctt ctc acc aag aga gat tct ttt ctt aaa cga cta tac agg gcc 192
 Leu Leu Leu Thr Lys Arg Asp Ser Phe Leu Lys Arg Leu Tyr Arg Ala
 50 55 60

cca att gac tgg ata gag gaa tac acc aca ggc atg gca gac tgc atc 240
 Pro Ile Asp Trp Ile Glu Glu Tyr Thr Thr Gly Met Ala Asp Cys Ile
 65 70 75 80

tta gtc aac agc cag ttc aca gct gct gtt ttt aag gaa aca ttc aag 288
 Leu Val Asn Ser Gln Phe Thr Ala Ala Val Phe Lys Glu Thr Phe Lys
 85 90 95

tcc ctg tct cac ata gac cct gat gtc ctc tat cca tct cta aat gtc 336
 Ser Leu Ser His Ile Asp Pro Asp Val Leu Tyr Pro Ser Leu Asn Val
 100 105 110

111

| | |
|---|-----|
| acc agc ttt gac tca gtt gtt cct gaa aag ctg gat gac cta gtc ccc Thr Ser Phe Asp Ser Val Val Pro Glu Lys Leu Asp Asp Leu Val Pro 115 120 125 | 384 |
| aag ggg aaa aaa ttc ctg ctg ctc tcc atc aac aga tac gaa agg aag Lys Gly Lys Lys Phe Leu Leu Leu Ser Ile Asn Arg Tyr Glu Arg Lys 130 135 140 | 432 |
| aaa aat ctg act ttg gca ctg gaa gcc cta gta cag ctg cgt gga aga Lys Asn Leu Thr Leu Ala Leu Glu Ala Leu Val Gln Leu Arg Gly Arg 145 150 155 160 | 480 |
| ttg aca tcc caa gat tgg gag agg gtt cat ctg atc gtg gca ggt ggt Leu Thr Ser Gln Asp Trp Glu Arg Val His Leu Ile Val Ala Gly Gly 165 170 175 | 528 |
| tat gac gag aga gtc ctg gag aat gtg gaa cat tat cag gaa ttg aag Tyr Asp Glu Arg Val Leu Glu Asn Val Glu His Tyr Gln Glu Leu Lys 180 185 190 | 576 |
| aaa atg gtc caa cag tcc gac ctt ggc cag tat gtg acc ttc ttg agg Lys Met Val Gln Gln Ser Asp Leu Gly Gln Tyr Val Thr Phe Leu Arg 195 200 205 | 624 |
| tct ttc tca gac aaa cag aaa atc tcc ctc ctc cac agc tgc acg tgt Ser Phe Ser Asp Lys Gln Lys Ile Ser Leu Leu His Ser Cys Thr Cys 210 215 220 | 672 |
| gtg ctt tac aca cca agc aat gag cac ttt ggc att gtc cct ctg gaa Val Leu Tyr Thr Pro Ser Asn Glu His Phe Gly Ile Val Pro Leu Glu 225 230 235 240 | 720 |
| gcc atg tac atg cag tgc cca gtc att gct gtt aat tcg ggt gga ccc Ala Met Tyr Met Gln Cys Pro Val Ile Ala Val Asn Ser Gly Gly Pro 245 250 255 | 768 |
| ttg gag tcc att gac cac agt gtc aca ggg ttt ctg tgt gag cct gac Leu Glu Ser Ile Asp His Ser Val Thr Gly Phe Leu Cys Glu Pro Asp 260 265 270 | 816 |
| ccg gtg cac ttc tca gaa gca ata gaa aag ttc atc cgt gaa cct tcc Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Arg Glu Pro Ser 275 280 285 | 864 |

112

tta aaa gcc acc atg ggc ctg gct gga aga gcc aga gtg aag gaa aaa 912
 Leu Lys Ala Thr Met Gly Leu Ala Gly Arg Ala Arg Val Lys Glu Lys
 290 295 300

 ttt tcc cct gaa gca ttt aca gaa cag ctc tac cga tat gtt acc aaa 960
 Phe Ser Pro Glu Ala Phe Thr Glu Gln Leu Tyr Arg Tyr Val Thr Lys
 305 310 315 320

 ctg ctg gta taa 972
 Leu Leu Val *

<210> 78
 <211> 323
 <212> PRT
 <213> Homo sapiens

<400> 78
 Met Pro Leu Leu Lys Leu Val His Gly Ser Pro Leu Val Phe Gly Glu
 1 5 10 15
 Lys Phe Lys Leu Phe Thr Leu Val Ser Ala Cys Ile Pro Val Phe Arg
 20 25 30
 Leu Ala Arg Arg Arg Lys Lys Ile Leu Phe Tyr Cys His Phe Pro Asp
 35 40 45
 Leu Leu Leu Thr Lys Arg Asp Ser Phe Leu Lys Arg Leu Tyr Arg Ala
 50 55 60
 Pro Ile Asp Trp Ile Glu Glu Tyr Thr Thr Gly Met Ala Asp Cys Ile
 65 70 75 80
 Leu Val Asn Ser Gln Phe Thr Ala Ala Val Phe Lys Glu Thr Phe Lys
 85 90 95
 Ser Leu Ser His Ile Asp Pro Asp Val Leu Tyr Pro Ser Leu Asn Val
 100 105 110
 Thr Ser Phe Asp Ser Val Val Pro Glu Lys Leu Asp Asp Leu Val Pro
 115 120 125
 Lys Gly Lys Lys Phe Leu Leu Leu Ser Ile Asn Arg Tyr Glu Arg Lys
 130 135 140
 Lys Asn Leu Thr Leu Ala Leu Glu Ala Leu Val Gln Leu Arg Gly Arg
 145 150 155 160
 Leu Thr Ser Gln Asp Trp Glu Arg Val His Leu Ile Val Ala Gly Gly
 165 170 175
 Tyr Asp Glu Arg Val Leu Glu Asn Val Glu His Tyr Gln Glu Leu Lys
 180 185 190

113

Lys Met Val Gln Gln Ser Asp Leu Gly Gln Tyr Val Thr Phe Leu Arg
 195 200 205
 Ser Phe Ser Asp Lys Gln Lys Ile Ser Leu Leu His Ser Cys Thr Cys
 210 215 220
 Val Leu Tyr Thr Pro Ser Asn Glu His Phe Gly Ile Val Pro Leu Glu
 225 230 235 240
 Ala Met Tyr Met Gln Cys Pro Val Ile Ala Val Asn Ser Gly Gly Pro
 245 250 255
 Leu Glu Ser Ile Asp His Ser Val Thr Gly Phe Leu Cys Glu Pro Asp
 260 265 270
 Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Arg Glu Pro Ser
 275 280 285
 Leu Lys Ala Thr Met Gly Leu Ala Gly Arg Ala Arg Val Lys Glu Lys
 290 295 300
 Phe Ser Pro Glu Ala Phe Thr Glu Gln Leu Tyr Arg Tyr Val Thr Lys
 305 310 315 320
 Leu Leu Val

<210> 79
 <211> 891
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(891)
 <223>

<221> misc_feature
 <222> (1)...(891)
 <223> n = A,T,C or G

<400> 79

atg cac ggg aag act gtg ctg atc acc ggg gcg aac agc ggc ctg ggc 48
 Met His Gly Lys Thr Val Leu Ile Thr Gly Ala Asn Ser Gly Leu Gly
 1 5 10 15

cgn tcc acg gcc gcc gag cta ctg cgc ctg gga gcg cgg gtg atc atg 96
 Xaa Ser Thr Ala Ala Glu Leu Leu Arg Leu Gly Ala Arg Val Ile Met

114

| 20 | 25 | 30 | |
|---|----|----|-----|
| ggc tgc cgc gac cgc gcg cgc gcc gag gag gcg gcg ggt cag ctc cgc Gly Cys Arg Asp Arg Ala Arg Ala Glu Glu Ala Ala Gly Gln Leu Arg 35 40 45 | | | 144 |
| cgc gag ctc cgc cag gcc gcg gag tgc ggc cca gag cct ggc gtc agc Arg Glu Leu Arg Gln Ala Ala Glu Cys Gly Pro Glu Pro Gly Val Ser 50 55 60 | | | 192 |
| ggg gtg ggc gag ctc ata gtc cgg gag ctg gac ctc gcc tcg ctg cgc Gly Val Gly Glu Leu Ile Val Arg Glu Leu Asp Leu Ala Ser Leu Arg 65 70 75 80 | | | 240 |
| tcg gtg cgc gcc ttc tgc cag gaa atg ctc cag gaa gag cct agg ctg Ser Val Arg Ala Phe Cys Gln Glu Met Leu Gln Glu Glu Pro Arg Leu 85 90 95 | | | 288 |
| gat gtc ttg atc aat aac gca ggg atc ttc cag tgc cct tac atg aag Asp Val Leu Ile Asn Asn Ala Gly Ile Phe Gln Cys Pro Tyr Met Lys 100 105 110 | | | 336 |
| act gaa gat ggg ttt gag atg cag ttc gga gtg aac cat ctg ggg cac Thr Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His 115 120 125 | | | 384 |
| ttt cta ctc acc aat ctt ctc ctt gga ctc ctc aaa agt tca gct ccc Phe Leu Leu Thr Asn Leu Leu Leu Gly Leu Leu Lys Ser Ser Ala Pro 130 135 140 | | | 432 |
| agc agg att gtg gta gtt tct tcc aaa ctt tat aaa tac gga gac atc Ser Arg Ile Val Val Val Ser Ser Lys Leu Tyr Lys Tyr Gly Asp Ile 145 150 155 160 | | | 480 |
| aat ttt gat gac ttg aac agt gaa caa agc tat aat aaa agc ttt tgt Asn Phe Asp Asp Leu Asn Ser Glu Gln Ser Tyr Asn Lys Ser Phe Cys 165 170 175 | | | 528 |
| tat agc cgg agc aaa ctg gct aac att ctt ttt acc agg gaa cta gcc Tyr Ser Arg Ser Lys Leu Ala Asn Ile Leu Phe Thr Arg Glu Leu Ala 180 185 190 | | | 576 |
| cgc cgc tta gaa ggc aca aat gtc acc gtc aat gtg ttg cat cct ggt Arg Arg Leu Glu Gly Thr Asn Val Thr Val Asn Val Leu His Pro Gly | | | 624 |

115

| | | | |
|---|-----|-----|-----|
| 195 | 200 | 205 | |
| att gta cgg aca aat ctg ggg agg cac ata cac att cca ctg ttg gtc | | | 672 |
| Ile Val Arg Thr Asn Leu Gly Arg His Ile His Ile Pro Leu Leu Val | | | |
| 210 | 215 | 220 | |
| aaa cca ctc ttc aat ttg gtg tca tgg gct ttt ttc aaa act cca gta | | | 720 |
| Lys Pro Leu Phe Asn Leu Val Ser Trp Ala Phe Phe Lys Thr Pro Val | | | |
| 225 | 230 | 235 | 240 |
| gaa ggt gcc cag act tcc att tat ttg gcc tct tca cct gag gta gaa | | | 768 |
| Glu Gly Ala Gln Thr Ser Ile Tyr Leu Ala Ser Ser Pro Glu Val Glu | | | |
| 245 | 250 | 255 | |
| gga gtg tca gga aga tac ttt ggg gat tgt aaa gag gaa gaa ctg ttg | | | 816 |
| Gly Val Ser Gly Arg Tyr Phe Gly Asp Cys Lys Glu Glu Glu Leu Leu | | | |
| 260 | 265 | 270 | |
| ccc aaa gct atg gat gaa tct gtt gca aga aaa ctc tgg gat atc agt | | | 864 |
| Pro Lys Ala Met Asp Glu Ser Val Ala Arg Lys Leu Trp Asp Ile Ser | | | |
| 275 | 280 | 285 | |
| gaa gtg atg gtt ggc ctg cta aaa tag | | | 891 |
| Glu Val Met Val Gly Leu Leu Lys * | | | |
| 290 | 295 | | |

<210> 80
 <211> 296
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(296)
 <223> Xaa = Any Amino Acid

| | |
|---|----|
| <400> 80 | |
| Met His Gly Lys Thr Val Leu Ile Thr Gly Ala Asn Ser Gly Leu Gly | |
| 1 | 15 |
| Xaa Ser Thr Ala Ala Glu Leu Leu Arg Leu Gly Ala Arg Val Ile Met | |
| 20 | 30 |
| Gly Cys Arg Asp Arg Ala Arg Ala Glu Glu Ala Ala Gly Gln Leu Arg | |
| 35 | 45 |

116

Arg Glu Leu Arg Gln Ala Ala Glu Cys Gly Pro Glu Pro Gly Val Ser
 50 55 60
 Gly Val Gly Glu Leu Ile Val Arg Glu Leu Asp Leu Ala Ser Leu Arg
 65 70 75 80
 Ser Val Arg Ala Phe Cys Gln Glu Met Leu Gln Glu Glu Pro Arg Leu
 85 90 95
 Asp Val Leu Ile Asn Asn Ala Gly Ile Phe Gln Cys Pro Tyr Met Lys
 100 105 110
 Thr Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His
 115 120 125
 Phe Leu Leu Thr Asn Leu Leu Leu Gly Leu Leu Lys Ser Ser Ala Pro
 130 135 140
 Ser Arg Ile Val Val Val Ser Ser Lys Leu Tyr Lys Tyr Gly Asp Ile
 145 150 155 160
 Asn Phe Asp Asp Leu Asn Ser Glu Gln Ser Tyr Asn Lys Ser Phe Cys
 165 170 175
 Tyr Ser Arg Ser Lys Leu Ala Asn Ile Leu Phe Thr Arg Glu Leu Ala
 180 185 190
 Arg Arg Leu Glu Gly Thr Asn Val Thr Val Asn Val Leu His Pro Gly
 195 200 205
 Ile Val Arg Thr Asn Leu Gly Arg His Ile His Ile Pro Leu Leu Val
 210 215 220
 Lys Pro Leu Phe Asn Leu Val Ser Trp Ala Phe Phe Lys Thr Pro Val
 225 230 235 240
 Glu Gly Ala Gln Thr Ser Ile Tyr Leu Ala Ser Ser Pro Glu Val Glu
 245 250 255
 Gly Val Ser Gly Arg Tyr Phe Gly Asp Cys Lys Glu Glu Glu Leu Leu
 260 265 270
 Pro Lys Ala Met Asp Glu Ser Val Ala Arg Lys Leu Trp Asp Ile Ser
 275 280 285
 Glu Val Met Val Gly Leu Leu Lys
 290 295

<210> 81

<211> 1716

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1716)

<400> 81

atg gta gaa tca att aaa cac tgc att gtg ttg ctg cag att gcc aaa

48

117

| | | | | | | | | | | | | | | | | |
|----------|-----|-----|-----|----------|-----|-----|-----|-----------|-----|-----|-----|-----|-----|-----------|-----|-----|
| Met 1 | Val | Glu | Ser | Ile 5 | Lys | His | Cys | Ile 10 | Val | Leu | Leu | Gln | Ile | Ala 15 | Lys | |
| gac | cag | agt | aat | gcg | gag | aag | cac | gca | gat | gga | atg | ata | agt | act | att | 96 |
| Asp | Gln | Ser | Asn | Ala | Glu | Lys | His | Ala | Asp | Gly | Met | Ile | Ser | Thr | Ile | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| aat | ccc | gta | gat | gca | ata | tat | caa | cct | agt | cct | ttg | gaa | cct | gtg | atc | 144 |
| Asn | Pro | Val | Asp | Ala | Ile | Tyr | Gln | Pro | Ser | Pro | Leu | Glu | Pro | Val | Ile | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| agc | aca | atg | cct | tcc | cag | act | gtg | tta | cct | cca | gaa | cct | gtt | cag | ttg | 192 |
| Ser | Thr | Met | Pro | Ser | Gln | Thr | Val | Leu | Pro | Pro | Glu | Pro | Val | Gln | Leu | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| tgt | aag | tca | gag | cag | cgt | cca | tct | tcc | cta | cca | gtt | gga | cct | gtg | ttg | 240 |
| Cys | Lys | Ser | Glu | Gln | Arg | Pro | Ser | Ser | Leu | Pro | Val | Gly | Pro | Val | Leu | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| gct | acc | ttg | gga | cat | cat | cag | act | cct | aca | cca | aat | agt | aca | ggc | agt | 288 |
| Ala | Thr | Leu | Gly | His | His | Gln | Thr | Pro | Thr | Pro | Asn | Ser | Thr | Gly | Ser | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| ggc | cat | tca | cca | ccg | agt | agc | agt | ctc | act | tct | cca | agc | cac | gtg | aac | 336 |
| Gly | His | Ser | Pro | Pro | Ser | Ser | Ser | Leu | Thr | Ser | Pro | Ser | His | Val | Asn | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| ttg | tct | cca | aat | aca | gtc | cca | gag | ttc | tct | tac | tcc | agc | agt | gaa | gat | 384 |
| Leu | Ser | Pro | Asn | Thr | Val | Pro | Glu | Phe | Ser | Tyr | Ser | Ser | Ser | Glu | Asp | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| gaa | ttt | tat | gat | gct | gat | gaa | ttc | cat | caa | agt | ggc | tca | tcc | cca | aag | 432 |
| Glu | Phe | Tyr | Asp | Ala | Asp | Glu | Phe | His | Gln | Ser | Gly | Ser | Ser | Pro | Lys | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| cgc | tta | ata | gat | tct | tct | gga | tct | gcc | tca | gtc | ctg | aca | cac | agc | agc | 480 |
| Arg | Leu | Ile | Asp | Ser | Ser | Gly | Ser | Ala | Ser | Val | Leu | Thr | His | Ser | Ser | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| tcg | gga | aat | agt | cta | aaa | cgc | cca | gat | acc | aca | gaa | tca | ctt | aat | tct | 528 |
| Ser | Gly | Asn | Ser | Leu | Lys | Arg | Pro | Asp | Thr | Thr | Glu | Ser | Leu | Asn | Ser | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| tcc | ttg | tcc | aat | gga | aca | agt | gat | gct | gac | ctg | ttt | gat | tca | cat | gat | 576 |

118

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| Ser | Leu | Ser | Asn | Gly | Thr | Ser | Asp | Ala | Asp | Leu | Phe | Asp | Ser | His | Asp | | |
| | | | 180 | | | | | 185 | | | | | 190 | | | | |
| gac | aga | gat | gat | gat | gcg | gag | gca | ggg | tct | gtg | gag | gag | cac | aag | agc | 624 | |
| Asp | Arg | Asp | Asp | Asp | Ala | Glu | Ala | Gly | Ser | Val | Glu | Glu | His | Lys | Ser | | |
| | | 195 | | | | | 200 | | | | 205 | | | | | | |
| gtt | atc | atg | cat | ctc | ttg | tcg | cag | gtt | aga | ctt | gga | atg | gat | ctt | act | 672 | |
| Val | Ile | Met | His | Leu | Leu | Ser | Gln | Val | Arg | Leu | Gly | Met | Asp | Leu | Thr | | |
| | 210 | | | | | 215 | | | | | 220 | | | | | | |
| aag | gta | gtt | ctt | cca | acg | ttt | att | ctt | gaa | aga | aga | tct | ctt | tta | gaa | 720 | |
| Lys | Val | Val | Leu | Pro | Thr | Phe | Ile | Leu | Glu | Arg | Arg | Ser | Leu | Leu | Glu | | |
| 225 | | | | | 230 | | | | 235 | | | | | 240 | | | |
| atg | tat | gca | gac | ttt | ttt | gca | cat | ccg | gac | ctg | ttt | gtg | agc | att | agt | 768 | |
| Met | Tyr | Ala | Asp | Phe | Phe | Ala | His | Pro | Asp | Leu | Phe | Val | Ser | Ile | Ser | | |
| | | | 245 | | | | | 250 | | | | | | 255 | | | |
| gac | cag | aag | gat | ccc | aag | gat | cga | atg | gtt | cag | gtt | gtg | aaa | tgg | tac | 816 | |
| Asp | Gln | Lys | Asp | Pro | Lys | Asp | Arg | Met | Val | Gln | Val | Val | Lys | Trp | Tyr | | |
| | | 260 | | | | | 265 | | | | | | 270 | | | | |
| ctc | tca | gcc | ttt | cat | gcg | gga | agg | aaa | gga | tca | gtt | gcc | aaa | aag | cca | 864 | |
| Leu | Ser | Ala | Phe | His | Ala | Gly | Arg | Lys | Gly | Ser | Val | Ala | Lys | Lys | Pro | | |
| | 275 | | | | | 280 | | | | | | 285 | | | | | |
| tac | aat | ccc | att | ttg | ggc | gag | att | ttt | cag | tgt | cat | tgg | aca | tta | cca | 912 | |
| Tyr | Asn | Pro | Ile | Leu | Gly | Glu | Ile | Phe | Gln | Cys | His | Trp | Thr | Leu | Pro | | |
| | 290 | | | | 295 | | | | | 300 | | | | | | | |
| aat | gat | act | gaa | gag | aac | aca | gaa | cta | gtt | tca | gaa | gga | cca | gtt | ccc | 960 | |
| Asn | Asp | Thr | Glu | Glu | Asn | Thr | Glu | Leu | Val | Ser | Glu | Gly | Pro | Val | Pro | | |
| 305 | | | | | 310 | | | | 315 | | | | | 320 | | | |
| tgg | gtt | tcc | aaa | aac | agt | gta | aca | ttt | gtg | gct | gag | cag | gtt | tcc | cat | 1008 | |
| Trp | Val | Ser | Lys | Asn | Ser | Val | Thr | Phe | Val | Ala | Glu | Gln | Val | Ser | His | | |
| | | | 325 | | | | | 330 | | | | | 335 | | | | |
| cat | cca | ccc | att | tca | gcc | ttt | tat | gct | gag | tgt | ttt | aac | aag | aag | ata | 1056 | |
| His | Pro | Pro | Ile | Ser | Ala | Phe | Tyr | Ala | Glu | Cys | Phe | Asn | Lys | Lys | Ile | | |
| | | | 340 | | | | | 345 | | | | | 350 | | | | |
| caa | ttc | aat | gct | cat | atc | tgg | acc | aaa | tca | aaa | ttc | ctt | ggg | atg | tca | 1104 | |

119

| | |
|---|------|
| Gln Phe Asn Ala His Ile Trp Thr Lys Ser Lys Phe Leu Gly Met Ser | |
| 355 360 365 | |
| att ggg gtg cac aac ata ggg cag ggc tgt gtc tca tgt cta gac tat | 1152 |
| Ile Gly Val His Asn Ile Gly Gln Gly Cys Val Ser Cys Leu Asp Tyr | |
| 370 375 380 | |
| gat gaa cat tac att ctc aca ttc ccc aat ggc tat gga agg tct atc | 1200 |
| Asp Glu His Tyr Ile Leu Thr Phe Pro Asn Gly Tyr Gly Arg Ser Ile | |
| 385 390 395 400 | |
| ctc aca gtg ccc tgg gtg gaa tta gga gga gaa tgc aat att aat tgt | 1248 |
| Leu Thr Val Pro Trp Val Glu Leu Gly Gly Glu Cys Asn Ile Asn Cys | |
| 405 410 415 | |
| tcc aaa aca ggc tat agt gca aat atc atc ttc cac act aaa ccc ttc | 1296 |
| Ser Lys Thr Gly Tyr Ser Ala Asn Ile Ile Phe His Thr Lys Pro Phe | |
| 420 425 430 | |
| tat ggg ggc aag aag cac aga att act gcc gag att ttt tct cca aat | 1344 |
| Tyr Gly Gly Lys Lys His Arg Ile Thr Ala Glu Ile Phe Ser Pro Asn | |
| 435 440 445 | |
| gac aag aag tct ttt tgc tca att gaa ggg gaa tgg aat ggt gtg atg | 1392 |
| Asp Lys Lys Ser Phe Cys Ser Ile Glu Gly Glu Trp Asn Gly Val Met | |
| 450 455 460 | |
| tat gca aaa tat gca aca ggg gaa aat aca gtc ttt gta gat acc aag | 1440 |
| Tyr Ala Lys Tyr Ala Thr Gly Glu Asn Thr Val Phe Val Asp Thr Lys | |
| 465 470 475 480 | |
| aag ttg cct ata atc aag aag aaa gtg agg aag ttg gaa gat cag aac | 1488 |
| Lys Leu Pro Ile Ile Lys Lys Lys Val Arg Lys Leu Glu Asp Gln Asn | |
| 485 490 495 | |
| gag tat gaa tcc cgc agc ctt tgg aag gat gtc act ttc aac tta aaa | 1536 |
| Glu Tyr Glu Ser Arg Ser Leu Trp Lys Asp Val Thr Phe Asn Leu Lys | |
| 500 505 510 | |
| atc aga gac att gat gca gca act gaa gca aag cac agg ctt gaa gaa | 1584 |
| Ile Arg Asp Ile Asp Ala Ala Thr Glu Ala Lys His Arg Leu Glu Glu | |
| 515 520 525 | |
| aga caa aga gca gaa gcc cga gaa agg aag gag aag gaa att cag tgg | 1632 |

120

Arg Gln Arg Ala Glu Ala Arg Glu Arg Lys Glu Lys Glu Ile Gln Trp
 530 535 540

gag aca agg tta ttt cat gaa gat gga gaa tgc tgg gtt tat gat gaa 1680
 Glu Thr Arg Leu Phe His Glu Asp Gly Glu Cys Trp Val Tyr Asp Glu
 545 550 555 560

cca tta ctg aaa cgt ctt ggt gct gcc aag cat tag 1716
 Pro Leu Leu Lys Arg Leu Gly Ala Ala Lys His *
 565 570

<210> 82

<211> 571

<212> PRT

<213> Homo sapiens

<400> 82

Met Val Glu Ser Ile Lys His Cys Ile Val Leu Leu Gln Ile Ala Lys
 1 5 10 15
 Asp Gln Ser Asn Ala Glu Lys His Ala Asp Gly Met Ile Ser Thr Ile
 20 25 30
 Asn Pro Val Asp Ala Ile Tyr Gln Pro Ser Pro Leu Glu Pro Val Ile
 35 40 45
 Ser Thr Met Pro Ser Gln Thr Val Leu Pro Pro Glu Pro Val Gln Leu
 50 55 60
 Cys Lys Ser Glu Gln Arg Pro Ser Ser Leu Pro Val Gly Pro Val Leu
 65 70 75 80
 Ala Thr Leu Gly His His Gln Thr Pro Thr Pro Asn Ser Thr Gly Ser
 85 90 95
 Gly His Ser Pro Pro Ser Ser Ser Leu Thr Ser Pro Ser His Val Asn
 100 105 110
 Leu Ser Pro Asn Thr Val Pro Glu Phe Ser Tyr Ser Ser Ser Glu Asp
 115 120 125
 Glu Phe Tyr Asp Ala Asp Glu Phe His Gln Ser Gly Ser Ser Pro Lys
 130 135 140
 Arg Leu Ile Asp Ser Ser Gly Ser Ala Ser Val Leu Thr His Ser Ser
 145 150 155 160
 Ser Gly Asn Ser Leu Lys Arg Pro Asp Thr Thr Glu Ser Leu Asn Ser
 165 170 175
 Ser Leu Ser Asn Gly Thr Ser Asp Ala Asp Leu Phe Asp Ser His Asp
 180 185 190
 Asp Arg Asp Asp Asp Ala Glu Ala Gly Ser Val Glu Glu His Lys Ser
 195 200 205

121

Val Ile Met His Leu Leu Ser Gln Val Arg Leu Gly Met Asp Leu Thr
 210 215 220
 Lys Val Val Leu Pro Thr Phe Ile Leu Glu Arg Arg Ser Leu Leu Glu
 225 230 235 240
 Met Tyr Ala Asp Phe Phe Ala His Pro Asp Leu Phe Val Ser Ile Ser
 245 250 255
 Asp Gln Lys Asp Pro Lys Asp Arg Met Val Gln Val Val Lys Trp Tyr
 260 265 270
 Leu Ser Ala Phe His Ala Gly Arg Lys Gly Ser Val Ala Lys Lys Pro
 275 280 285
 Tyr Asn Pro Ile Leu Gly Glu Ile Phe Gln Cys His Trp Thr Leu Pro
 290 295 300
 Asn Asp Thr Glu Glu Asn Thr Glu Leu Val Ser Glu Gly Pro Val Pro
 305 310 315 320
 Trp Val Ser Lys Asn Ser Val Thr Phe Val Ala Glu Gln Val Ser His
 325 330 335
 His Pro Pro Ile Ser Ala Phe Tyr Ala Glu Cys Phe Asn Lys Lys Ile
 340 345 350
 Gln Phe Asn Ala His Ile Trp Thr Lys Ser Lys Phe Leu Gly Met Ser
 355 360 365
 Ile Gly Val His Asn Ile Gly Gln Gly Cys Val Ser Cys Leu Asp Tyr
 370 375 380
 Asp Glu His Tyr Ile Leu Thr Phe Pro Asn Gly Tyr Gly Arg Ser Ile
 385 390 395 400
 Leu Thr Val Pro Trp Val Glu Leu Gly Gly Glu Cys Asn Ile Asn Cys
 405 410 415
 Ser Lys Thr Gly Tyr Ser Ala Asn Ile Ile Phe His Thr Lys Pro Phe
 420 425 430
 Tyr Gly Gly Lys Lys His Arg Ile Thr Ala Glu Ile Phe Ser Pro Asn
 435 440 445
 Asp Lys Lys Ser Phe Cys Ser Ile Glu Gly Glu Trp Asn Gly Val Met
 450 455 460
 Tyr Ala Lys Tyr Ala Thr Gly Glu Asn Thr Val Phe Val Asp Thr Lys
 465 470 475 480
 Lys Leu Pro Ile Ile Lys Lys Lys Val Arg Lys Leu Glu Asp Gln Asn
 485 490 495
 Glu Tyr Glu Ser Arg Ser Leu Trp Lys Asp Val Thr Phe Asn Leu Lys
 500 505 510
 Ile Arg Asp Ile Asp Ala Ala Thr Glu Ala Lys His Arg Leu Glu Glu
 515 520 525
 Arg Gln Arg Ala Glu Ala Arg Glu Arg Lys Glu Lys Glu Ile Gln Trp
 530 535 540
 Glu Thr Arg Leu Phe His Glu Asp Gly Glu Cys Trp Val Tyr Asp Glu
 545 550 555 560

122

Pro Leu Leu Lys Arg Leu Gly Ala Ala Lys His
 565 570

<210> 83
 <211> 648
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(648)

<400> 83
 atg ctt ttg caa gtt gta cga gaa ggg aag ttc tcg ggg ttt ctg acc 48
 Met Leu Leu Gln Val Val Arg Glu Gly Lys Phe Ser Gly Phe Leu Thr
 1 5 10 15

tcc tgc agc ctc ctc ttg cct cgg gct gcc cag atc ttg gcg gct gag 96
 Ser Cys Ser Leu Leu Leu Pro Arg Ala Ala Gln Ile Leu Ala Ala Glu
 20 25 30

gct ggc tta cct tcg agc cgt tcc ttc atg gga ttt gct gct ccc ttc 144
 Ala Gly Leu Pro Ser Ser Arg Ser Phe Met Gly Phe Ala Ala Pro Phe
 35 40 45

acc aac aag cga aag gct tac tcg gag cgt aga atc atg ggg tac tca 192
 Thr Asn Lys Arg Lys Ala Tyr Ser Glu Arg Arg Ile Met Gly Tyr Ser
 50 55 60

atg cag gag atg tat gag gtg gtg tcc aac gtc cag gag tat cgt gag 240
 Met Gln Glu Met Tyr Glu Val Val Ser Asn Val Gln Glu Tyr Arg Glu
 65 70 75 80

ttt gtg ccc tgg tgt aag aag tct ctg gtg gta tcc agc cgt aag ggt 288
 Phe Val Pro Trp Cys Lys Lys Ser Leu Val Val Ser Ser Arg Lys Gly
 85 90 95

cat ttg aaa gcc cag ctg gag gtt ggc ttt cca cct gtc atg gaa cgt 336
 His Leu Lys Ala Gln Leu Glu Val Gly Phe Pro Pro Val Met Glu Arg
 100 105 110

tac acc tct gca gtt tcc atg gtc aaa cct cac atg gtc aag gct gtt 384
 Tyr Thr Ser Ala Val Ser Met Val Lys Pro His Met Val Lys Ala Val
 115 120 125

123

| | |
|---|-----|
| tgt act gat ggc aag ctc ttc aac cac tta gag act att tgg cga ttc | 432 |
| Cys Thr Asp Gly Lys Leu Phe Asn His Leu Glu Thr Ile Trp Arg Phe | |
| 130 135 140 | |
| agc cct ggt att cct gcc tat cct cga acc tgc act gtg gac ttt tcg | 480 |
| Ser Pro Gly Ile Pro Ala Tyr Pro Arg Thr Cys Thr Val Asp Phe Ser | |
| 145 150 155 160 | |
| att tcc ttt gaa ttt cgt tct ctg ctg cac tcc cag ctg gcc acc atg | 528 |
| Ile Ser Phe Glu Phe Arg Ser Leu Leu His Ser Gln Leu Ala Thr Met | |
| 165 170 175 | |
| ttt ttt gat gag gtt gtc aaa cag aat gtt gct gcc ttt gag cgt cgg | 576 |
| Phe Phe Asp Glu Val Val Lys Gln Asn Val Ala Ala Phe Glu Arg Arg | |
| 180 185 190 | |
| gca gcc acc aag ttt ggt cca gaa aca gcc atc ccc cgt gaa ctg atg | 624 |
| Ala Ala Thr Lys Phe Gly Pro Glu Thr Ala Ile Pro Arg Glu Leu Met | |
| 195 200 205 | |
| ttc cat gag gtg cac cag act tga | 648 |
| Phe His Glu Val His Gln Thr * | |
| 210 215 | |

<210> 84
 <211> 215
 <212> PRT
 <213> Homo sapiens

<400> 84

| | |
|---|--|
| Met Leu Leu Gln Val Val Arg Glu Gly Lys Phe Ser Gly Phe Leu Thr | |
| 1 5 10 15 | |
| Ser Cys Ser Leu Leu Leu Pro Arg Ala Ala Gln Ile Leu Ala Ala Glu | |
| 20 25 30 | |
| Ala Gly Leu Pro Ser Ser Arg Ser Phe Met Gly Phe Ala Ala Pro Phe | |
| 35 40 45 | |
| Thr Asn Lys Arg Lys Ala Tyr Ser Glu Arg Arg Ile Met Gly Tyr Ser | |
| 50 55 60 | |
| Met Gln Glu Met Tyr Glu Val Val Ser Asn Val Gln Glu Tyr Arg Glu | |
| 65 70 75 80 | |
| Phe Val Pro Trp Cys Lys Lys Ser Leu Val Val Ser Ser Arg Lys Gly | |
| 85 90 95 | |

124

His Leu Lys Ala Gln Leu Glu Val Gly Phe Pro Pro Val Met Glu Arg
 100 105 110
 Tyr Thr Ser Ala Val Ser Met Val Lys Pro His Met Val Lys Ala Val
 115 120 125
 Cys Thr Asp Gly Lys Leu Phe Asn His Leu Glu Thr Ile Trp Arg Phe
 130 135 140
 Ser Pro Gly Ile Pro Ala Tyr Pro Arg Thr Cys Thr Val Asp Phe Ser
 145 150 155 160
 Ile Ser Phe Glu Phe Arg Ser Leu Leu His Ser Gln Leu Ala Thr Met
 165 170 175
 Phe Phe Asp Glu Val Val Lys Gln Asn Val Ala Ala Phe Glu Arg Arg
 180 185 190
 Ala Ala Thr Lys Phe Gly Pro Glu Thr Ala Ile Pro Arg Glu Leu Met
 195 200 205
 Phe His Glu Val His Gln Thr
 210 215

<210> 85

<211> 615

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(615)

<400> 85

atg ggg ttt ctg acc tcc tgc agc ctc ctc ttg cct cgg gct gcc cag 48
 Met Gly Phe Leu Thr Ser Cys Ser Leu Leu Leu Pro Arg Ala Ala Gln
 1 5 10 15

atc ttg gcg gct gag gct ggc tta cct tcg agc cgt tcc ttc atg gga 96
 Ile Leu Ala Ala Glu Ala Gly Leu Pro Ser Ser Arg Ser Phe Met Gly
 20 25 30

ttt gct gct ccc ttc acc aac aag cga aag gct tac tcg gag cgt aga 144
 Phe Ala Ala Pro Phe Thr Asn Lys Arg Lys Ala Tyr Ser Glu Arg Arg
 35 40 45

atc atg ggg tac tca atg cag gag atg tat gag gtg gtg tcc aac gtc 192
 Ile Met Gly Tyr Ser Met Gln Glu Met Tyr Glu Val Val Ser Asn Val
 50 55 60

cag gag tat cgt gag ttt gtg ccc tgg tgt aag aag tct ctg gtg gta 240

125

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|
| Gln | Glu | Tyr | Arg | Glu | Phe | Val | Pro | Trp | Cys | Lys | Lys | Ser | Leu | Val | Val | | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | | |
| tcc | agc | cgt | aag | ggt | cat | ttg | aaa | gcc | cag | ctg | gag | gtt | ggc | ttt | cca | | 288 |
| Ser | Ser | Arg | Lys | Gly | His | Leu | Lys | Ala | Gln | Leu | Glu | Val | Gly | Phe | Pro | | |
| | | | 85 | | | | | | 90 | | | | | 95 | | | |
| cct | gtc | atg | gaa | cgt | tac | acc | tct | gca | gtt | tcc | atg | gtc | aaa | cct | cac | | 336 |
| Pro | Val | Met | Glu | Arg | Tyr | Thr | Ser | Ala | Val | Ser | Met | Val | Lys | Pro | His | | |
| | | | 100 | | | | | | 105 | | | | | 110 | | | |
| atg | gtc | aag | gct | gtt | tgt | act | gat | ggc | aag | ctc | ttc | aac | cac | tta | gag | | 384 |
| Met | Val | Lys | Ala | Val | Cys | Thr | Asp | Gly | Lys | Leu | Phe | Asn | His | Leu | Glu | | |
| | | | 115 | | | | | | 120 | | | | | 125 | | | |
| act | att | tgg | cga | ttc | agc | cct | ggt | att | cct | gcc | tat | cct | cga | acc | tgc | | 432 |
| Thr | Ile | Trp | Arg | Phe | Ser | Pro | Gly | Ile | Pro | Ala | Tyr | Pro | Arg | Thr | Cys | | |
| | | | 130 | | | | | | 135 | | | | | 140 | | | |
| act | gtg | gac | ttt | tcg | att | tcc | ttt | gaa | ttt | cgt | tct | ctg | ctg | cac | tcc | | 480 |
| Thr | Val | Asp | Phe | Ser | Ile | Ser | Phe | Glu | Phe | Arg | Ser | Leu | Leu | His | Ser | | |
| | | | 145 | | | | | | 150 | | | | | 155 | | | |
| cag | ctg | gcc | acc | atg | ttt | ttt | gat | gag | gtt | gtc | aaa | cag | aat | gtt | gct | | 528 |
| Gln | Leu | Ala | Thr | Met | Phe | Phe | Asp | Glu | Val | Val | Lys | Gln | Asn | Val | Ala | | |
| | | | 165 | | | | | | 170 | | | | | 175 | | | |
| gcc | ttt | gag | cgt | cgg | gca | gcc | acc | aag | ttt | ggt | cca | gaa | aca | gcc | atc | | 576 |
| Ala | Phe | Glu | Arg | Arg | Ala | Ala | Thr | Lys | Phe | Gly | Pro | Glu | Thr | Ala | Ile | | |
| | | | 180 | | | | | | 185 | | | | | 190 | | | |
| ccc | cgt | gaa | ctg | atg | ttc | cat | gag | gtg | cac | cag | act | tga | | | | | 615 |
| Pro | Arg | Glu | Leu | Met | Phe | His | Glu | Val | His | Gln | Thr | * | | | | | |
| | | | 195 | | | | | | 200 | | | | | | | | |

<210> 86

<211> 204

<212> PRT

<213> Homo sapiens

<400> 86

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Gly | Phe | Leu | Thr | Ser | Cys | Ser | Leu | Leu | Leu | Pro | Arg | Ala | Ala | Gln | | |
| 1 | | | | | 5 | | | | | 10 | | | | | 15 | | |

126

Ile Leu Ala Ala Glu Ala Gly Leu Pro Ser Ser Arg Ser Phe Met Gly
 20 25 30
 Phe Ala Ala Pro Phe Thr Asn Lys Arg Lys Ala Tyr Ser Glu Arg Arg
 35 40 45
 Ile Met Gly Tyr Ser Met Gln Glu Met Tyr Glu Val Val Ser Asn Val
 50 55 60
 Gln Glu Tyr Arg Glu Phe Val Pro Trp Cys Lys Lys Ser Leu Val Val
 65 70 75 80
 Ser Ser Arg Lys Gly His Leu Lys Ala Gln Leu Glu Val Gly Phe Pro
 85 90 95
 Pro Val Met Glu Arg Tyr Thr Ser Ala Val Ser Met Val Lys Pro His
 100 105 110
 Met Val Lys Ala Val Cys Thr Asp Gly Lys Leu Phe Asn His Leu Glu
 115 120 125
 Thr Ile Trp Arg Phe Ser Pro Gly Ile Pro Ala Tyr Pro Arg Thr Cys
 130 135 140
 Thr Val Asp Phe Ser Ile Ser Phe Glu Phe Arg Ser Leu Leu His Ser
 145 150 155 160
 Gln Leu Ala Thr Met Phe Phe Asp Glu Val Val Lys Gln Asn Val Ala
 165 170 175
 Ala Phe Glu Arg Arg Ala Ala Thr Lys Phe Gly Pro Glu Thr Ala Ile
 180 185 190
 Pro Arg Glu Leu Met Phe His Glu Val His Gln Thr
 195 200

<210> 87

<211> 570

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(570)

<400> 87

atg gcc ctg ctc tcg cgc ccc gcg ctc acc ctc ctg ctc ctc ctc atg
 Met Ala Leu Leu Ser Arg Pro Ala Leu Thr Leu Leu Leu Leu Met
 1 5 10 15

gcc gct gtt gtc agg tgc cag gag cag gcc cag acc acc gac tgg aga
 Ala Ala Val Val Arg Cys Gln Glu Gln Ala Gln Thr Thr Asp Trp Arg
 20 25 30

gcc acc ctg aag acc atc cgg aac ggc gtt cat aag ata gac acg tac
 144

127

| | |
|---|-----|
| Ala Thr Leu Lys Thr Ile Arg Asn Gly Val His Lys Ile Asp Thr Tyr | |
| 35 40 45 | |
| ctg aac gcc gcc ttg gac ctc ctg gga ggc gag gac ggt ctc tgc cag | 192 |
| Leu Asn Ala Ala Leu Asp Leu Leu Gly Gly Glu Asp Gly Leu Cys Gln | |
| 50 55 60 | |
| tat aaa tgc agt gac gga tct aag cct ttc cca cgt tat ggt tat aaa | 240 |
| Tyr Lys Cys Ser Asp Gly Ser Lys Pro Phe Pro Arg Tyr Gly Tyr Lys | |
| 65 70 75 80 | |
| ccc tcc cca ccg aat gga tgt ggc tct cca ctg ttt ggt gtt cat ctt | 288 |
| Pro Ser Pro Pro Asn Gly Cys Gly Ser Pro Leu Phe Gly Val His Leu | |
| 85 90 95 | |
| aac att ggt atc cct tcc ctg aca aag tgt tgc aac caa cac gac agg | 336 |
| Asn Ile Gly Ile Pro Ser Leu Thr Lys Cys Cys Asn Gln His Asp Arg | |
| 100 105 110 | |
| tgc tat gaa acc tgt ggc aaa agc aag aat gac tgt gat gaa gaa ttc | 384 |
| Cys Tyr Glu Thr Cys Gly Lys Ser Lys Asn Asp Cys Asp Glu Glu Phe | |
| 115 120 125 | |
| cag tat tgc ctc tcc aag atc tgc cga gat gta cag aaa aca cta gga | 432 |
| Gln Tyr Cys Leu Ser Lys Ile Cys Arg Asp Val Gln Lys Thr Leu Gly | |
| 130 135 140 | |
| cta act cag cat gtt cag gca tgt gaa aca aca gtg gag ctc ttg ttt | 480 |
| Leu Thr Gln His Val Gln Ala Cys Glu Thr Thr Val Glu Leu Leu Phe | |
| 145 150 155 160 | |
| gac agt gtt ata cat tta ggt tgt aaa cca tat ctg gac agc caa cga | 528 |
| Asp Ser Val Ile His Leu Gly Cys Lys Pro Tyr Leu Asp Ser Gln Arg | |
| 165 170 175 | |
| gcc gca tgc agg tgt cat tat gaa gaa aaa act gat ctt taa | 570 |
| Ala Ala Cys Arg Cys His Tyr Glu Glu Lys Thr Asp Leu * | |
| 180 185 | |

<210> 88

<211> 189

<212> PRT

<213> Homo sapiens

128

<400> 88

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Met Ala Leu Leu Ser Arg Pro Ala Leu Thr Leu Leu Leu Leu Met
 1           5           10           15
Ala Ala Val Val Arg Cys Gln Glu Gln Ala Gln Thr Thr Asp Trp Arg
 20           25           30
Ala Thr Leu Lys Thr Ile Arg Asn Gly Val His Lys Ile Asp Thr Tyr
 35           40           45
Leu Asn Ala Ala Leu Asp Leu Leu Gly Gly Glu Asp Gly Leu Cys Gln
 50           55           60
Tyr Lys Cys Ser Asp Gly Ser Lys Pro Phe Pro Arg Tyr Gly Tyr Lys
 65           70           75           80
Pro Ser Pro Pro Asn Gly Cys Gly Ser Pro Leu Phe Gly Val His Leu
 85           90           95
Asn Ile Gly Ile Pro Ser Leu Thr Lys Cys Cys Asn Gln His Asp Arg
100           105           110
Cys Tyr Glu Thr Cys Gly Lys Ser Lys Asn Asp Cys Asp Glu Glu Phe
115           120           125
Gln Tyr Cys Leu Ser Lys Ile Cys Arg Asp Val Gln Lys Thr Leu Gly
130           135           140
Leu Thr Gln His Val Gln Ala Cys Glu Thr Thr Val Glu Leu Leu Phe
145           150           155           160
Asp Ser Val Ile His Leu Gly Cys Lys Pro Tyr Leu Asp Ser Gln Arg
165           170           175
Ala Ala Cys Arg Cys His Tyr Glu Glu Lys Thr Asp Leu
180           185

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<210> 89

<211> 696

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(696)

<400> 89

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atg ttt ctg gtg ggc ctg aca ggg ggc att gcc tca ggc aag agc tca      48
Met Phe Leu Val Gly Leu Thr Gly Gly Ile Ala Ser Gly Lys Ser Ser
 1           5           10           15

gtg atc cag gtg ttc cag cag ctg ggc tgt gcg gtg att gac gtg gac      96
Val Ile Gln Val Phe Gln Gln Leu Gly Cys Ala Val Ile Asp Val Asp
 20           25           30

```

129

| | |
|---|-----|
| gtg atg gcc cgg cac gtc gtc cag cca gga tac cct gcc cac cgg cgc Val Met Ala Arg His Val Val Gln Pro Gly Tyr Pro Ala His Arg Arg 35 40 45 | 144 |
| atc gta gag gtc ttc ggc act gag gtc ttg ctg gag aac ggc gac ata Ile Val Glu Val Phe Gly Thr Glu Val Leu Leu Glu Asn Gly Asp Ile 50 55 60 | 192 |
| aat cgc aag gtc ctg ggg gac ctg atc ttt aac cag cct gac cgg cgg Asn Arg Lys Val Leu Gly Asp Leu Ile Phe Asn Gln Pro Asp Arg Arg 65 70 75 80 | 240 |
| cag ctg ctc aac gcc atc acc cac ccc gag att cgc aag gag atg atg Gln Leu Leu Asn Ala Ile Thr His Pro Glu Ile Arg Lys Glu Met Met 85 90 95 | 288 |
| aag gag acg ttc aag tac ttc ctc cgg gga tac cgc tac gtg att ctg Lys Glu Thr Phe Lys Tyr Phe Leu Arg Gly Tyr Arg Tyr Val Ile Leu 100 105 110 | 336 |
| gat atc ccc ctg ctg ttt gag acc aag aag ttg ctc aag tac atg aag Asp Ile Pro Leu Leu Phe Glu Thr Lys Lys Leu Leu Lys Tyr Met Lys 115 120 125 | 384 |
| cac acc gtg gta gta tac tgc gac cgg gac aca cag ctg gca cgg ctg His Thr Val Val Val Tyr Cys Asp Arg Asp Thr Gln Leu Ala Arg Leu 130 135 140 | 432 |
| atg cgg cgg aac agc ctg aac cgc aag gac gca gag gcc cgc atc aat Met Arg Arg Asn Ser Leu Asn Arg Lys Asp Ala Glu Ala Arg Ile Asn 145 150 155 160 | 480 |
| gcc cag ctg ccc ctg aca gac aag gcc cgc atg gcc cgc cat gtc cta Ala Gln Leu Pro Leu Thr Asp Lys Ala Arg Met Ala Arg His Val Leu 165 170 175 | 528 |
| gac aac tcg ggc gag tgg agt gtc acc aaa cgc cag gtc atc ctc ttg Asp Asn Ser Gly Glu Trp Ser Val Thr Lys Arg Gln Val Ile Leu Leu 180 185 190 | 576 |
| cac act gag ctg gag cgc tcc ctg gag tac ctg ccg ctg agg ttt ggg His Thr Glu Leu Glu Arg Ser Leu Glu Tyr Leu Pro Leu Arg Phe Gly 195 200 205 | 624 |

gtc ctc aca ggg ctc gct gcc att gcc agc ctc ctc tac ctg ctc acc 672
Val Leu Thr Gly Leu Ala Ala Ile Ala Ser Leu Leu Tyr Leu Leu Thr
210 215 220

cac tac ctt ctg cct tac gcc tag 696
His Tyr Leu Leu Pro Tyr Ala *
225 230

```
<210> 90
<211> 231
<212> PRT
<213> Homo sapiens
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| <400> 90 | | | | | | | | | | | | | | |
|----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | Leu | Val | Gly | Leu | Thr | Gly | Gly | Ile | Ala | Ser | Gly | Lys | Ser |
| 1 | | | | 5 | | | | | 10 | | | | | 15 |
| Val | Ile | Gln | Val | Phe | Gln | Gln | Leu | Gly | Cys | Ala | Val | Ile | Asp | Val |
| | | | 20 | | | | | 25 | | | | | 30 | |
| Val | Met | Ala | Arg | His | Val | Val | Gln | Pro | Gly | Tyr | Pro | Ala | His | Arg |
| | | 35 | | | | | 40 | | | | | 45 | | |
| Ile | Val | Glu | Val | Phe | Gly | Thr | Glu | Val | Leu | Leu | Glu | Asn | Gly | Asp |
| | 50 | | | | | 55 | | | | | 60 | | | |
| Asn | Arg | Lys | Val | Leu | Gly | Asp | Leu | Ile | Phe | Asn | Gln | Pro | Asp | Arg |
| 65 | | | | 70 | | | | | 75 | | | | | 80 |
| Gln | Leu | Leu | Asn | Ala | Ile | Thr | His | Pro | Glu | Ile | Arg | Lys | Glu | Met |
| | | | 85 | | | | | 90 | | | | | 95 | |
| Lys | Glu | Thr | Phe | Lys | Tyr | Phe | Leu | Arg | Gly | Tyr | Arg | Tyr | Val | Ile |
| | | | 100 | | | | | 105 | | | | | 110 | |
| Asp | Ile | Pro | Leu | Leu | Phe | Glu | Thr | Lys | Lys | Leu | Leu | Lys | Tyr | Met |
| | | 115 | | | | 120 | | | | | | 125 | | |
| His | Thr | Val | Val | Val | Tyr | Cys | Asp | Arg | Asp | Thr | Gln | Leu | Ala | Arg |
| | 130 | | | | | 135 | | | | | 140 | | | |
| Met | Arg | Arg | Asn | Ser | Leu | Asn | Arg | Lys | Asp | Ala | Glu | Ala | Arg | Ile |
| 145 | | | | 150 | | | | | 155 | | | | | 160 |
| Ala | Gln | Leu | Pro | Leu | Thr | Asp | Lys | Ala | Arg | Met | Ala | Arg | His | Val |
| | | | 165 | | | | | 170 | | | | | 175 | |
| Asp | Asn | Ser | Gly | Glu | Trp | Ser | Val | Thr | Lys | Arg | Gln | Val | Ile | Leu |
| | | | 180 | | | | | 185 | | | | | 190 | |
| His | Thr | Glu | Leu | Glu | Arg | Ser | Leu | Glu | Tyr | Leu | Pro | Leu | Arg | Phe |
| | | 195 | | | | 200 | | | | | 205 | | | |
| Val | Leu | Thr | Gly | Leu | Ala | Ala | Ile | Ala | Ser | Leu | Leu | Tyr | Leu | Leu |
| | 210 | | | | | 215 | | | | | 220 | | | |

131

His Tyr Leu Leu Pro Tyr Ala
 225 230

<210> 91
 <211> 198
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(198)

<221> misc_feature
 <222> (1)...(198)
 <223> n = A,T,C or G

<400> 91
 atg gac gca ctg gcg ctg ctt ggg gga ctg gta aat nta gcc cgt ctg 48
 Met Asp Ala Leu Ala Leu Leu Gly Gly Leu Val Asn Xaa Ala Arg Leu
 1 5 10 15
 ccc gag cgc tgg gga cct ggc cgc ttt gac tac tgg ggc aac tcc cac 96
 Pro Glu Arg Trp Gly Pro Gly Arg Phe Asp Tyr Trp Gly Asn Ser His
 20 25 30
 cag atc atg cac ctg ctg agc gtg ggc tcc atc ctg cag ctg cac gcc 144
 Gln Ile Met His Leu Leu Ser Val Gly Ser Ile Leu Gln Leu His Ala
 35 40 45
 ggc gtc gtg ccc gac ctg ctc tgg gct gcc cac cac gcc tgt ccc cgg 192
 Gly Val Val Pro Asp Leu Leu Trp Ala Ala His His Ala Cys Pro Arg
 50 55 60
 gac tga 198
 Asp *
 65

<210> 92
 <211> 65
 <212> PRT
 <213> Homo sapiens

<220>

132

<221> VARIANT

<222> (1)...(65)

<223> Xaa = Any Amino Acid

<400> 92

```

Met Asp Ala Leu Ala Leu Leu Gly Gly Leu Val Asn Xaa Ala Arg Leu
 1             5             10             15
Pro Glu Arg Trp Gly Pro Gly Arg Phe Asp Tyr Trp Gly Asn Ser His
          20             25             30
Gln Ile Met His Leu Leu Ser Val Gly Ser Ile Leu Gln Leu His Ala
          35             40             45
Gly Val Val Pro Asp Leu Leu Trp Ala Ala His His Ala Cys Pro Arg
          50             55             60
Asp
65

```

<210> 93

<211> 498

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(498)

<400> 93

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atg gtg tct aca gtg ttc tcg act tcg tcg ctg atg ctt gct ctg tca      48
Met Val Ser Thr Val Phe Ser Thr Ser Ser Leu Met Leu Ala Leu Ser
 1             5             10             15

agg cac agc cta ttg tct cct ttg ctc agt gtg aca tca ttc aga cgc      96
Arg His Ser Leu Leu Ser Pro Leu Leu Ser Val Thr Ser Phe Arg Arg
          20             25             30

ttc tac aga ggt gac agc cca aca gat tcc caa aag gac atg att gaa      144
Phe Tyr Arg Gly Asp Ser Pro Thr Asp Ser Gln Lys Asp Met Ile Glu
          35             40             45

atc cct ttg cct cca tgg cag gag aga act gat gaa tcc ata gaa acc      192
Ile Pro Leu Pro Pro Trp Gln Glu Arg Thr Asp Glu Ser Ile Glu Thr
          50             55             60

aaa aga gcc cgc ctg ctc tat gag agc aga aag agg gga atg ttg gaa      240
Lys Arg Ala Arg Leu Leu Tyr Glu Ser Arg Lys Arg Gly Met Leu Glu

```


133

| | | | | |
|---|-----|-----|-----|-----|
| 65 | 70 | 75 | 80 | |
| aac tgc att ctt ctt agt ctt ttt gct aaa gaa cat ctg cag cac atg | | | | 288 |
| Asn Cys Ile Leu Leu Ser Leu Phe Ala Lys Glu His Leu Gln His Met | | | | |
| | 85 | 90 | 95 | |
| aca gaa aag cag ctg aac ctc tat gac cgc ctg att aac gag cct agt | | | | 336 |
| Thr Glu Lys Gln Leu Asn Leu Tyr Asp Arg Leu Ile Asn Glu Pro Ser | | | | |
| | 100 | 105 | 110 | |
| aat gac tgg gat att tac tac tgg gcc aca gaa gct aaa cca gcc cca | | | | 384 |
| Asn Asp Trp Asp Ile Tyr Tyr Trp Ala Thr Glu Ala Lys Pro Ala Pro | | | | |
| | 115 | 120 | 125 | |
| gaa ata ttt gaa aat gaa gtc atg gcc ctg ctg aga gac ttt gct aaa | | | | 432 |
| Glu Ile Phe Glu Asn Glu Val Met Ala Leu Leu Arg Asp Phe Ala Lys | | | | |
| | 130 | 135 | 140 | |
| aac aaa aac aaa gag cag aga ctg cgt gcc cca gat ctt gag tac ctc | | | | 480 |
| Asn Lys Asn Lys Glu Gln Arg Leu Arg Ala Pro Asp Leu Glu Tyr Leu | | | | |
| | 145 | 150 | 155 | 160 |
| ttt gaa aag cca cgt tga | | | | 498 |
| Phe Glu Lys Pro Arg * | | | | |
| | 165 | | | |

<210> 94

<211> 165

<212> PRT

<213> Homo sapiens

<400> 94

| | | | | |
|---|----|----|----|--|
| Met Val Ser Thr Val Phe Ser Thr Ser Ser Leu Met Leu Ala Leu Ser | | | | |
| 1 | 5 | 10 | 15 | |
| Arg His Ser Leu Leu Ser Pro Leu Leu Ser Val Thr Ser Phe Arg Arg | | | | |
| | 20 | 25 | 30 | |
| Phe Tyr Arg Gly Asp Ser Pro Thr Asp Ser Gln Lys Asp Met Ile Glu | | | | |
| | 35 | 40 | 45 | |
| Ile Pro Leu Pro Pro Trp Gln Glu Arg Thr Asp Glu Ser Ile Glu Thr | | | | |
| | 50 | 55 | 60 | |
| Lys Arg Ala Arg Leu Leu Tyr Glu Ser Arg Lys Arg Gly Met Leu Glu | | | | |
| 65 | 70 | 75 | 80 | |
| Asn Cys Ile Leu Leu Ser Leu Phe Ala Lys Glu His Leu Gln His Met | | | | |

[illegible]

```
<220>  
<221> CDS  
<222> (1)...(501)
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| | | | | | | | | | | | | | | | | |
|----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> 95 | | | | | | | | | | | | | | | | |
| atg | gcg | gtg | tct | aca | gtg | ttc | tcg | act | tcg | tcg | ctg | atg | ctt | gct | ctg | 48 |
| Met | Ala | Val | Ser | Thr | Val | Phe | Ser | Thr | Ser | Ser | Leu | Met | Leu | Ala | Leu | |
| 1 | | | | 5 | | | | 10 | | | | 15 | | | | |
| | | | | | | | | | | | | | | | | |
| tca | agg | cac | agc | cta | ttg | tct | cct | ttg | ctc | agt | gtg | aca | tca | ttc | aga | 96 |
| Ser | Arg | His | Ser | Leu | Leu | Ser | Pro | Leu | Leu | Ser | Val | Thr | Ser | Phe | Arg | |
| 20 | | | | 25 | | | | 30 | | | | | | | | |
| | | | | | | | | | | | | | | | | |
| cgc | ttc | tac | aga | ggt | gac | agc | cca | aca | gat | tcc | caa | aag | gac | atg | att | 144 |
| Arg | Phe | Tyr | Arg | Gly | Asp | Ser | Pro | Thr | Asp | Ser | Gln | Lys | Asp | Met | Ile | |
| 35 | | | | 40 | | | | 45 | | | | | | | | |
| | | | | | | | | | | | | | | | | |
| gaa | atc | cct | ttg | cct | cca | tgg | cag | gag | aga | act | gat | gaa | tcc | ata | gaa | 192 |
| Glu | Ile | Pro | Leu | Pro | Pro | Trp | Gln | Glu | Arg | Thr | Asp | Glu | Ser | Ile | Glu | |
| 50 | | | | 55 | | | | 60 | | | | | | | | |
| | | | | | | | | | | | | | | | | |
| acc | aaa | aga | gcc | cgc | ctg | ctc | tat | gag | agc | aga | aag | agg | gga | atg | ttg | 240 |
| Thr | Lys | Arg | Ala | Arg | Leu | Leu | Tyr | Glu | Ser | Arg | Lys | Arg | Gly | Met | Leu | |
| 65 | | | | 70 | | | | 75 | | | | 80 | | | | |
| | | | | | | | | | | | | | | | | |
| gaa | aac | tgc | att | ctt | ctt | agt | ctt | ttt | gct | aaa | gaa | cat | ctg | cag | cac | 288 |
| Glu | Asn | Cys | Ile | Leu | Leu | Ser | Leu | Phe | Ala | Lys | Glu | His | Leu | Gln | His | |

135

85

90

95

atg aca gaa aag cag ctg aac ctc tat gac cgc ctg att aac gag cct 336
 Met Thr Glu Lys Gln Leu Asn Leu Tyr Asp Arg Leu Ile Asn Glu Pro
 100 105 110

agt aat gac tgg gat att tac tac tgg gcc aca gaa gct aaa cca gcc 384
 Ser Asn Asp Trp Asp Ile Tyr Tyr Trp Ala Thr Glu Ala Lys Pro Ala
 115 120 125

cca gaa ata ttt gaa aat gaa gtc atg gcc ctg ctg aga gac ttt gct 432
 Pro Glu Ile Phe Glu Asn Glu Val Met Ala Leu Leu Arg Asp Phe Ala
 130 135 140

aaa aac aaa aac aaa gag cag aga ctg cgt gcc cca gat ctt gag tac 480
 Lys Asn Lys Asn Lys Glu Gln Arg Leu Arg Ala Pro Asp Leu Glu Tyr
 145 150 155 160

ctc ttt gaa aag cca cgt tga 501
 Leu Phe Glu Lys Pro Arg *
 165

<210> 96

<211> 166

<212> PRT

<213> Homo sapiens

<400> 96

Met Ala Val Ser Thr Val Phe Ser Thr Ser Ser Leu Met Leu Ala Leu
 1 5 10 15
 Ser Arg His Ser Leu Leu Ser Pro Leu Leu Ser Val Thr Ser Phe Arg
 20 25 30
 Arg Phe Tyr Arg Gly Asp Ser Pro Thr Asp Ser Gln Lys Asp Met Ile
 35 40 45
 Glu Ile Pro Leu Pro Pro Trp Gln Glu Arg Thr Asp Glu Ser Ile Glu
 50 55 60
 Thr Lys Arg Ala Arg Leu Leu Tyr Glu Ser Arg Lys Arg Gly Met Leu
 65 70 75 80
 Glu Asn Cys Ile Leu Leu Ser Leu Phe Ala Lys Glu His Leu Gln His
 85 90 95
 Met Thr Glu Lys Gln Leu Asn Leu Tyr Asp Arg Leu Ile Asn Glu Pro
 100 105 110
 Ser Asn Asp Trp Asp Ile Tyr Tyr Trp Ala Thr Glu Ala Lys Pro Ala

136

115 120 125
 Pro Glu Ile Phe Glu Asn Glu Val Met Ala Leu Leu Arg Asp Phe Ala
 130 135 140
 Lys Asn Lys Asn Lys Glu Gln Arg Leu Arg Ala Pro Asp Leu Glu Tyr
 145 150 155 160
 Leu Phe Glu Lys Pro Arg
 165

<210> 97
 <211> 492
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(492)

<400> 97
 atg gct ggc ttc tat gga ttg tat acc tgg ctg act cat act atg ttt 48
 Met Ala Gly Phe Tyr Gly Leu Tyr Thr Trp Leu Thr His Thr Met Phe
 1 5 10 15
 ggc atc aat att gtc ttc ata cca tca gca tta gca gca atc ctt gga 96
 Gly Ile Asn Ile Val Phe Ile Pro Ser Ala Leu Ala Ala Ile Leu Gly
 20 25 30
 gca gtg cca ttc ctg ggg aca tac tgg gca gca gta cct gca gtt ctt 144
 Ala Val Pro Phe Leu Gly Thr Tyr Trp Ala Ala Val Pro Ala Val Leu
 35 40 45
 gac ctg tgg ctg aca caa ggg tta gga tgc aag gcc att tta ctg ttg 192
 Asp Leu Trp Leu Thr Gln Gly Leu Gly Cys Lys Ala Ile Leu Leu Leu
 50 55 60
 att ttt cat ctc ttg cca aca tac ttt gta gat act gca atc tac tct 240
 Ile Phe His Leu Leu Pro Thr Tyr Phe Val Asp Thr Ala Ile Tyr Ser
 65 70 75 80
 gac ata tca gga ggt ggc cat cct tac ctg aca ggc ttg gca gtg gcc 288
 Asp Ile Ser Gly Gly Gly His Pro Tyr Leu Thr Gly Leu Ala Val Ala
 85 90 95
 ggt gga gca tac tac cta ggc ctg gaa gga gca atc atc ggt cct att 336
 Gly Gly Ala Tyr Tyr Leu Gly Leu Glu Gly Ala Ile Ile Gly Pro Ile

137

| 100 | 105 | 110 | |
|---|-----|-----|-----|
| ctt ctc tgc ata ctt gtg gtt gct tcc aat atc tat agt gcc atg cta | | | 384 |
| Leu Leu Cys Ile Leu Val Val Ala Ser Asn Ile Tyr Ser Ala Met Leu | | | |
| 115 | 120 | 125 | |
| gtg agt ccc acg aat tca gtt ccc acg cca aac cag acc cca tgg cct | | | 432 |
| Val Ser Pro Thr Asn Ser Val Pro Thr Pro Asn Gln Thr Pro Trp Pro | | | |
| 130 | 135 | 140 | |
| gct cag cct cag cgg act ttc cgt gac att tct gaa gat ctg aaa tct | | | 480 |
| Ala Gln Pro Gln Arg Thr Phe Arg Asp Ile Ser Glu Asp Leu Lys Ser | | | |
| 145 | 150 | 155 | 160 |
| tca gta ggt tga | | | 492 |
| Ser Val Gly * | | | |

<210> 98
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 98

| | | | |
|---|-----|-----|----|
| Met Ala Gly Phe Tyr Gly Leu Tyr Thr Trp Leu Thr His Thr Met Phe | | | |
| 1 | 5 | 10 | 15 |
| Gly Ile Asn Ile Val Phe Ile Pro Ser Ala Leu Ala Ala Ile Leu Gly | | | |
| 20 | 25 | 30 | |
| Ala Val Pro Phe Leu Gly Thr Tyr Trp Ala Ala Val Pro Ala Val Leu | | | |
| 35 | 40 | 45 | |
| Asp Leu Trp Leu Thr Gln Gly Leu Gly Cys Lys Ala Ile Leu Leu Leu | | | |
| 50 | 55 | 60 | |
| Ile Phe His Leu Leu Pro Thr Tyr Phe Val Asp Thr Ala Ile Tyr Ser | | | |
| 65 | 70 | 75 | 80 |
| Asp Ile Ser Gly Gly Gly His Pro Tyr Leu Thr Gly Leu Ala Val Ala | | | |
| 85 | 90 | 95 | |
| Gly Gly Ala Tyr Tyr Leu Gly Leu Glu Gly Ala Ile Ile Gly Pro Ile | | | |
| 100 | 105 | 110 | |
| Leu Leu Cys Ile Leu Val Val Ala Ser Asn Ile Tyr Ser Ala Met Leu | | | |
| 115 | 120 | 125 | |
| Val Ser Pro Thr Asn Ser Val Pro Thr Pro Asn Gln Thr Pro Trp Pro | | | |
| 130 | 135 | 140 | |
| Ala Gln Pro Gln Arg Thr Phe Arg Asp Ile Ser Glu Asp Leu Lys Ser | | | |

138

145 150 155 160
 Ser Val Gly

<210> 99
 <211> 1464
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1464)

<221> misc_feature
 <222> (1)...(1464)
 <223> n = A,T,C or G

<400> 99

atg tgg gga cct aac tcc tat gca tgg gtg ctc atg cag ttg gcc acc 48
 Met Trp Gly Pro Asn Ser Tyr Ala Trp Val Leu Met Gln Leu Ala Thr
 1 5 10 15

gcc cag gcg ggc atc att ctg gtg tct gtg aac cca gcc tac cag gct 96
 Ala Gln Ala Gly Ile Ile Leu Val Ser Val Asn Pro Ala Tyr Gln Ala
 20 25 30

atg gaa ctg gag tac gtc ctc aag aag gtg ggc tgc aag gcc ctt gtg 144
 Met Glu Leu Glu Tyr Val Leu Lys Lys Val Gly Cys Lys Ala Leu Val
 35 40 45

ttc ccc aag caa ttc aag acc cag caa tac tac aac gtc ctg aag cag 192
 Phe Pro Lys Gln Phe Lys Thr Gln Gln Tyr Tyr Asn Val Leu Lys Gln
 50 55 60

atc tgt cca gaa gtg gag aat gcc cag cca ggg gcc ttg aag agt cag 240
 Ile Cys Pro Glu Val Glu Asn Ala Gln Pro Gly Ala Leu Lys Ser Gln
 65 70 75 80

agg ctc cca gat ctg acc aca gtc atc tcg gtg gat gcc cct ttg ccg 288
 Arg Leu Pro Asp Leu Thr Thr Val Ile Ser Val Asp Ala Pro Leu Pro
 85 90 95

ggg acc ctg ctc ctg gat gaa gtg gtg gcg gct ggc agc aca cgg cag 336
 Gly Thr Leu Leu Leu Asp Glu Val Val Ala Ala Gly Ser Thr Arg Gln

139

| 100 | 105 | 110 | |
|---|-----|-----|-----|
| cat ctg gac cag ctc caa tac aac cag cag ttc ctg tcc tgc cat gac | | | 384 |
| His Leu Asp Gln Leu Gln Tyr Asn Gln Gln Phe Leu Ser Cys His Asp | | | |
| 115 | 120 | 125 | |
| ccc atc aac atc cag ttc acc tcg ggg aca aca ggc agc ccc aag ggg | | | 432 |
| Pro Ile Asn Ile Gln Phe Thr Ser Gly Thr Thr Gly Ser Pro Lys Gly | | | |
| 130 | 135 | 140 | |
| gcc acc ctc tcc cac tac aac att gtc aac aac tcc aac att tta gga | | | 480 |
| Ala Thr Leu Ser His Tyr Asn Ile Val Asn Asn Ser Asn Ile Leu Gly | | | |
| 145 | 150 | 155 | 160 |
| gag cgc ctg aaa ctg cat gag aag aca cca gag cag ttg cgg atg atc | | | 528 |
| Glu Arg Leu Lys Leu His Glu Lys Thr Pro Glu Gln Leu Arg Met Ile | | | |
| 165 | 170 | 175 | |
| ctg ccc aac ccc ctg tac cat tgc ctg ggt tcc gtg gca ggc aca atg | | | 576 |
| Leu Pro Asn Pro Leu Tyr His Cys Leu Gly Ser Val Ala Gly Thr Met | | | |
| 180 | 185 | 190 | |
| atg tgt ctg atg tac ggt gcc acc ctc atc ctg gcc tct ccc atc ttc | | | 624 |
| Met Cys Leu Met Tyr Gly Ala Thr Leu Ile Leu Ala Ser Pro Ile Phe | | | |
| 195 | 200 | 205 | |
| aat ggc aag aag gca ctg gag gcc atc agc aga gag aga ggc acc ttc | | | 672 |
| Asn Gly Lys Lys Ala Leu Glu Ala Ile Ser Arg Glu Arg Gly Thr Phe | | | |
| 210 | 215 | 220 | |
| ctg tat ggt acc ccc acg atg ttc gtg gac att ctg aac cag cca gac | | | 720 |
| Leu Tyr Gly Thr Pro Thr Met Phe Val Asp Ile Leu Asn Gln Pro Asp | | | |
| 225 | 230 | 235 | 240 |
| ttc tcc agt tat gac atc tcg acc atg tgt gga ggt gtc att gct ggg | | | 768 |
| Phe Ser Ser Tyr Asp Ile Ser Thr Met Cys Gly Gly Val Ile Ala Gly | | | |
| 245 | 250 | 255 | |
| tcc cct gca cct cca gag ttg atc cga gcc atc atc aac aag ata aat | | | 816 |
| Ser Pro Ala Pro Pro Glu Leu Ile Arg Ala Ile Ile Asn Lys Ile Asn | | | |
| 260 | 265 | 270 | |
| atg aag gac ctg gtg gtt gct tat gga acc aca gag aac agt ccc gtg | | | 864 |
| Met Lys Asp Leu Val Val Ala Tyr Gly Thr Thr Glu Asn Ser Pro Val | | | |

140

| 275 | 280 | 285 | |
|---|-----|-----|------|
| aca ttc gcg cac ttc cct gag gac act gtg gag cag aag gca gaa agc | | | 912 |
| Thr Phe Ala His Phe Pro Glu Asp Thr Val Glu Gln Lys Ala Glu Ser | | | |
| 290 | 295 | 300 | |
| gtg ggc aga att atg cct cac acg gag gcc cgg atc atg aac atg gag | | | 960 |
| Val Gly Arg Ile Met Pro His Thr Glu Ala Arg Ile Met Asn Met Glu | | | |
| 305 | 310 | 315 | 320 |
| gca ggg acg ctg gca aag ctg aac acg ccc ggg gag ctg tgc atc cga | | | 1008 |
| Ala Gly Thr Leu Ala Lys Leu Asn Thr Pro Gly Glu Leu Cys Ile Arg | | | |
| 325 | 330 | 335 | |
| ggg tac tgc gtc atg ctg ggc tac tgg ggt gag cct cag aag aca gag | | | 1056 |
| Gly Tyr Cys Val Met Leu Gly Tyr Trp Gly Glu Pro Gln Lys Thr Glu | | | |
| 340 | 345 | 350 | |
| gaa gca gtg gat cag gac aag tgg tat tgg aca gga gat gtc gcc aca | | | 1104 |
| Glu Ala Val Asp Gln Asp Lys Trp Tyr Trp Thr Gly Asp Val Ala Thr | | | |
| 355 | 360 | 365 | |
| atg aat gag cag ggc ttc tgc aag atc gtg ggc cgc tct aag gat atg | | | 1152 |
| Met Asn Glu Gln Gly Phe Cys Lys Ile Val Gly Arg Ser Lys Asp Met | | | |
| 370 | 375 | 380 | |
| atc atc cgg ggt ggt gag aac atc tac ccc gca gag ctc gag gac ttc | | | 1200 |
| Ile Ile Arg Gly Gly Glu Asn Ile Tyr Pro Ala Glu Leu Glu Asp Phe | | | |
| 385 | 390 | 395 | 400 |
| ttt cac aca cac ccg aag ntg cag gaa gtg cag gtg gtg gga gtg aag | | | 1248 |
| Phe His Thr His Pro Lys Xaa Gln Glu Val Gln Val Val Gly Val Lys | | | |
| 405 | 410 | 415 | |
| gac gat cgg atg ggg gaa gag att tgt gcc tgc att cgg ctg aag gac | | | 1296 |
| Asp Asp Arg Met Gly Glu Glu Ile Cys Ala Cys Ile Arg Leu Lys Asp | | | |
| 420 | 425 | 430 | |
| ggg gag gag acc acg gtg gag gag ata aaa gct ttc tgc aaa ggg aag | | | 1344 |
| Gly Glu Glu Thr Thr Val Glu Glu Ile Lys Ala Phe Cys Lys Gly Lys | | | |
| 435 | 440 | 445 | |
| atc tct cac ttc aag att ccg aag tac atc gtg ttt gtc aca aac tac | | | 1392 |
| Ile Ser His Phe Lys Ile Pro Lys Tyr Ile Val Phe Val Thr Asn Tyr | | | |

141

450 455 460
 ccc ctc acc att tca gga aag atc cag aaa ttc aaa ctt cga gag cag 1440
 Pro Leu Thr Ile Ser Gly Lys Ile Gln Lys Phe Lys Leu Arg Glu Gln
 465 470 475 480

 atg gaa cga cat cta aat ctg tga 1464
 Met Glu Arg His Leu Asn Leu *
 485

<210> 100
 <211> 487
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(487).
 <223> Xaa = Any Amino Acid

<400> 100
 Met Trp Gly Pro Asn Ser Tyr Ala Trp Val Leu Met Gln Leu Ala Thr
 1 5 10 15
 Ala Gln Ala Gly Ile Ile Leu Val Ser Val Asn Pro Ala Tyr Gln Ala
 20 25 30
 Met Glu Leu Glu Tyr Val Leu Lys Lys Val Gly Cys Lys Ala Leu Val
 35 40 45
 Phe Pro Lys Gln Phe Lys Thr Gln Gln Tyr Tyr Asn Val Leu Lys Gln
 50 55 60
 Ile Cys Pro Glu Val Glu Asn Ala Gln Pro Gly Ala Leu Lys Ser Gln
 65 70 75 80
 Arg Leu Pro Asp Leu Thr Thr Val Ile Ser Val Asp Ala Pro Leu Pro
 85 90 95
 Gly Thr Leu Leu Leu Asp Glu Val Val Ala Ala Gly Ser Thr Arg Gln
 100 105 110
 His Leu Asp Gln Leu Gln Tyr Asn Gln Gln Phe Leu Ser Cys His Asp
 115 120 125
 Pro Ile Asn Ile Gln Phe Thr Ser Gly Thr Thr Gly Ser Pro Lys Gly
 130 135 140
 Ala Thr Leu Ser His Tyr Asn Ile Val Asn Asn Ser Asn Ile Leu Gly
 145 150 155 160
 Glu Arg Leu Lys Leu His Glu Lys Thr Pro Glu Gln Leu Arg Met Ile
 165 170 175

142

Leu Pro Asn Pro Leu Tyr His Cys Leu Gly Ser Val Ala Gly Thr Met
 180 185 190
 Met Cys Leu Met Tyr Gly Ala Thr Leu Ile Leu Ala Ser Pro Ile Phe
 195 200 205
 Asn Gly Lys Lys Ala Leu Glu Ala Ile Ser Arg Glu Arg Gly Thr Phe
 210 215 220
 Leu Tyr Gly Thr Pro Thr Met Phe Val Asp Ile Leu Asn Gln Pro Asp
 225 230 235 240
 Phe Ser Ser Tyr Asp Ile Ser Thr Met Cys Gly Gly Val Ile Ala Gly
 245 250 255
 Ser Pro Ala Pro Pro Glu Leu Ile Arg Ala Ile Ile Asn Lys Ile Asn
 260 265 270
 Met Lys Asp Leu Val Val Ala Tyr Gly Thr Thr Glu Asn Ser Pro Val
 275 280 285
 Thr Phe Ala His Phe Pro Glu Asp Thr Val Glu Gln Lys Ala Glu Ser
 290 295 300
 Val Gly Arg Ile Met Pro His Thr Glu Ala Arg Ile Met Asn Met Glu
 305 310 315 320
 Ala Gly Thr Leu Ala Lys Leu Asn Thr Pro Gly Glu Leu Cys Ile Arg
 325 330 335
 Gly Tyr Cys Val Met Leu Gly Tyr Trp Gly Glu Pro Gln Lys Thr Glu
 340 345 350
 Glu Ala Val Asp Gln Asp Lys Trp Tyr Trp Thr Gly Asp Val Ala Thr
 355 360 365
 Met Asn Glu Gln Gly Phe Cys Lys Ile Val Gly Arg Ser Lys Asp Met
 370 375 380
 Ile Ile Arg Gly Gly Glu Asn Ile Tyr Pro Ala Glu Leu Glu Asp Phe
 385 390 395 400
 Phe His Thr His Pro Lys Xaa Gln Glu Val Gln Val Val Gly Val Lys
 405 410 415
 Asp Asp Arg Met Gly Glu Glu Ile Cys Ala Cys Ile Arg Leu Lys Asp
 420 425 430
 Gly Glu Glu Thr Thr Val Glu Glu Ile Lys Ala Phe Cys Lys Gly Lys
 435 440 445
 Ile Ser His Phe Lys Ile Pro Lys Tyr Ile Val Phe Val Thr Asn Tyr
 450 455 460
 Pro Leu Thr Ile Ser Gly Lys Ile Gln Lys Phe Lys Leu Arg Glu Gln
 465 470 475 480
 Met Glu Arg His Leu Asn Leu
 485

<210> 101

<211> 348

<212> DNA

143

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(348)

<400> 101

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| atg | ggg | atc | acc | ttc | ctg | gct | gct | ggg | acc | agc | gtg | cct | gac | tgc | atg | 48 |
| Met | Gly | Ile | Thr | Phe | Leu | Ala | Ala | Gly | Thr | Ser | Val | Pro | Asp | Cys | Met | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| gcc | agc | ctc | att | gtg | gcc | aga | caa | ggg | atg | ggg | gac | atg | gct | gtg | tcc | 96 |
| Ala | Ser | Leu | Ile | Val | Ala | Arg | Gln | Gly | Met | Gly | Asp | Met | Ala | Val | Ser | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| aac | tcc | att | ggg | agc | aac | gtg | ttt | gac | atc | ctg | att | ggc | ctc | ggt | ctc | 144 |
| Asn | Ser | Ile | Gly | Ser | Asn | Val | Phe | Asp | Ile | Leu | Ile | Gly | Leu | Gly | Leu | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ccc | tgg | gct | ctg | cag | acc | ctg | gct | gtg | gat | tac | gga | tcc | tac | atc | cgg | 192 |
| Pro | Trp | Ala | Leu | Gln | Thr | Leu | Ala | Val | Asp | Tyr | Gly | Ser | Tyr | Ile | Arg | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ctg | aat | agc | agg | ggg | ctg | atc | tac | tcc | gta | ggc | ttg | ctc | ctg | gcc | tct | 240 |
| Leu | Asn | Ser | Arg | Gly | Leu | Ile | Tyr | Ser | Val | Gly | Leu | Leu | Leu | Ala | Ser | |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gtt | ttt | gtc | acg | gtg | ttc | ggc | gtc | cac | ctg | aac | aag | tgg | cag | ctg | gac | 288 |
| Val | Phe | Val | Thr | Val | Phe | Gly | Val | His | Leu | Asn | Lys | Trp | Gln | Leu | Asp | |
| | | | 85 | | | | | 90 | | | | | | 95 | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| aag | aag | ctg | ggc | tgt | ggg | tgc | ctc | ctc | ctg | tat | ggg | tgt | tcc | tgt | gct | 336 |
| Lys | Lys | Leu | Gly | Cys | Gly | Cys | Leu | Leu | Leu | Tyr | Gly | Cys | Ser | Cys | Ala | |
| | | 100 | | | | | 105 | | | | | | 110 | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|--|--|--|--|--|--|--|--|--|--|--|--|-----|
| tct | cca | tca | tga | | | | | | | | | | | | | 348 |
| Ser | Pro | Ser | * | | | | | | | | | | | | | |
| | | 115 | | | | | | | | | | | | | | |

<210> 102

<211> 115

<212> PRT

<213> Homo sapiens

144

<400> 102

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Met Gly Ile Thr Phe Leu Ala Ala Gly Thr Ser Val Pro Asp Cys Met
 1           5           10           15
Ala Ser Leu Ile Val Ala Arg Gln Gly Met Gly Asp Met Ala Val Ser
      20           25           30
Asn Ser Ile Gly Ser Asn Val Phe Asp Ile Leu Ile Gly Leu Gly Leu
      35           40           45
Pro Trp Ala Leu Gln Thr Leu Ala Val Asp Tyr Gly Ser Tyr Ile Arg
      50           55           60
Leu Asn Ser Arg Gly Leu Ile Tyr Ser Val Gly Leu Leu Leu Ala Ser
65           70           75           80
Val Phe Val Thr Val Phe Gly Val His Leu Asn Lys Trp Gln Leu Asp
      85           90           95
Lys Lys Leu Gly Cys Gly Cys Leu Leu Tyr Gly Cys Ser Cys Ala
      100           105           110
Ser Pro Ser
      115

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<210> 103

<211> 1239

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1239)

<400> 103

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atg gcg ggc tct gtg gga ctg gcg ttg tgc ggg cag acg ttg gtg gtg      48
Met Ala Gly Ser Val Gly Leu Ala Leu Cys Gly Gln Thr Leu Val Val
 1           5           10           15

cgg ggc ggc agc cga ttc ctg gcc acc tcc ata gca agc agt gat gat      96
Arg Gly Gly Ser Arg Phe Leu Ala Thr Ser Ile Ala Ser Ser Asp Asp
      20           25           30

gac agc ctc ttc atc tat gac tgc agt gct gca gaa aag aag tca caa      144
Asp Ser Leu Phe Ile Tyr Asp Cys Ser Ala Ala Glu Lys Lys Ser Gln
      35           40           45

gaa aat aaa ggg gag gac gcg ccc ttg gac cag ggg agc ggt gcg att      192
Glu Asn Lys Gly Glu Asp Ala Pro Leu Asp Gln Gly Ser Gly Ala Ile
      50           55           60

```

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ctg | gcg | tcc | acc | ttc | tcc | aag | tct | ggc | agc | tat | ttt | gct | tta | acc | gat | 240 |
| Leu | Ala | Ser | Thr | Phe | Ser | Lys | Ser | Gly | Ser | Tyr | Phe | Ala | Leu | Thr | Asp | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| gac | agt | aag | cgt | ctg | att | ctt | ttc | cgt | aca | aaa | cca | tgg | caa | tgt | ctg | 288 |
| Asp | Ser | Lys | Arg | Leu | Ile | Leu | Phe | Arg | Thr | Lys | Pro | Trp | Gln | Cys | Leu | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| agt | gtc | agg | acc | gtg | gca | agg | agg | tgt | aca | gcc | ctg | act | ttc | ata | gcc | 336 |
| Ser | Val | Arg | Thr | Val | Ala | Arg | Arg | Cys | Thr | Ala | Leu | Thr | Phe | Ile | Ala | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| tcg | gag | gag | aag | gtc | ttg | gtg | gcc | gac | aag | tct | gga | gac | gtc | tac | tcc | 384 |
| Ser | Glu | Glu | Lys | Val | Leu | Val | Ala | Asp | Lys | Ser | Gly | Asp | Val | Tyr | Ser | |
| | 115 | | | | | | 120 | | | | | 125 | | | | |
| ttt | tcg | gtg | ctg | gag | cca | cac | ggg | tgt | ggc | cgt | cta | gag | ctg | ggg | cac | 432 |
| Phe | Ser | Val | Leu | Glu | Pro | His | Gly | Cys | Gly | Arg | Leu | Glu | Leu | Gly | His | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| ctg | tct | atg | ctg | tta | gat | gtg | gct | gtg | agt | cct | gat | gac | cgc | ttc | atc | 480 |
| Leu | Ser | Met | Leu | Leu | Asp | Val | Ala | Val | Ser | Pro | Asp | Asp | Arg | Phe | Ile | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| ctc | act | gcc | gac | cgg | gac | gag | aag | atc | cga | gtc | agc | tgg | gcc | gcg | gcg | 528 |
| Leu | Thr | Ala | Asp | Arg | Asp | Glu | Lys | Ile | Arg | Val | Ser | Trp | Ala | Ala | Ala | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| ccc | cat | agc | atc | gag | tcc | ttc | tgc | ttg | ggg | cac | aca | gag | ttt | gtg | agc | 576 |
| Pro | His | Ser | Ile | Glu | Ser | Phe | Cys | Leu | Gly | His | Thr | Glu | Phe | Val | Ser | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| cgt | atc | tcc | gtg | gtg | cca | act | cag | ccc | ggg | ctg | ctt | ctg | tcc | tcc | tct | 624 |
| Arg | Ile | Ser | Val | Val | Pro | Thr | Gln | Pro | Gly | Leu | Leu | Leu | Ser | Ser | Ser | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| ggg | gac | ggc | acc | ctg | agg | ctc | tgg | gag | tac | agg | agc | ggc | cgc | cag | ctg | 672 |
| Gly | Asp | Gly | Thr | Leu | Arg | Leu | Trp | Glu | Tyr | Arg | Ser | Gly | Arg | Gln | Leu | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| cac | tgc | tgt | cac | ctg | gcc | agt | ctg | cag | gag | ctg | gtg | gac | ccc | cag | gcc | 720 |
| His | Cys | Cys | His | Leu | Ala | Ser | Leu | Gln | Glu | Leu | Val | Asp | Pro | Gln | Ala | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |

146

| | |
|---|------|
| ccc cag aag ttt gcc gcg tcc agg att gca ttc tgg tgc cag gag aac | 768 |
| Pro Gln Lys Phe Ala Ala Ser Arg Ile Ala Phe Trp Cys Gln Glu Asn | |
| 245 250 255 | |
| tgc gtg gcg ctc ctg tgc gac ggc act cct gtg gtc tac atc ttc cag | 816 |
| Cys Val Ala Leu Leu Cys Asp Gly Thr Pro Val Val Tyr Ile Phe Gln | |
| 260 265 270 | |
| ctg gac gcc cgc aga cag cag ttg gtg tac agg cag cag ctg gcg ttc | 864 |
| Leu Asp Ala Arg Arg Gln Gln Leu Val Tyr Arg Gln Gln Leu Ala Phe | |
| 275 280 285 | |
| cag cac caa gtg tgg gac gtg gct ttc gag gag acc cag ggg ctg tgg | 912 |
| Gln His Gln Val Trp Asp Val Ala Phe Glu Glu Thr Gln Gly Leu Trp | |
| 290 295 300 | |
| gtg ctc cag gac tgc cag gaa gcc ccc ctg gtg ctc tac agg cct gtg | 960 |
| Val Leu Gln Asp Cys Gln Glu Ala Pro Leu Val Leu Tyr Arg Pro Val | |
| 305 310 315 320 | |
| ggc gac cag tgg cag tct gtt cct gag agc acc gtg tta aag aaa gtc | 1008 |
| Gly Asp Gln Trp Gln Ser Val Pro Glu Ser Thr Val Leu Lys Lys Val | |
| 325 330 335 | |
| tct ggt gtt ctt cgt ggg aac tgg gcc atg ctg gaa ggc tct gcc ggc | 1056 |
| Ser Gly Val Leu Arg Gly Asn Trp Ala Met Leu Glu Gly Ser Ala Gly | |
| 340 345 350 | |
| gca gac gcc agc ttc agc agt ctc tac aag gcc acg ttc gac aac gtg | 1104 |
| Ala Asp Ala Ser Phe Ser Ser Leu Tyr Lys Ala Thr Phe Asp Asn Val | |
| 355 360 365 | |
| acc tcc tac ctg aag aag aaa gag gag aga ctg cag cag cag cta gag | 1152 |
| Thr Ser Tyr Leu Lys Lys Lys Glu Glu Arg Leu Gln Gln Gln Leu Glu | |
| 370 375 380 | |
| aag aag cag cgg cgc cgg agt ccc ccg cct ggg ccc gac ggg cat gcc | 1200 |
| Lys Lys Gln Arg Arg Arg Ser Pro Pro Pro Gly Pro Asp Gly His Ala | |
| 385 390 395 400 | |
| aag aag atg aga ccg ggg gag gcg acg cta agt tgc tga | 1239 |
| Lys Lys Met Arg Pro Gly Glu Ala Thr Leu Ser Cys * | |
| 405 410 | |

<210> 104
 <211> 412
 <212> PRT
 <213> Homo sapiens

<400> 104

```

Met Ala Gly Ser Val Gly Leu Ala Leu Cys Gly Gln Thr Leu Val Val
 1           5           10           15
Arg Gly Gly Ser Arg Phe Leu Ala Thr Ser Ile Ala Ser Ser Asp Asp
      20           25           30
Asp Ser Leu Phe Ile Tyr Asp Cys Ser Ala Ala Glu Lys Lys Ser Gln
      35           40           45
Glu Asn Lys Gly Glu Asp Ala Pro Leu Asp Gln Gly Ser Gly Ala Ile
      50           55           60
Leu Ala Ser Thr Phe Ser Lys Ser Gly Ser Tyr Phe Ala Leu Thr Asp
65           70           75           80
Asp Ser Lys Arg Leu Ile Leu Phe Arg Thr Lys Pro Trp Gln Cys Leu
      85           90           95
Ser Val Arg Thr Val Ala Arg Arg Cys Thr Ala Leu Thr Phe Ile Ala
      100          105          110
Ser Glu Glu Lys Val Leu Val Ala Asp Lys Ser Gly Asp Val Tyr Ser
      115          120          125
Phe Ser Val Leu Glu Pro His Gly Cys Gly Arg Leu Glu Leu Gly His
      130          135          140
Leu Ser Met Leu Leu Asp Val Ala Val Ser Pro Asp Asp Arg Phe Ile
145          150          155          160
Leu Thr Ala Asp Arg Asp Glu Lys Ile Arg Val Ser Trp Ala Ala Ala
      165          170          175
Pro His Ser Ile Glu Ser Phe Cys Leu Gly His Thr Glu Phe Val Ser
      180          185          190
Arg Ile Ser Val Val Pro Thr Gln Pro Gly Leu Leu Leu Ser Ser Ser
      195          200          205
Gly Asp Gly Thr Leu Arg Leu Trp Glu Tyr Arg Ser Gly Arg Gln Leu
      210          215          220
His Cys Cys His Leu Ala Ser Leu Gln Glu Leu Val Asp Pro Gln Ala
225          230          235          240
Pro Gln Lys Phe Ala Ala Ser Arg Ile Ala Phe Trp Cys Gln Glu Asn
      245          250          255
Cys Val Ala Leu Leu Cys Asp Gly Thr Pro Val Val Tyr Ile Phe Gln
      260          265          270
Leu Asp Ala Arg Arg Gln Gln Leu Val Tyr Arg Gln Gln Leu Ala Phe
      275          280          285

```

148

Gln His Gln Val Trp Asp Val Ala Phe Glu Glu Thr Gln Gly Leu Trp
 290 295 300
 Val Leu Gln Asp Cys Gln Glu Ala Pro Leu Val Leu Tyr Arg Pro Val
 305 310 315 320
 Gly Asp Gln Trp Gln Ser Val Pro Glu Ser Thr Val Leu Lys Lys Val
 325 330 335
 Ser Gly Val Leu Arg Gly Asn Trp Ala Met Leu Glu Gly Ser Ala Gly
 340 345 350
 Ala Asp Ala Ser Phe Ser Ser Leu Tyr Lys Ala Thr Phe Asp Asn Val
 355 360 365
 Thr Ser Tyr Leu Lys Lys Lys Glu Glu Arg Leu Gln Gln Gln Leu Glu
 370 375 380
 Lys Lys Gln Arg Arg Arg Ser Pro Pro Pro Gly Pro Asp Gly His Ala
 385 390 395 400
 Lys Lys Met Arg Pro Gly Glu Ala Thr Leu Ser Cys
 405 410

<210> 105
 <211> 645
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(645)

<400> 105
 atg agt gat ttg gaa gat gat gag aca ccc cag ctt tct gcc cat gcc 48
 Met Ser Asp Leu Glu Asp Asp Glu Thr Pro Gln Leu Ser Ala His Ala
 1 5 10 15
 tta gca gct ctc cag gaa ttt tat gct gag caa aag caa caa att gag 96
 Leu Ala Ala Leu Gln Glu Phe Tyr Ala Glu Gln Lys Gln Gln Ile Glu
 20 25 30
 cca ggc gag gat gat aaa tat aac att gga ata ata gaa gag aat tgg 144
 Pro Gly Glu Asp Asp Lys Tyr Asn Ile Gly Ile Ile Glu Glu Asn Trp
 35 40 45
 caa ctg agc cag ttt tgg tat agt cag gaa act gct ctg cag ctg gca 192
 Gln Leu Ser Gln Phe Trp Tyr Ser Gln Glu Thr Ala Leu Gln Leu Ala
 50 55 60
 cag gag gca att gca gct gta gga gaa ggt ggc aga atc gca tgt gtg 240

[illegible]

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<210> 106
<211> 214
<212> PRT
<213> Homo sapiens
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150

<400> 106

```

Met Ser Asp Leu Glu Asp Asp Glu Thr Pro Gln Leu Ser Ala His Ala
 1           5           10           15
Leu Ala Ala Leu Gln Glu Phe Tyr Ala Glu Gln Lys Gln Gln Ile Glu
      20           25           30
Pro Gly Glu Asp Asp Lys Tyr Asn Ile Gly Ile Ile Glu Glu Asn Trp
      35           40           45
Gln Leu Ser Gln Phe Trp Tyr Ser Gln Glu Thr Ala Leu Gln Leu Ala
      50           55           60
Gln Glu Ala Ile Ala Ala Val Gly Glu Gly Gly Arg Ile Ala Cys Val
65           70           75           80
Ser Ala Pro Ser Val Tyr Gln Lys Leu Arg Glu Leu Cys Arg Glu Asn
      85           90           95
Phe Ser Ile Tyr Ile Phe Glu Tyr Asp Lys Arg Phe Ala Met Tyr Gly
      100          105          110
Glu Glu Phe Ile Phe Tyr Asp Tyr Asn Asn Pro Leu Asp Leu Pro Glu
      115          120          125
Arg Ile Ala Ala His Ser Phe Asp Ile Val Ile Ala Asp Pro Pro Tyr
      130          135          140
Leu Ser Glu Glu Cys Leu Arg Lys Thr Ser Glu Thr Val Lys Tyr Leu
145          150          155          160
Thr Arg Gly Lys Ile Leu Leu Cys Thr Gly Ala Ile Met Glu Glu Gln
      165          170          175
Ala Ala Glu Leu Leu Gly Val Lys Met Cys Thr Phe Val Pro Arg His
      180          185          190
Thr Arg Asn Leu Ala Asn Glu Phe Arg Cys Tyr Val Asn Tyr Asp Ser
      195          200          205
Gly Leu Asp Cys Gly Ile
210

```

<210> 107

<211> 264

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(264)

<400> 107

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atg aag agc agc act ctg ttg acg atc cta gtt ctc cag gcc ctt ctg
Met Lys Ser Ser Thr Leu Leu Thr Ile Leu Val Leu Gln Ala Leu Leu
 1           5           10           15

```

48

151

gtc tct acg gcc gtg ccc aaa gga cct gca ggc ccg aag aag cag tgc 96
 Val Ser Thr Ala Val Pro Lys Gly Pro Ala Gly Pro Lys Lys Gln Cys
 20 25 30

tgg tgc ggc gag tgc acc agc tgg tcg ggc gtg tgg acc tgc gac gac 144
 Trp Cys Gly Glu Cys Thr Ser Trp Ser Gly Val Trp Thr Cys Asp Asp
 35 40 45

ctc ctc acc aag tgc gcc gcc acc tgc aag aac tgc gtc ccc gtc tcc 192
 Leu Leu Thr Lys Cys Ala Ala Thr Cys Lys Asn Cys Val Pro Val Ser
 50 55 60

acg gac aag ggc gcc acc aag tac aga tgc cgc gac ttc ctc ccc gaa 240
 Thr Asp Lys Gly Ala Thr Lys Tyr Arg Cys Arg Asp Phe Leu Pro Glu
 65 70 75 80

aac tgc ggc tgc aag atc cac tag 264
 Asn Cys Gly Cys Lys Ile His *
 85

<210> 108
 <211> 87
 <212> PRT
 <213> Homo sapiens

<400> 108
 Met Lys Ser Ser Thr Leu Leu Thr Ile Leu Val Leu Gln Ala Leu Leu
 1 5 10 15
 Val Ser Thr Ala Val Pro Lys Gly Pro Ala Gly Pro Lys Lys Gln Cys
 20 25 30
 Trp Cys Gly Glu Cys Thr Ser Trp Ser Gly Val Trp Thr Cys Asp Asp
 35 40 45
 Leu Leu Thr Lys Cys Ala Ala Thr Cys Lys Asn Cys Val Pro Val Ser
 50 55 60
 Thr Asp Lys Gly Ala Thr Lys Tyr Arg Cys Arg Asp Phe Leu Pro Glu
 65 70 75 80
 Asn Cys Gly Cys Lys Ile His
 85

<210> 109
 <211> 378
 <212> DNA

152

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(378)

<400> 109

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| atg | aag | gaa | gaa | gga | aaa | ctc | cta | ttt | tat | gcg | aca | agc | cgt | gcc | tat | 48 |
| Met | Lys | Glu | Glu | Gly | Lys | Leu | Leu | Phe | Tyr | Ala | Thr | Ser | Arg | Ala | Tyr | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| gtg | gaa | tct | atc | tgt | tcg | aat | aat | ttt | gac | agt | ttc | cta | cat | gaa | act | 96 |
| Val | Glu | Ser | Ile | Cys | Ser | Asn | Asn | Phe | Asp | Ser | Phe | Leu | His | Glu | Thr | |
| | | | 20 | | | | | 25 | | | | 30 | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| cat | gaa | aac | aaa | tac | gga | aaa | gga | att | tac | ttt | gca | aaa | gat | gcc | atc | 144 |
| His | Glu | Asn | Lys | Tyr | Gly | Lys | Gly | Ile | Tyr | Phe | Ala | Lys | Asp | Ala | Ile | |
| | | 35 | | | | 40 | | | | | 45 | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| tat | tcc | cac | aaa | aat | tgc | ccg | tat | gat | gcc | aaa | aac | gtc | gtt | atg | ttt | 192 |
| Tyr | Ser | His | Lys | Asn | Cys | Pro | Tyr | Asp | Ala | Lys | Asn | Val | Val | Met | Phe | |
| | 50 | | | | 55 | | | | | 60 | | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gta | gcc | caa | gtt | ctg | gtt | gga | aag | ttt | act | gaa | gga | aat | ata | acg | tac | 240 |
| Val | Ala | Gln | Val | Leu | Val | Gly | Lys | Phe | Thr | Glu | Gly | Asn | Ile | Thr | Tyr | |
| 65 | | | | 70 | | | | | 75 | | | | 80 | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| acg | agc | cct | cct | cca | cag | ttc | gac | agc | tgt | gtg | gat | acc | aga | tcg | aat | 288 |
| Thr | Ser | Pro | Pro | Pro | Gln | Phe | Asp | Ser | Cys | Val | Asp | Thr | Arg | Ser | Asn | |
| | | | 85 | | | | | 90 | | | | | 95 | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ccc | tcc | gtt | ttt | gtc | atc | ttt | cag | aaa | gat | cag | gtt | tac | cca | caa | tat | 336 |
| Pro | Ser | Val | Phe | Val | Ile | Phe | Gln | Lys | Asp | Gln | Val | Tyr | Pro | Gln | Tyr | |
| | | | 100 | | | | 105 | | | | | 110 | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|-----|
| gtg | att | gaa | tat | act | gaa | gac | aaa | gcc | tgc | gtg | att | agt | tag | | | 378 |
| Val | Ile | Glu | Tyr | Thr | Glu | Asp | Lys | Ala | Cys | Val | Ile | Ser | * | | | |
| | | 115 | | | | 120 | | | | | 125 | | | | | |

<210> 110

<211> 125

<212> PRT

<213> Homo sapiens

153

<400> 110

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Met Lys Glu Glu Gly Lys Leu Leu Phe Tyr Ala Thr Ser Arg Ala Tyr
 1           5           10           15
Val Glu Ser Ile Cys Ser Asn Asn Phe Asp Ser Phe Leu His Glu Thr
           20           25           30
His Glu Asn Lys Tyr Gly Lys Gly Ile Tyr Phe Ala Lys Asp Ala Ile
           35           40           45
Tyr Ser His Lys Asn Cys Pro Tyr Asp Ala Lys Asn Val Val Met Phe
           50           55           60
Val Ala Gln Val Leu Val Gly Lys Phe Thr Glu Gly Asn Ile Thr Tyr
65           70           75           80
Thr Ser Pro Pro Pro Gln Phe Asp Ser Cys Val Asp Thr Arg Ser Asn
           85           90           95
Pro Ser Val Phe Val Ile Phe Gln Lys Asp Gln Val Tyr Pro Gln Tyr
           100          105          110
Val Ile Glu Tyr Thr Glu Asp Lys Ala Cys Val Ile Ser
           115          120          125

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<210> 111

<211> 1965

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1965)

<400> 111

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atg gcg gcg gcg gca ttg ggc agc tcc tca ggc tcg gcg tcc ccg gcc      48
Met Ala Ala Ala Ala Leu Gly Ser Ser Ser Gly Ser Ala Ser Pro Ala
 1           5           10           15

gtg gct gag ctc tgc cag aac acc ccg gag acc ttt ttg gag gcc tcc      96
Val Ala Glu Leu Cys Gln Asn Thr Pro Glu Thr Phe Leu Glu Ala Ser
           20           25           30

aag ctg ctg ctc acc tat gct gac aac atc ctc aga aac cct aat gat      144
Lys Leu Leu Leu Thr Tyr Ala Asp Asn Ile Leu Arg Asn Pro Asn Asp
           35           40           45

gaa aaa tat aga tcc atc cgg att gga aac aca gcc ttt tct act aga      192
Glu Lys Tyr Arg Ser Ile Arg Ile Gly Asn Thr Ala Phe Ser Thr Arg
           50           55           60

```

154

| | |
|---|-----|
| ctc ttg cct gtc aga gga gct gtt gaa tgt tta ttt gaa atg ggc ttt | 240 |
| Leu Leu Pro Val Arg Gly Ala Val Glu Cys Leu Phe Glu Met Gly Phe | |
| 65 70 75 80 | |
| gaa gag gga gaa aca cat ctc atc ttt cct aaa aaa gct tca gtg gag | 288 |
| Glu Glu Gly Glu Thr His Leu Ile Phe Pro Lys Lys Ala Ser Val Glu | |
| 85 90 95 | |
| cag ctg caa aaa att cgt gac ctg att gcc ata gag aga agt agc aga | 336 |
| Gln Leu Gln Lys Ile Arg Asp Leu Ile Ala Ile Glu Arg Ser Ser Arg | |
| 100 105 110 | |
| ctg gat ggc tca aat aag agc cac aaa gta aag tca tct cag caa cct | 384 |
| Leu Asp Gly Ser Asn Lys Ser His Lys Val Lys Ser Ser Gln Gln Pro | |
| 115 120 125 | |
| gca gcc agt acc cag ctt cct aca aca cca tct tca aat ccc agt ggg | 432 |
| Ala Ala Ser Thr Gln Leu Pro Thr Thr Pro Ser Ser Asn Pro Ser Gly | |
| 130 135 140 | |
| tta aac cag cac aca agg aac cgt caa ggg cag tca tca gat cca cca | 480 |
| Leu Asn Gln His Thr Arg Asn Arg Gln Gly Gln Ser Ser Asp Pro Pro | |
| 145 150 155 160 | |
| tct gct tca acg gtt gct gct gac tca gcc att cta gaa gtt ctt cag | 528 |
| Ser Ala Ser Thr Val Ala Ala Asp Ser Ala Ile Leu Glu Val Leu Gln | |
| 165 170 175 | |
| tcc aac att cag cat gtg ctg gtc tat gaa aat cct gct ctt cag gag | 576 |
| Ser Asn Ile Gln His Val Leu Val Tyr Glu Asn Pro Ala Leu Gln Glu | |
| 180 185 190 | |
| aaa gcg ttg gct tgt att ccg gtc caa gaa cta aaa agg aaa tca caa | 624 |
| Lys Ala Leu Ala Cys Ile Pro Val Gln Glu Leu Lys Arg Lys Ser Gln | |
| 195 200 205 | |
| gaa aag tta tcg aga gct aga aaa ttg gat aaa ggt atc aat ata agt | 672 |
| Glu Lys Leu Ser Arg Ala Arg Lys Leu Asp Lys Gly Ile Asn Ile Ser | |
| 210 215 220 | |
| gat gag gat ttt ctt ttg ctg gag ctt ttg cac tgg ttt aag gaa gaa | 720 |
| Asp Glu Asp Phe Leu Leu Leu Glu Leu Leu His Trp Phe Lys Glu Glu | |
| 225 230 235 240 | |

155

| | |
|---|------|
| ttt ttt cac tgg gtg aat aac gtt ttg tgc agc aaa tgt ggt gga cag Phe Phe His Trp Val Asn Asn Val Leu Cys Ser Lys Cys Gly Gly Gln 245 250 255 | 768 |
| act agg tct aga gat aga tca tta ctg ccc agt gat gat gag ctg aag Thr Arg Ser Arg Asp Arg Ser Leu Leu Pro Ser Asp Asp Glu Leu Lys 260 265 270 | 816 |
| tgg ggt gca aag gaa gtg gaa gat cat tac tgt gat gcc tgc cag ttc Trp Gly Ala Lys Glu Val Glu Asp His Tyr Cys Asp Ala Cys Gln Phe 275 280 285 | 864 |
| agc aat cga ttc cca aga tat aat aac cct gag aaa ctt ttg gaa aca Ser Asn Arg Phe Pro Arg Tyr Asn Asn Pro Glu Lys Leu Leu Glu Thr 290 295 300 | 912 |
| aga tgt gga cgg tgt ggc gag tgg gcc aat tgt ttt aca ctg tgc tgc Arg Cys Gly Arg Cys Gly Glu Trp Ala Asn Cys Phe Thr Leu Cys Cys 305 310 315 320 | 960 |
| cga gct gta ggg ttt gaa gct cgc tat gtt tgg gat tac aca gac cat Arg Ala Val Gly Phe Glu Ala Arg Tyr Val Trp Asp Tyr Thr Asp His 325 330 335 | 1008 |
| gtc tgg aca gaa gtc tat tct cct tct cag cag cgg tgg ctg cac tgt Val Trp Thr Glu Val Tyr Ser Pro Ser Gln Gln Arg Trp Leu His Cys 340 345 350 | 1056 |
| gat gca tgt gaa gat gtc tgt gac aag cca ctc ctt tat gaa ata gga Asp Ala Cys Glu Asp Val Cys Asp Lys Pro Leu Leu Tyr Glu Ile Gly 355 360 365 | 1104 |
| tgg ggc aag aag ctt tcc tat gtc ata gca ttt tca aaa gat gag gta Trp Gly Lys Lys Leu Ser Tyr Val Ile Ala Phe Ser Lys Asp Glu Val 370 375 380 | 1152 |
| gtt gat gtc act tgg cga tat tcc tgc aaa cat gaa gag gtg att gcc Val Asp Val Thr Trp Arg Tyr Ser Cys Lys His Glu Glu Val Ile Ala 385 390 395 400 | 1200 |
| aga aga act aag gtt aaa gaa gca tta ctt cga gac act att aat ggg Arg Arg Thr Lys Val Lys Glu Ala Leu Leu Arg Asp Thr Ile Asn Gly 405 410 415 | 1248 |

| | |
|---|------|
| ctt aat aag cag agg caa ctg ttt ttg tca gaa aac aga agg aaa gaa Leu Asn Lys Gln Arg Gln Leu Phe Leu Ser Glu Asn Arg Arg Lys Glu 420 425 430 | 1296 |
| ctt ctc cag agg ata att gtg gag ctt gtt gaa ttt ata tct ccc aaa Leu Leu Gln Arg Ile Ile Val Glu Leu Val Glu Phe Ile Ser Pro Lys 435 440 445 | 1344 |
| acc cct aaa cct gga gaa ctt ggg gga aga ata tct ggg tca gtg gct Thr Pro Lys Pro Gly Glu Leu Gly Gly Arg Ile Ser Gly Ser Val Ala 450 455 460 | 1392 |
| tgg aga gta gcc cga ggt gaa atg ggt cta cag aga aaa gaa acc ttg Trp Arg Val Ala Arg Gly Glu Met Gly Leu Gln Arg Lys Glu Thr Leu 465 470 475 480 | 1440 |
| ttt att ccc tgt gaa aat gag aag att tct aaa cag ctc cac ctt tgt Phe Ile Pro Cys Glu Asn Glu Lys Ile Ser Lys Gln Leu His Leu Cys 485 490 495 | 1488 |
| tac aat att gtg aaa gat cgt tat gtt cga gtt tca aat aac aat caa Tyr Asn Ile Val Lys Asp Arg Tyr Val Arg Val Ser Asn Asn Asn Gln 500 505 510 | 1536 |
| acc att tct gga tgg gag aat ggc gtg tgg aaa atg gaa tct ata ttc Thr Ile Ser Gly Trp Glu Asn Gly Val Trp Lys Met Glu Ser Ile Phe 515 520 525 | 1584 |
| aga aaa gtt gaa aca gac tgg cac atg gta tat ttg gcc cga aag gaa Arg Lys Val Glu Thr Asp Trp His Met Val Tyr Leu Ala Arg Lys Glu 530 535 540 | 1632 |
| gga tca tct ttt gct tat att tcc tgg aag ttt gag tgt ggg tca gtt Gly Ser Ser Phe Ala Tyr Ile Ser Trp Lys Phe Glu Cys Gly Ser Val 545 550 555 560 | 1680 |
| ggc cta aaa gta gat agc att tct att aga aca agt agt caa act ttt Gly Leu Lys Val Asp Ser Ile Ser Ile Arg Thr Ser Ser Gln Thr Phe 565 570 575 | 1728 |
| cag act gga aca gta gaa tgg aaa ttg cga tct gat aca gca caa gta Gln Thr Gly Thr Val Glu Trp Lys Leu Arg Ser Asp Thr Ala Gln Val 580 585 590 | 1776 |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| gaa | ctg | aca | ggc | gat | aac | agt | ctt | cac | tcc | tat | gct | gat | ttt | tct | ggg | 1824 |
| Glu | Leu | Thr | Gly | Asp | Asn | Ser | Leu | His | Ser | Tyr | Ala | Asp | Phe | Ser | Gly | |
| | | 595 | | | | | 600 | | | | | 605 | | | | |
| | | | | | | | | | | | | | | | | |
| gcc | act | gaa | gtt | att | ttg | gaa | gca | gaa | tta | agc | aga | gga | gat | ggg | gat | 1872 |
| Ala | Thr | Glu | Val | Ile | Leu | Glu | Ala | Glu | Leu | Ser | Arg | Gly | Asp | Gly | Asp | |
| | | 610 | | | | 615 | | | | | 620 | | | | | |
| | | | | | | | | | | | | | | | | |
| gtc | gct | tgg | caa | cac | acc | cag | ctg | ttt | aga | caa | agc | tta | aat | gac | cat | 1920 |
| Val | Ala | Trp | Gln | His | Thr | Gln | Leu | Phe | Arg | Gln | Ser | Leu | Asn | Asp | His | |
| | | 625 | | | 630 | | | | | 635 | | | | | 640 | |
| | | | | | | | | | | | | | | | | |
| gaa | gaa | aat | tgt | ttg | gag | ata | att | ata | aaa | ttc | agt | gac | ctt | tga | | 1965 |
| Glu | Glu | Asn | Cys | Leu | Glu | Ile | Ile | Ile | Lys | Phe | Ser | Asp | Leu | * | | |
| | | | | 645 | | | | | 650 | | | | | | | |

```
<210> 112
<211> 654
<212> PRT
<213> Homo sapiens
```

| | | | | | | | | | | | | | | | |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> 112 | | | | | | | | | | | | | | | |
| Met | Ala | Ala | Ala | Ala | Leu | Gly | Ser | Ser | Ser | Gly | Ser | Ala | Ser | Pro | Ala |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Val | Ala | Glu | Leu | Cys | Gln | Asn | Thr | Pro | Glu | Thr | Phe | Leu | Glu | Ala | Ser |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Lys | Leu | Leu | Leu | Thr | Tyr | Ala | Asp | Asn | Ile | Leu | Arg | Asn | Pro | Asn | Asp |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Glu | Lys | Tyr | Arg | Ser | Ile | Arg | Ile | Gly | Asn | Thr | Ala | Phe | Ser | Thr | Arg |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Leu | Leu | Pro | Val | Arg | Gly | Ala | Val | Glu | Cys | Leu | Phe | Glu | Met | Gly | Phe |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Glu | Glu | Gly | Glu | Thr | His | Leu | Ile | Phe | Pro | Lys | Lys | Ala | Ser | Val | Glu |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Gln | Leu | Gln | Lys | Ile | Arg | Asp | Leu | Ile | Ala | Ile | Glu | Arg | Ser | Ser | Arg |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Leu | Asp | Gly | Ser | Asn | Lys | Ser | His | Lys | Val | Lys | Ser | Ser | Gln | Gln | Pro |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Ala | Ala | Ser | Thr | Gln | Leu | Pro | Thr | Thr | Pro | Ser | Ser | Asn | Pro | Ser | Gly |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Leu | Asn | Gln | His | Thr | Arg | Asn | Arg | Gln | Gly | Gln | Ser | Ser | Asp | Pro | Pro |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |

158

Ser Ala Ser Thr Val Ala Ala Asp Ser Ala Ile Leu Glu Val Leu Gln
 165 170 175
 Ser Asn Ile Gln His Val Leu Val Tyr Glu Asn Pro Ala Leu Gln Glu
 180 185 190
 Lys Ala Leu Ala Cys Ile Pro Val Gln Glu Leu Lys Arg Lys Ser Gln
 195 200 205
 Glu Lys Leu Ser Arg Ala Arg Lys Leu Asp Lys Gly Ile Asn Ile Ser
 210 215 220
 Asp Glu Asp Phe Leu Leu Leu Glu Leu Leu His Trp Phe Lys Glu Glu
 225 230 235 240
 Phe Phe His Trp Val Asn Asn Val Leu Cys Ser Lys Cys Gly Gly Gln
 245 250 255
 Thr Arg Ser Arg Asp Arg Ser Leu Leu Pro Ser Asp Asp Glu Leu Lys
 260 265 270
 Trp Gly Ala Lys Glu Val Glu Asp His Tyr Cys Asp Ala Cys Gln Phe
 275 280 285
 Ser Asn Arg Phe Pro Arg Tyr Asn Asn Pro Glu Lys Leu Leu Glu Thr
 290 295 300
 Arg Cys Gly Arg Cys Gly Glu Trp Ala Asn Cys Phe Thr Leu Cys Cys
 305 310 315 320
 Arg Ala Val Gly Phe Glu Ala Arg Tyr Val Trp Asp Tyr Thr Asp His
 325 330 335
 Val Trp Thr Glu Val Tyr Ser Pro Ser Gln Gln Arg Trp Leu His Cys
 340 345 350
 Asp Ala Cys Glu Asp Val Cys Asp Lys Pro Leu Leu Tyr Glu Ile Gly
 355 360 365
 Trp Gly Lys Lys Leu Ser Tyr Val Ile Ala Phe Ser Lys Asp Glu Val
 370 375 380
 Val Asp Val Thr Trp Arg Tyr Ser Cys Lys His Glu Glu Val Ile Ala
 385 390 395 400
 Arg Arg Thr Lys Val Lys Glu Ala Leu Leu Arg Asp Thr Ile Asn Gly
 405 410 415
 Leu Asn Lys Gln Arg Gln Leu Phe Leu Ser Glu Asn Arg Arg Lys Glu
 420 425 430
 Leu Leu Gln Arg Ile Ile Val Glu Leu Val Glu Phe Ile Ser Pro Lys
 435 440 445
 Thr Pro Lys Pro Gly Glu Leu Gly Gly Arg Ile Ser Gly Ser Val Ala
 450 455 460
 Trp Arg Val Ala Arg Gly Glu Met Gly Leu Gln Arg Lys Glu Thr Leu
 465 470 475 480
 Phe Ile Pro Cys Glu Asn Glu Lys Ile Ser Lys Gln Leu His Leu Cys
 485 490 495
 Tyr Asn Ile Val Lys Asp Arg Tyr Val Arg Val Ser Asn Asn Asn Gln
 500 505 510

159

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ile | Ser | Gly | Trp | Glu | Asn | Gly | Val | Trp | Lys | Met | Glu | Ser | Ile | Phe |
| | | 515 | | | | | 520 | | | | | 525 | | | |
| Arg | Lys | Val | Glu | Thr | Asp | Trp | His | Met | Val | Tyr | Leu | Ala | Arg | Lys | Glu |
| | | 530 | | | | 535 | | | | | 540 | | | | |
| Gly | Ser | Ser | Phe | Ala | Tyr | Ile | Ser | Trp | Lys | Phe | Glu | Cys | Gly | Ser | Val |
| 545 | | | | | 550 | | | | | 555 | | | | | 560 |
| Gly | Leu | Lys | Val | Asp | Ser | Ile | Ser | Ile | Arg | Thr | Ser | Ser | Gln | Thr | Phe |
| | | | | 565 | | | | | 570 | | | | | 575 | |
| Gln | Thr | Gly | Thr | Val | Glu | Trp | Lys | Leu | Arg | Ser | Asp | Thr | Ala | Gln | Val |
| | | | 580 | | | | | 585 | | | | | 590 | | |
| Glu | Leu | Thr | Gly | Asp | Asn | Ser | Leu | His | Ser | Tyr | Ala | Asp | Phe | Ser | Gly |
| | | 595 | | | | | 600 | | | | | 605 | | | |
| Ala | Thr | Glu | Val | Ile | Leu | Glu | Ala | Glu | Leu | Ser | Arg | Gly | Asp | Gly | Asp |
| | | 610 | | | | 615 | | | | | 620 | | | | |
| Val | Ala | Trp | Gln | His | Thr | Gln | Leu | Phe | Arg | Gln | Ser | Leu | Asn | Asp | His |
| 625 | | | | 630 | | | | | | 635 | | | | | 640 |
| Glu | Glu | Asn | Cys | Leu | Glu | Ile | Ile | Ile | Lys | Phe | Ser | Asp | Leu | | |
| | | | | 645 | | | | | 650 | | | | | | |

```
<210> 113
<211> 585
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (1)...(585)

| | | | | | | | | | | | | | | | | |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> 113 | | | | | | | | | | | | | | | | |
| atg | tct | gca | ttg | tgg | ctg | ctg | ctg | ggc | ctc | ctt | gcc | ctg | atg | gac | ttg | 48 |
| Met | Ser | Ala | Leu | Trp | Leu | Leu | Leu | Gly | Leu | Leu | Ala | Leu | Met | Asp | Leu | |
| 1 | | 5 | | | 10 | | | | | 15 | | | | | | |
| | | | | | | | | | | | | | | | | |
| tct | gaa | agc | agc | aac | tgg | gga | tgc | tat | gga | aac | atc | caa | agc | ctg | gac | 96 |
| Ser | Glu | Ser | Ser | Asn | Trp | Gly | Cys | Tyr | Gly | Asn | Ile | Gln | Ser | Leu | Asp | |
| 20 | | | | 25 | | | | | 30 | | | | | | | |
| | | | | | | | | | | | | | | | | |
| acc | cct | gga | gca | tct | tgt | ggg | att | gga | aga | cgt | cac | ggc | ctg | aac | tac | 144 |
| Thr | Pro | Gly | Ala | Ser | Cys | Gly | Ile | Gly | Arg | Arg | His | Gly | Leu | Asn | Tyr | |
| 35 | | | 40 | | | | | 45 | | | | | | | | |
| | | | | | | | | | | | | | | | | |
| tgt | gga | gtt | cgt | gct | tct | gaa | agg | ctg | gct | gaa | ata | gac | atg | cca | tac | 192 |
| Cys | Gly | Val | Arg | Ala | Ser | Glu | Arg | Leu | Ala | Glu | Ile | Asp | Met | Pro | Tyr | |
| 50 | | 55 | | | | | 60 | | | | | | | | | |

[illegible]

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<210> 114
<211> 194
<212> PRT
<213> Homo sapiens
<400> 114
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161

Met Ser Ala Leu Trp Leu Leu Leu Gly Leu Leu Ala Leu Met Asp Leu
 1 5 10 15
 Ser Glu Ser Ser Asn Trp Gly Cys Tyr Gly Asn Ile Gln Ser Leu Asp
 20 25 30
 Thr Pro Gly Ala Ser Cys Gly Ile Gly Arg Arg His Gly Leu Asn Tyr
 35 40 45
 Cys Gly Val Arg Ala Ser Glu Arg Leu Ala Glu Ile Asp Met Pro Tyr
 50 55 60
 Leu Leu Lys Tyr Gln Pro Met Met Gln Thr Ile Gly Gln Lys Tyr Cys
 65 70 75 80
 Met Asp Pro Ala Val Ile Ala Gly Val Leu Ser Arg Lys Ser Pro Gly
 85 90 95
 Asp Lys Ile Leu Val Asn Met Gly Asp Arg Thr Ser Met Val Gln Asp
 100 105 110
 Pro Gly Ser Gln Ala Pro Thr Ser Trp Ile Ser Glu Ser Gln Val Ser
 115 120 125
 Gln Thr Thr Glu Val Leu Thr Thr Arg Ile Lys Glu Ile Gln Arg Arg
 130 135 140
 Phe Pro Thr Trp Thr Pro Asp Gln Tyr Leu Arg Gly Gly Leu Cys Ala
 145 150 155 160
 Tyr Ser Gly Gly Ala Gly Tyr Val Arg Ser Ser Gln Asp Leu Ser Cys
 165 170 175
 Asp Phe Cys Asn Asp Val Leu Ala Arg Ala Lys Tyr Leu Lys Arg His
 180 185 190
 Gly Phe

<210> 115
 <211> 933
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(933)

<221> misc_feature
 <222> (1)...(933)
 <223> n = A,T,C or G

<400> 115

atg ctg gtg gtg gag gtg gcg aac ggc cgc tcc ctg gtg tgg gga gcc
 Met Leu Val Val Glu Val Ala Asn Gly Arg Ser Leu Val Trp Gly Ala
 1 5 10 15

162

| | |
|---|-----|
| gag gcg gtg cag gcc ctc cgg gag cgc ctg ggt gtg ggg ggc cgc acg Glu Ala Val Gln Ala Leu Arg Glu Arg Leu Gly Val Gly Gly Arg Thr 20 25 30 | 96 |
| gta ggc gcc ctg ccc cgc ggg ccc cgc cag aac tcg cgc ctg ggc ctc Val Gly Ala Leu Pro Arg Gly Pro Arg Gln Asn Ser Arg Leu Gly Leu 35 40 45 | 144 |
| ccg ctg ctg ctg atg ccc gaa gag gcg cgg ctc ttg gcc gag atc ggc Pro Leu Leu Leu Met Pro Glu Glu Ala Arg Leu Leu Ala Glu Ile Gly 50 55 60 | 192 |
| gcc gtg act ctg gtc agc gcc ccg cgt cca gac tct cgg cac cac agc Ala Val Thr Leu Val Ser Ala Pro Arg Pro Asp Ser Arg His His Ser 65 70 75 80 | 240 |
| ctg gcc ctg aca tcc ttc aag cgc can caa gag gag agc ttc cag gag Leu Ala Leu Thr Ser Phe Lys Arg Xaa Gln Glu Glu Ser Phe Gln Glu 85 90 95 | 288 |
| cag agc gcc ttg gca gct gag gcc cgg gag acc cgt cgt cag gag ctc Gln Ser Ala Leu Ala Ala Glu Ala Arg Glu Thr Arg Arg Gln Glu Leu 100 105 110 | 336 |
| ctg gag aag att acg gag ggc cag gct gct aag aag cag aaa cta gaa Leu Glu Lys Ile Thr Glu Gly Gln Ala Ala Lys Lys Gln Lys Leu Glu 115 120 125 | 384 |
| cag gct tca ggg gcc agc tca agc cag gag gcc ggc tcg agc cag gct Gln Ala Ser Gly Ala Ser Ser Ser Gln Glu Ala Gly Ser Ser Gln Ala 130 135 140 | 432 |
| gcc aaa gag gat gag acc agt gat ggc cag gct tcg gga gag cag gag Ala Lys Glu Asp Glu Thr Ser Asp Gly Gln Ala Ser Gly Glu Gln Glu 145 150 155 160 | 480 |
| gaa gct ggc ccc tcg tct tcc caa gca gga ccc tca aat ggg gta gcc Glu Ala Gly Pro Ser Ser Ser Gln Ala Gly Pro Ser Asn Gly Val Ala 165 170 175 | 528 |
| ccc ttg ccc aga tct gct ctc ctt gtc cag ctg gcc act gcc agg cct Pro Leu Pro Arg Ser Ala Leu Leu Val Gln Leu Ala Thr Ala Arg Pro 180 185 190 | 576 |

163

| | |
|---|-----|
| cga ccg gtc aag gcc agg ccc ctg gac tgg cgt gtc cag tct aaa gac | 624 |
| Arg Pro Val Lys Ala Arg Pro Leu Asp Trp Arg Val Gln Ser Lys Asp | |
| 195 200 205 | |
| tggtccc cac gcc ggc cgc cct gcc cac gag ctg cgc tac agt atc tac | 672 |
| Trp Pro His Ala Gly Arg Pro Ala His Glu Leu Arg Tyr Ser Ile Tyr | |
| 210 215 220 | |
| aga gac ctg tgg gag cga ggc ttc ttc ctc agt gcg gct gcc aag ttc | 720 |
| Arg Asp Leu Trp Glu Arg Gly Phe Phe Leu Ser Ala Ala Gly Lys Phe | |
| 225 230 235 240 | |
| gga ggt gac ttc ctg gtc tat cct ggt gac ccc ctc cgc ttc cac gcc | 768 |
| Gly Gly Asp Phe Leu Val Tyr Pro Gly Asp Pro Leu Arg Phe His Ala | |
| 245 250 255 | |
| cat tat atc gct cag tgc tgg gcc cct gag gac acc atc cca ctc caa | 816 |
| His Tyr Ile Ala Gln Cys Trp Ala Pro Glu Asp Thr Ile Pro Leu Gln | |
| 260 265 270 | |
| gac ctg gtt gct gct ggg cgc ctt gga acc agc gtc aga aag acc ctg | 864 |
| Asp Leu Val Ala Ala Gly Arg Leu Gly Thr Ser Val Arg Lys Thr Leu | |
| 275 280 285 | |
| ctc ctc tgt tct ccg cag cct gat ggt aag gtg gtc tac acc tcc ctg | 912 |
| Leu Leu Cys Ser Pro Gln Pro Asp Gly Lys Val Val Tyr Thr Ser Leu | |
| 290 295 300 | |
| caa tgg gcc agc ctg cag tga | 933 |
| Gln Trp Ala Ser Leu Gln * | |
| 305 310 | |

<210> 116

<211> 310

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(310)

<223> Xaa = Any Amino Acid

164

<400> 116

Met Leu Val Val Glu Val Ala Asn Gly Arg Ser Leu Val Trp Gly Ala
 1 5 10 15
 Glu Ala Val Gln Ala Leu Arg Glu Arg Leu Gly Val Gly Gly Arg Thr
 20 25 30
 Val Gly Ala Leu Pro Arg Gly Pro Arg Gln Asn Ser Arg Leu Gly Leu
 35 40 45
 Pro Leu Leu Leu Met Pro Glu Glu Ala Arg Leu Leu Ala Glu Ile Gly
 50 55 60
 Ala Val Thr Leu Val Ser Ala Pro Arg Pro Asp Ser Arg His His Ser
 65 70 75 80
 Leu Ala Leu Thr Ser Phe Lys Arg Xaa Gln Glu Glu Ser Phe Gln Glu
 85 90 95
 Gln Ser Ala Leu Ala Ala Glu Ala Arg Glu Thr Arg Arg Gln Glu Leu
 100 105 110
 Leu Glu Lys Ile Thr Glu Gly Gln Ala Ala Lys Lys Gln Lys Leu Glu
 115 120 125
 Gln Ala Ser Gly Ala Ser Ser Ser Gln Glu Ala Gly Ser Ser Gln Ala
 130 135 140
 Ala Lys Glu Asp Glu Thr Ser Asp Gly Gln Ala Ser Gly Glu Gln Glu
 145 150 155 160
 Glu Ala Gly Pro Ser Ser Ser Gln Ala Gly Pro Ser Asn Gly Val Ala
 165 170 175
 Pro Leu Pro Arg Ser Ala Leu Leu Val Gln Leu Ala Thr Ala Arg Pro
 180 185 190
 Arg Pro Val Lys Ala Arg Pro Leu Asp Trp Arg Val Gln Ser Lys Asp
 195 200 205
 Trp Pro His Ala Gly Arg Pro Ala His Glu Leu Arg Tyr Ser Ile Tyr
 210 215 220
 Arg Asp Leu Trp Glu Arg Gly Phe Phe Leu Ser Ala Ala Gly Lys Phe
 225 230 235 240
 Gly Gly Asp Phe Leu Val Tyr Pro Gly Asp Pro Leu Arg Phe His Ala
 245 250 255
 His Tyr Ile Ala Gln Cys Trp Ala Pro Glu Asp Thr Ile Pro Leu Gln
 260 265 270
 Asp Leu Val Ala Ala Gly Arg Leu Gly Thr Ser Val Arg Lys Thr Leu
 275 280 285
 Leu Leu Cys Ser Pro Gln Pro Asp Gly Lys Val Val Tyr Thr Ser Leu
 290 295 300
 Gln Trp Ala Ser Leu Gln
 305 310

<210> 117

<211> 828

165

<212> DNA

<213> Homo sapiens

 $\langle 220 \rangle$

<221> CDS

<222> (1)...(828)

<400> 117

atg gca aat ttc aag ggc cac gcg ctt cca ggg agt ttc ttc ctg atc 48
Met Ala Asn Phe Lys Gly His Ala Leu Pro Gly Ser Phe Phe Leu Ile
1 5 10 15

att ggg ctg tgt tgg tca gtg aag tac ccg ctg aag tac ttt agc cac 96
Ile Gly Leu Cys Trp Ser Val Lys Tyr Pro Leu Lys Tyr Phe Ser His
20 25 30

acg cgg aag aac agc cca cta cat tac tat cag cgt ctc gag atc gtc 144
Thr Arg. Lys Asn Ser Pro Leu His Tyr Tyr Gln Arg Leu Glu Ile Val
35 40 45

gaa gcc gca att agg act ttg ttt tcc gtc act ggg atc ctg gca gag 192
Glu Ala Ala Ile Arg Thr Leu Phe Ser Val Thr Gly Ile Leu Ala Glu
50 55 60

cag ttt gtt ccg gat ggg ccc cac ctg cac ctc tac cat gag aac cac 240
Gln Phe Val Pro Asp Gly Pro His Leu His Leu Tyr His Glu Asn His
65 70 75 80

tgg ata aag tta atg aat tgg cag cac agc acc atg tac cta ttc ttt 288
Trp Ile Lys Leu Met Asn Trp Gln His Ser Thr Met Tyr Leu Phe Phe
85 90 95

gca gtc tca gga att gtt gac atg ctc acc tat ctg gtc agc cac gtt 336
Ala Val Ser Gly Ile Val Asp Met Leu Thr Tyr Leu Val Ser His Val
100 105 110

ccc ttg ggg gtg gac aga ctg gtt atg gct gtg gca gta ttc atg gaa 384
Pro Leu Gly Val Asp Arg Leu Val Met Ala Val Ala Val Phe Met Glu
115 120 125

ggt ttc ctc ttc tac tac cac gtc cac aac cgg cct ccg ctg gac cag 432
Gly Phe Leu Phe Tyr Tyr His Val His Asn Arg Pro Pro Leu Asp Gln
130 135 140

| | |
|---|-----|
| cac atc cac tca ctc ctg ctg tat gct ctg ttc gga ggg tgt gtt agt | 480 |
| His Ile His Ser Leu Leu Leu Tyr Ala Leu Phe Gly Gly Cys Val Ser | |
| 145 150 155 160 | |
| atc tcc cta gag gtg atc ttc cgg gac cac att gtg ctg gaa ctt ttc | 528 |
| Ile Ser Leu Glu Val Ile Phe Arg Asp His Ile Val Leu Glu Leu Phe | |
| 165 170 175 | |
| cga acc agt ctc atc att ctt cag gga acc tgg ttc tgg cag att ggg | 576 |
| Arg Thr Ser Leu Ile Ile Leu Gln Gly Thr Trp Phe Trp Gln Ile Gly | |
| 180 185 190 | |
| ttt gtg ctg ttc cca cct ttt gga aca ccc gaa tgg gac cag aag gat | 624 |
| Phe Val Leu Phe Pro Pro Phe Gly Thr Pro Glu Trp Asp Gln Lys Asp | |
| 195 200 205 | |
| gat gcc aac ctc atg ttc atc acc atg tgc ttc tgc tgg cac tac ctg | 672 |
| Asp Ala Asn Leu Met Phe Ile Thr Met Cys Phe Cys Trp His Tyr Leu | |
| 210 215 220 | |
| gct gcc ctc agc att gtg gcc gtc aac tat tct ctt gtt tac tgc ctt | 720 |
| Ala Ala Leu Ser Ile Val Ala Val Asn Tyr Ser Leu Val Tyr Cys Leu | |
| 225 230 235 240 | |
| ttg act cgg atg aag aga cac gga agg gga gaa atc att gga att cag | 768 |
| Leu Thr Arg Met Lys Arg His Gly Arg Gly Glu Ile Ile Gly Ile Gln | |
| 245 250 255 | |
| aag ctg aat tca gat gac act tac cag acc gcc ctc ttg agt ggc tca | 816 |
| Lys Leu Asn Ser Asp Asp Thr Tyr Gln Thr Ala Leu Leu Ser Gly Ser | |
| 260 265 270 | |
| gat gag gaa tga | 828 |
| Asp Glu Glu * | |
| 275 | |

```
<210> 118
<211> 275
<212> PRT
<213> Homo sapiens
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<400> 118
Met Ala Asn Phe Lys Gly His Ala Leu Pro Gly Ser Phe Phe Leu Ile

167

1 5 10 15
 Ile Gly Leu Cys Trp Ser Val Lys Tyr Pro Leu Lys Tyr Phe Ser His
 20 25 30
 Thr Arg Lys Asn Ser Pro Leu His Tyr Tyr Gln Arg Leu Glu Ile Val
 35 40 45
 Glu Ala Ala Ile Arg Thr Leu Phe Ser Val Thr Gly Ile Leu Ala Glu
 50 55 60
 Gln Phe Val Pro Asp Gly Pro His Leu His Leu Tyr His Glu Asn His
 65 70 75 80
 Trp Ile Lys Leu Met Asn Trp Gln His Ser Thr Met Tyr Leu Phe Phe
 85 90 95
 Ala Val Ser Gly Ile Val Asp Met Leu Thr Tyr Leu Val Ser His Val
 100 105 110
 Pro Leu Gly Val Asp Arg Leu Val Met Ala Val Ala Val Phe Met Glu
 115 120 125
 Gly Phe Leu Phe Tyr Tyr His Val His Asn Arg Pro Pro Leu Asp Gln
 130 135 140
 His Ile His Ser Leu Leu Leu Tyr Ala Leu Phe Gly Gly Cys Val Ser
 145 150 155 160
 Ile Ser Leu Glu Val Ile Phe Arg Asp His Ile Val Leu Glu Leu Phe
 165 170 175
 Arg Thr Ser Leu Ile Ile Leu Gln Gly Thr Trp Phe Trp Gln Ile Gly
 180 185 190
 Phe Val Leu Phe Pro Pro Phe Gly Thr Pro Glu Trp Asp Gln Lys Asp
 195 200 205
 Asp Ala Asn Leu Met Phe Ile Thr Met Cys Phe Cys Trp His Tyr Leu
 210 215 220
 Ala Ala Leu Ser Ile Val Ala Val Asn Tyr Ser Leu Val Tyr Cys Leu
 225 230 235 240
 Leu Thr Arg Met Lys Arg His Gly Arg Gly Glu Ile Ile Gly Ile Gln
 245 250 255
 Lys Leu Asn Ser Asp Asp Thr Tyr Gln Thr Ala Leu Leu Ser Gly Ser
 260 265 270
 Asp Glu Glu
 275

<210> 119
 <211> 867
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(867)

168

<400> 119

| | |
|---|-----|
| atg ggg cgc ctg acg gaa gcg gcg gca gcg ggc agc ggc tct cgg gct | 48 |
| Met Gly Arg Leu Thr Glu Ala Ala Ala Ala Gly Ser Gly Ser Arg Ala | |
| 1 5 10 15 | |
| gca ggc tgg gca ggg tcc cct ccc acg ctc ctg ccg ctg tct ccc acg | 96 |
| Ala Gly Trp Ala Gly Ser Pro Pro Thr Leu Leu Pro Leu Ser Pro Thr | |
| 20 25 30 | |
| tcc ccc agg tgc gcg gcc acc atg gcg tcc agc gac gag gac ggc acc | 144 |
| Ser Pro Arg Cys Ala Ala Thr Met Ala Ser Ser Asp Glu Asp Gly Thr | |
| 35 40 45 | |
| aac ggc ggc gcc tcg gag gcc ggc gag gac cgg gag gct ccc ggc aag | 192 |
| Asn Gly Gly Ala Ser Glu Ala Gly Glu Asp Arg Glu Ala Pro Gly Lys | |
| 50 55 60 | |
| cgg agg cgc ctg ggg ttc ttg gcc acc gcc tgg ctc acc ttc tac gac | 240 |
| Arg Arg Arg Leu Gly Phe Leu Ala Thr Ala Trp Leu Thr Phe Tyr Asp | |
| 65 70 75 80 | |
| atc gcc atg acc gcg ggg tgg ttg gtt cta gct att gcc atg gta cgt | 288 |
| Ile Ala Met Thr Ala Gly Trp Leu Val Leu Ala Ile Ala Met Val Arg | |
| 85 90 95 | |
| ttt tat atg gaa aaa gga aca cac aga ggt tta tat aaa agt att cag | 336 |
| Phe Tyr Met Glu Lys Gly Thr His Arg Gly Leu Tyr Lys Ser Ile Gln | |
| 100 105 110 | |
| aag aca ctt aaa ttt ttc cag aca ttt gcc ttg ctt gag ata gtt cac | 384 |
| Lys Thr Leu Lys Phe Phe Gln Thr Phe Ala Leu Leu Glu Ile Val His | |
| 115 120 125 | |
| tgt tta att gga att gta cct act tct gtg att gtg act ggg gtc caa | 432 |
| Cys Leu Ile Gly Ile Val Pro Thr Ser Val Ile Val Thr Gly Val Gln | |
| 130 135 140 | |
| gtg agt tca aga atc ttt atg gtg tgg ctc att act cac agt ata aaa | 480 |
| Val Ser Ser Arg Ile Phe Met Val Trp Leu Ile Thr His Ser Ile Lys | |
| 145 150 155 160 | |
| cca atc cag aat gaa gag agt gtg gtg ctt ttt ctg gtc gcg tgg act | 528 |
| Pro Ile Gln Asn Glu Glu Ser Val Val Leu Phe Leu Val Ala Trp Thr | |

169

| 165 | 170 | 175 | |
|---|-----|-----|-----|
| gtg aca gag atc act cgc tat tcc ttc tac aca ttc agc ctt ctt gac | | | 576 |
| Val Thr Glu Ile Thr Arg Tyr Ser Phe Tyr Thr Phe Ser Leu Leu Asp | | | |
| 180 | 185 | 190 | |
| cac ttg cca tac ttc att aaa tgg gcc aga tat aat ttt ttt atc atc | | | 624 |
| His Leu Pro Tyr Phe Ile Lys Trp Ala Arg Tyr Asn Phe Phe Ile Ile | | | |
| 195 | 200 | 205 | |
| tta tat cct gtt gga gtt gct ggt gaa ctt ctt aca ata tac gct gcc | | | 672 |
| Leu Tyr Pro Val Gly Val Ala Gly Glu Leu Leu Thr Ile Tyr Ala Ala | | | |
| 210 | 215 | 220 | |
| ttg ccg cat gtg aag aaa aca gga atg ttt tca ata aga ctt cct aac | | | 720 |
| Leu Pro His Val Lys Lys Thr Gly Met Phe Ser Ile Arg Leu Pro Asn | | | |
| 225 | 230 | 235 | 240 |
| aaa tac aat gtc tct ttt gac tac tat tat ttt ctt ctt ata acc atg | | | 768 |
| Lys Tyr Asn Val Ser Phe Asp Tyr Tyr Tyr Phe Leu Leu Ile Thr Met | | | |
| 245 | 250 | 255 | |
| gca tca tat ata cct ttg ttt cca caa ctc tat ttt cat atg tta cgt | | | 816 |
| Ala Ser Tyr Ile Pro Leu Phe Pro Gln Leu Tyr Phe His Met Leu Arg | | | |
| 260 | 265 | 270 | |
| caa aga aga aag gtg ctt cat gga gag gtg att gta gaa aag gat gat | | | 864 |
| Gln Arg Arg Lys Val Leu His Gly Glu Val Ile Val Glu Lys Asp Asp | | | |
| 275 | 280 | 285 | |
| taa | | | 867 |
| * | | | |

<210> 120

<211> 288

<212> PRT

<213> Homo sapiens

<400> 120

| | |
|---|----|
| Met Gly Arg Leu Thr Glu Ala Ala Ala Ala Gly Ser Gly Ser Arg Ala | |
| 1 | 5 |
| 10 | 15 |
| Ala Gly Trp Ala Gly Ser Pro Pro Thr Leu Leu Pro Leu Ser Pro Thr | |

170

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| | | | 20 | | | | | 25 | | | | | | 30 | | | |
| Ser | Pro | Arg | Cys | Ala | Ala | Thr | Met | Ala | Ser | Ser | Asp | Glu | Asp | Gly | Thr | | |
| | | 35 | | | | | 40 | | | | | 45 | | | | | |
| Asn | Gly | Gly | Ala | Ser | Glu | Ala | Gly | Glu | Asp | Arg | Glu | Ala | Pro | Gly | Lys | | |
| | 50 | | | | | 55 | | | | | 60 | | | | | | |
| Arg | Arg | Arg | Leu | Gly | Phe | Leu | Ala | Thr | Ala | Trp | Leu | Thr | Phe | Tyr | Asp | | |
| 65 | | | | 70 | | | | | | 75 | | | | | 80 | | |
| Ile | Ala | Met | Thr | Ala | Gly | Trp | Leu | Val | Leu | Ala | Ile | Ala | Met | Val | Arg | | |
| | | | | 85 | | | | | 90 | | | | | 95 | | | |
| Phe | Tyr | Met | Glu | Lys | Gly | Thr | His | Arg | Gly | Leu | Tyr | Lys | Ser | Ile | Gln | | |
| | | 100 | | | | | | 105 | | | | | 110 | | | | |
| Lys | Thr | Leu | Lys | Phe | Phe | Gln | Thr | Phe | Ala | Leu | Leu | Glu | Ile | Val | His | | |
| | 115 | | | | | 120 | | | | | | 125 | | | | | |
| Cys | Leu | Ile | Gly | Ile | Val | Pro | Thr | Ser | Val | Ile | Val | Thr | Gly | Val | Gln | | |
| | 130 | | | | | 135 | | | | 140 | | | | | | | |
| Val | Ser | Ser | Arg | Ile | Phe | Met | Val | Trp | Leu | Ile | Thr | His | Ser | Ile | Lys | | |
| 145 | | | | 150 | | | | | | 155 | | | | | 160 | | |
| Pro | Ile | Gln | Asn | Glu | Glu | Ser | Val | Val | Leu | Phe | Leu | Val | Ala | Trp | Thr | | |
| | | | 165 | | | | | | 170 | | | | | 175 | | | |
| Val | Thr | Glu | Ile | Thr | Arg | Tyr | Ser | Phe | Tyr | Thr | Phe | Ser | Leu | Leu | Asp | | |
| | | 180 | | | | | | 185 | | | | | 190 | | | | |
| His | Leu | Pro | Tyr | Phe | Ile | Lys | Trp | Ala | Arg | Tyr | Asn | Phe | Phe | Ile | Ile | | |
| | 195 | | | | | 200 | | | | | 205 | | | | | | |
| Leu | Tyr | Pro | Val | Gly | Val | Ala | Gly | Glu | Leu | Leu | Thr | Ile | Tyr | Ala | Ala | | |
| | 210 | | | | | 215 | | | | | 220 | | | | | | |
| Leu | Pro | His | Val | Lys | Lys | Thr | Gly | Met | Phe | Ser | Ile | Arg | Leu | Pro | Asn | | |
| 225 | | | | 230 | | | | | | 235 | | | | | 240 | | |
| Lys | Tyr | Asn | Val | Ser | Phe | Asp | Tyr | Tyr | Tyr | Phe | Leu | Leu | Ile | Thr | Met | | |
| | | 245 | | | | | | | 250 | | | | | 255 | | | |
| Ala | Ser | Tyr | Ile | Pro | Leu | Phe | Pro | Gln | Leu | Tyr | Phe | His | Met | Leu | Arg | | |
| | | 260 | | | | | | 265 | | | | | 270 | | | | |
| Gln | Arg | Arg | Lys | Val | Leu | His | Gly | Glu | Val | Ile | Val | Glu | Lys | Asp | Asp | | |
| | 275 | | | | | 280 | | | | | | 285 | | | | | |

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<210> 121
<211> 177
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (1)...(177)
```

<400> 121

171

atg gcc gcc acc ttc gac gac tgc ctg tat gcc ttg tgc gtg gtg gac 48
 Met Ala Ala Thr Phe Asp Asp Cys Leu Tyr Ala Leu Cys Val Val Asp
 1 5 10 15

acc atc aag agg tcc agc cag acg ggc gag tgg cag aac att gcc atc 96
 Thr Ile Lys Arg Ser Ser Gln Thr Gly Glu Trp Gln Asn Ile Ala Ile
 20 25 30

atg acc gag gag ccg gag ctg agc ccc gcc tac ctg atc agc gag gcc 144
 Met Thr Glu Glu Pro Glu Leu Ser Pro Ala Tyr Leu Ile Ser Glu Ala
 35 40 45

atg cgc cgc agc agg atg tcc ctc tac tgt tag 177
 Met Arg Arg Ser Arg Met Ser Leu Tyr Cys *
 50 55

<210> 122

<211> 58

<212> PRT

<213> Homo sapiens

<400> 122

Met Ala Ala Thr Phe Asp Asp Cys Leu Tyr Ala Leu Cys Val Val Asp
 1 5 10 15
 Thr Ile Lys Arg Ser Ser Gln Thr Gly Glu Trp Gln Asn Ile Ala Ile
 20 25 30
 Met Thr Glu Glu Pro Glu Leu Ser Pro Ala Tyr Leu Ile Ser Glu Ala
 35 40 45
 Met Arg Arg Ser Arg Met Ser Leu Tyr Cys
 50 55

<210> 123

<211> 1158

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1158)

<400> 123

atg cag tac cac gcg ctg tcg ttg gcc atg cac ggc ttc tcg gtg acc 48
 Met Gln Tyr His Ala Leu Ser Leu Ala Met His Gly Phe Ser Val Thr

172

| 1 | 5 | 10 | 15 | |
|---|-----|-----|---------|-----|
| ctc ctg ggg ttc tgc aac tcc aaa ccc cat gat gag ctc ttg cag aac | | | | 96 |
| Leu Leu Gly Phe Cys Asn Ser Lys Pro His Asp Glu Leu Leu Gln Asn | | | | |
| | 20 | 25 | 30 | |
| aac aga att cag att gtg ggg ttg aca gaa ctt cag agt ctt gca gtt | | | | 144 |
| Asn Arg Ile Gln Ile Val Gly Leu Thr Glu Leu Gln Ser Leu Ala Val | | | | |
| | 35 | 40 | 45 | |
| ggg ccc cga gtt ttc cag tac gga gtc aaa gtt gta ctt cag gct atg | | | | 192 |
| Gly Pro Arg Val Phe Gln Tyr Gly Val Lys Val Val Leu Gln Ala Met | | | | |
| | 50 | 55 | 60 | |
| tac ttg ctg tgg aag ttg atg tgg agg gag cca ggt gcc tat atc ttt | | | | 240 |
| Tyr Leu Leu Trp Lys Leu Met Trp Arg Glu Pro Gly Ala Tyr Ile Phe | | | | |
| | 65 | 70 | 75 80 | |
| ctc cag aac ccc cca ggt ctg cct agc att gct gtc tgc tgg ttc gtg | | | | 288 |
| Leu Gln Asn Pro Pro Gly Leu Pro Ser Ile Ala Val Cys Trp Phe Val | | | | |
| | 85 | 90 | 95 | |
| ggc tgc ctt tgt gga agc aag ctc gtc att gac tgg cac aac tat ggc | | | | 336 |
| Gly Cys Leu Cys Gly Ser Lys Leu Val Ile Asp Trp His Asn Tyr Gly | | | | |
| | 100 | 105 | 110 | |
| tac tcc atc atg ggt ctg gtg cat ggc ccc aac cat ccc ctc gtt ctg | | | | 384 |
| Tyr Ser Ile Met Gly Leu Val His Gly Pro Asn His Pro Leu Val Leu | | | | |
| | 115 | 120 | 125 | |
| ctg gcc aag tgg tac gag aag ttc ttt ggg cgc ctg tcc cac ctg aac | | | | 432 |
| Leu Ala Lys Trp Tyr Glu Lys Phe Phe Gly Arg Leu Ser His Leu Asn | | | | |
| | 130 | 135 | 140 | |
| ctg tgt gtt acc aat gct atg cga gaa gac ctg gcg gat aac tgg cac | | | | 480 |
| Leu Cys Val Thr Asn Ala Met Arg Glu Asp Leu Ala Asp Asn Trp His | | | | |
| | 145 | 150 | 155 160 | |
| atc agg gct gtg acc gtc tac gac aag ccc gca tct ttc ttt aaa gag | | | | 528 |
| Ile Arg Ala Val Thr Val Tyr Asp Lys Pro Ala Ser Phe Phe Lys Glu | | | | |
| | 165 | 170 | 175 | |
| aca cct ctg gac ctg cag cac cgg ctc ttc atg aag ctg ggc agc atg | | | | 576 |
| Thr Pro Leu Asp Leu Gln His Arg Leu Phe Met Lys Leu Gly Ser Met | | | | |

173

| 180 | 185 | 190 | |
|---|-----|-----|------|
| cac tct ccg ttc agg gcc cgc tca gaa cct gag gac cca gtc acg gag His Ser Pro Phe Arg Ala Arg Ser Glu Pro Glu Asp Pro Val Thr Glu 195 200 205 | | | 624 |
| cgg tcg gcc ttc acg gag cgg gat gct ggg agc ggg ctg gtg acg cgt Arg Ser Ala Phe Thr Glu Arg Asp Ala Gly Ser Gly Leu Val Thr Arg 210 215 220 | | | 672 |
| ctc cgt gag cgg cca gcc ctg ctg gtc agc agc acg agc tgg aca gag Leu Arg Glu Arg Pro Ala Leu Leu Val Ser Ser Thr Ser Trp Thr Glu 225 230 235 240 | | | 720 |
| gac gaa gac ttc tcc atc ctg ctg gca gct tta gaa aag ttt gaa caa Asp Glu Asp Phe Ser Ile Leu Leu Ala Ala Leu Glu Lys Phe Glu Gln 245 250 255 | | | 768 |
| ctg act ctt gat gga cac aac ctt cct tct ctc gtc tgt gtg ata aca Leu Thr Leu Asp Gly His Asn Leu Pro Ser Leu Val Cys Val Ile Thr 260 265 270 | | | 816 |
| ggc aaa ggg cct ctg agg gag tat tat agc cgc ctc atc cac cag aag Gly Lys Gly Pro Leu Arg Glu Tyr Tyr Ser Arg Leu Ile His Gln Lys 275 280 285 | | | 864 |
| cac ttc cag cac atc cag gtc tgc acc ccc tgg ctg gag gcc gag gac His Phe Gln His Ile Gln Val Cys Thr Pro Trp Leu Glu Ala Glu Asp 290 295 300 | | | 912 |
| tac ccc ctg ctt cta ggg tcg gcg gac ctg ggt gtc tgt ctg cac acg Tyr Pro Leu Leu Leu Gly Ser Ala Asp Leu Gly Val Cys Leu His Thr 305 310 315 320 | | | 960 |
| tcc tcc agt ggc ctg gac ctg ccc atg aag gtg gtg gac atg ttc ggg Ser Ser Ser Gly Leu Asp Leu Pro Met Lys Val Val Asp Met Phe Gly 325 330 335 | | | 1008 |
| tgc tgt ttg cct gtg tgt gct gtg aac ttc aag tgt tta cat gag ctg Cys Cys Leu Pro Val Cys Ala Val Asn Phe Lys Cys Leu His Glu Leu 340 345 350 | | | 1056 |
| gtg aaa cat gaa gaa aat ggc ctg gtc ttt gag gac tca gag gaa ctg Val Lys His Glu Glu Asn Gly Leu Val Phe Glu Asp Ser Glu Glu Leu | | | 1104 |

174

| | | | |
|---|-----|-----|------|
| 355 | 360 | 365 | |
| gca gct cag ctg cag atg ctt ttc tca aac ttt cct gat ctg cgg gca | | | 1152 |
| Ala Ala Gln Leu Gln Met Leu Phe Ser Asn Phe Pro Asp Leu Arg Ala | | | |
| 370 | 375 | 380 | |
| agc taa | | | 1158 |
| Ser * | | | |
| 385 | | | |

<210> 124

<211> 385

<212> PRT

<213> Homo sapiens

<400> 124

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Tyr | His | Ala | Leu | Ser | Leu | Ala | Met | His | Gly | Phe | Ser | Val | Thr |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Leu | Leu | Gly | Phe | Cys | Asn | Ser | Lys | Pro | His | Asp | Glu | Leu | Leu | Gln | Asn |
| | | 20 | | | | | 25 | | | | | | 30 | | |
| Asn | Arg | Ile | Gln | Ile | Val | Gly | Leu | Thr | Glu | Leu | Gln | Ser | Leu | Ala | Val |
| | | 35 | | | | 40 | | | | | | 45 | | | |
| Gly | Pro | Arg | Val | Phe | Gln | Tyr | Gly | Val | Lys | Val | Val | Leu | Gln | Ala | Met |
| | 50 | | | | 55 | | | | | 60 | | | | | |
| Tyr | Leu | Leu | Trp | Lys | Leu | Met | Trp | Arg | Glu | Pro | Gly | Ala | Tyr | Ile | Phe |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| Leu | Gln | Asn | Pro | Pro | Gly | Leu | Pro | Ser | Ile | Ala | Val | Cys | Trp | Phe | Val |
| | | | 85 | | | | | 90 | | | | | 95 | | |
| Gly | Cys | Leu | Cys | Gly | Ser | Lys | Leu | Val | Ile | Asp | Trp | His | Asn | Tyr | Gly |
| | | 100 | | | | | 105 | | | | | | 110 | | |
| Tyr | Ser | Ile | Met | Gly | Leu | Val | His | Gly | Pro | Asn | His | Pro | Leu | Val | Leu |
| | 115 | | | | 120 | | | | | | | 125 | | | |
| Leu | Ala | Lys | Trp | Tyr | Glu | Lys | Phe | Phe | Gly | Arg | Leu | Ser | His | Leu | Asn |
| | 130 | | | | 135 | | | | | 140 | | | | | |
| Leu | Cys | Val | Thr | Asn | Ala | Met | Arg | Glu | Asp | Leu | Ala | Asp | Asn | Trp | His |
| 145 | | | | 150 | | | | | 155 | | | | | 160 | |
| Ile | Arg | Ala | Val | Thr | Val | Tyr | Asp | Lys | Pro | Ala | Ser | Phe | Phe | Lys | Glu |
| | | 165 | | | | | | 170 | | | | | | 175 | |
| Thr | Pro | Leu | Asp | Leu | Gln | His | Arg | Leu | Phe | Met | Lys | Leu | Gly | Ser | Met |
| | | 180 | | | | | 185 | | | | | | 190 | | |
| His | Ser | Pro | Phe | Arg | Ala | Arg | Ser | Glu | Pro | Glu | Asp | Pro | Val | Thr | Glu |
| | 195 | | | | | | 200 | | | | | 205 | | | |
| Arg | Ser | Ala | Phe | Thr | Glu | Arg | Asp | Ala | Gly | Ser | Gly | Leu | Val | Thr | Arg |

175

210 215 220
 Leu Arg Glu Arg Pro Ala Leu Leu Val Ser Ser Thr Ser Trp Thr Glu
 225 230 235 240
 Asp Glu Asp Phe Ser Ile Leu Leu Ala Ala Leu Glu Lys Phe Glu Gln
 245 250 255
 Leu Thr Leu Asp Gly His Asn Leu Pro Ser Leu Val Cys Val Ile Thr
 260 265 270
 Gly Lys Gly Pro Leu Arg Glu Tyr Tyr Ser Arg Leu Ile His Gln Lys
 275 280 285
 His Phe Gln His Ile Gln Val Cys Thr Pro Trp Leu Glu Ala Glu Asp
 290 295 300
 Tyr Pro Leu Leu Leu Gly Ser Ala Asp Leu Gly Val Cys Leu His Thr
 305 310 315 320
 Ser Ser Ser Gly Leu Asp Leu Pro Met Lys Val Val Asp Met Phe Gly
 325 330 335
 Cys Cys Leu Pro Val Cys Ala Val Asn Phe Lys Cys Leu His Glu Leu
 340 345 350
 Val Lys His Glu Glu Asn Gly Leu Val Phe Glu Asp Ser Glu Glu Leu
 355 360 365
 Ala Ala Gln Leu Gln Met Leu Phe Ser Asn Phe Pro Asp Leu Arg Ala
 370 375 380
 Ser
 385

<210> 125
 <211> 1002
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1002)

<221> misc_feature
 <222> (1)...(1002)
 <223> n = A,T,C or G

<400> 125

atg gcg gcc gcc gca ggn nga ncg ctc ctg ctg ctc ctc tcc tct cgg 48
 Met Ala Ala Ala Ala Xaa Xaa Xaa Leu Leu Leu Leu Ser Ser Arg
 1 5 10 15

ggc ggc ggc ggc ggg ggc gcc ggc ggc tgc ggg gcg ctg act gcc ggc 96
 Gly Gly Gly Gly Gly Gly Ala Gly Gly Cys Gly Ala Leu Thr Ala Gly

176

| 20 | 25 | 30 | |
|---|----|----|-----|
| tgc ttc cct ggg ctg ggc gtc agc cgc cac cgg cag cag cac cac Cys Phe Pro Gly Leu Gly Val Ser Arg His Arg Gln Gln Gln His His 35 40 45 | | | 144 |
| cgg acg gta cac cag agg atc gct tcc tgg cag aat ttg gga gct gtt Arg Thr Val His Gln Arg Ile Ala Ser Trp Gln Asn Leu Gly Ala Val 50 55 60 | | | 192 |
| tat tgc agc act gtt gtg ccc tct gat gat gtt aca gtg gtt tat caa Tyr Cys Ser Thr Val Val Pro Ser Asp Asp Val Thr Val Val Tyr Gln 65 70 75 80 | | | 240 |
| aat ggg tta cct gtg ata tct gtg agg cta cca tcc cgg cgt gaa cgc Asn Gly Leu Pro Val Ile Ser Val Arg Leu Pro Ser Arg Arg Glu Arg 85 90 95 | | | 288 |
| tgt cag ttc aca ctc aag cct atc tct gac tct gtt ggt gta ttt tta Cys Gln Phe Thr Leu Lys Pro Ile Ser Asp Ser Val Gly Val Phe Leu 100 105 110 | | | 336 |
| cga caa ctg caa gaa gag gat cgg gga att gac aga gtt gct atc tat Arg Gln Leu Gln Glu Glu Asp Arg Gly Ile Asp Arg Val Ala Ile Tyr 115 120 125 | | | 384 |
| tca cca gat ggt gtt cgc gtt gct gct tca aca gga ata gac ctc ctc Ser Pro Asp Gly Val Arg Val Ala Ala Ser Thr Gly Ile Asp Leu Leu 130 135 140 | | | 432 |
| ctc ctt gat gac ttt aag ctg gtc att aat gac tta aca tac cac gta Leu Leu Asp Asp Phe Lys Leu Val Ile Asn Asp Leu Thr Tyr His Val 145 150 155 160 | | | 480 |
| cga cca cca aaa aga gac ctc tta agt cat gaa aat gca gca acg ctg Arg Pro Pro Lys Arg Asp Leu Leu Ser His Glu Asn Ala Ala Thr Leu 165 170 175 | | | 528 |
| aat gat gta aag aca ttg gtc cag caa cta tac acc aca ctg tgc att Asn Asp Val Lys Thr Leu Val Gln Gln Leu Tyr Thr Thr Leu Cys Ile 180 185 190 | | | 576 |
| gag cag cac cag tta aac aag gaa agg gag ctt att gaa aga cta gag Glu Gln His Gln Leu Asn Lys Glu Arg Glu Leu Ile Glu Arg Leu Glu 200 205 210 215 220 225 230 235 240 | | | 624 |

177

| 195 | 200 | 205 | |
|---|-----|-----|------|
| gat ctc aaa gag cag ctg gct ccc ctg gaa aag gta cga att gag att | | | 672 |
| Asp Leu Lys Glu Gln Leu Ala Pro Leu Glu Lys Val Arg Ile Glu Ile | | | |
| 210 | 215 | 220 | |
| agc aga aaa gct gag aag agg acc act ttg gtg cta tgg ggt ggc ctt | | | 720 |
| Ser Arg Lys Ala Glu Lys Arg Thr Thr Leu Val Leu Trp Gly Gly Leu | | | |
| 225 | 230 | 235 | 240 |
| gcc tac atg gcc aca cag ttt ggc att ttg gcc cgg ctt acc tgg tgg | | | 768 |
| Ala Tyr Met Ala Thr Gln Phe Gly Ile Leu Ala Arg Leu Thr Trp Trp | | | |
| 245 | 250 | 255 | |
| gaa tat tcc tgg gac atc atg gag cca gta aca tac ttc atc act tat | | | 816 |
| Glu Tyr Ser Trp Asp Ile Met Glu Pro Val Thr Tyr Phe Ile Thr Tyr | | | |
| 260 | 265 | 270 | |
| gga agt gcc atg gca atg tat gca tat ttt gta atg aca cgc cag gaa | | | 864 |
| Gly Ser Ala Met Ala Met Tyr Ala Tyr Phe Val Met Thr Arg Gln Glu | | | |
| 275 | 280 | 285 | |
| tat gtt tat cca gaa gcc aga gac aga caa tac tta cta ttt ttc cat | | | 912 |
| Tyr Val Tyr Pro Glu Ala Arg Asp Arg Gln Tyr Leu Leu Phe Phe His | | | |
| 290 | 295 | 300 | |
| aaa gga gcc aaa aag tca cgt ttt gac cta gag aaa tac aat caa ctc | | | 960 |
| Lys Gly Ala Lys Lys Ser Arg Phe Asp Leu Glu Lys Tyr Asn Gln Leu | | | |
| 305 | 310 | 315 | 320 |
| aag gat gca att gct cag cag aaa tgg acc tta aga gac tga | | | 1002 |
| Lys Asp Ala Ile Ala Gln Gln Lys Trp Thr Leu Arg Asp * | | | |
| 325 | 330 | | |

<210> 126

<211> 333

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(333)

<223> Xaa = Any Amino Acid

<400> 126

Met Ala Ala Ala Ala Xaa Xaa Xaa Leu Leu Leu Leu Leu Ser Ser Arg
 1 5 10 15
 Gly Gly Gly Gly Gly Ala Gly Gly Cys Gly Ala Leu Thr Ala Gly
 20 25 30
 Cys Phe Pro Gly Leu Gly Val Ser Arg His Arg Gln Gln His His
 35 40 45
 Arg Thr Val His Gln Arg Ile Ala Ser Trp Gln Asn Leu Gly Ala Val
 50 55 60
 Tyr Cys Ser Thr Val Val Pro Ser Asp Asp Val Thr Val Val Tyr Gln
 65 70 75 80
 Asn Gly Leu Pro Val Ile Ser Val Arg Leu Pro Ser Arg Arg Glu Arg
 85 90 95
 Cys Gln Phe Thr Leu Lys Pro Ile Ser Asp Ser Val Gly Val Phe Leu
 100 105 110
 Arg Gln Leu Gln Glu Glu Asp Arg Gly Ile Asp Arg Val Ala Ile Tyr
 115 120 125
 Ser Pro Asp Gly Val Arg Val Ala Ala Ser Thr Gly Ile Asp Leu Leu
 130 135 140
 Leu Leu Asp Asp Phe Lys Leu Val Ile Asn Asp Leu Thr Tyr His Val
 145 150 155 160
 Arg Pro Pro Lys Arg Asp Leu Leu Ser His Glu Asn Ala Ala Thr Leu
 165 170 175
 Asn Asp Val Lys Thr Leu Val Gln Gln Leu Tyr Thr Thr Leu Cys Ile
 180 185 190
 Glu Gln His Gln Leu Asn Lys Glu Arg Glu Leu Ile Glu Arg Leu Glu
 195 200 205
 Asp Leu Lys Glu Gln Leu Ala Pro Leu Glu Lys Val Arg Ile Glu Ile
 210 215 220
 Ser Arg Lys Ala Glu Lys Arg Thr Thr Leu Val Leu Trp Gly Gly Leu
 225 230 235 240
 Ala Tyr Met Ala Thr Gln Phe Gly Ile Leu Ala Arg Leu Thr Trp Trp
 245 250 255
 Glu Tyr Ser Trp Asp Ile Met Glu Pro Val Thr Tyr Phe Ile Thr Tyr
 260 265 270
 Gly Ser Ala Met Ala Met Tyr Ala Tyr Phe Val Met Thr Arg Gln Glu
 275 280 285
 Tyr Val Tyr Pro Glu Ala Arg Asp Arg Gln Tyr Leu Leu Phe Phe His
 290 295 300
 Lys Gly Ala Lys Lys Ser Arg Phe Asp Leu Glu Lys Tyr Asn Gln Leu
 305 310 315 320
 Lys Asp Ala Ile Ala Gln Gln Lys Trp Thr Leu Arg Asp
 325 330

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<220>
<221> CDS
<222> (1)...(1164)

<221> misc_feature
<222> (1)...(1164)
<223> n = A,T,C or G
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| | | | | | | | | | | | | | | | | |
|---|----|--|--|--|--|--|--|--|--|--|--|--|--|--|--|-----|
| <400> 127 | | | | | | | | | | | | | | | | |
| atg gtc ata ccc act ttg gcc tcc ctg gct tct cca act aca cta cag | 48 | | | | | | | | | | | | | | | |
| Met Val Ile Pro Thr Leu Ala Ser Leu Ala Ser Pro Thr Thr Leu Gln | | | | | | | | | | | | | | | | |
| 1 5 10 15 | | | | | | | | | | | | | | | | |
| tcc cag atg ctt ggg ggc cta gga cag gat gtt ttg tta aat aat tca | | | | | | | | | | | | | | | | 96 |
| Ser Gln Met Leu Gly Gly Leu Gly Gln Asp Val Leu Leu Asn Asn Ser | | | | | | | | | | | | | | | | |
| 20 25 30 | | | | | | | | | | | | | | | | |
| ctc act cct aaa tat ctt ggc tgt aag caa gac aac agc tct tcc cct | | | | | | | | | | | | | | | | 144 |
| Leu Thr Pro Lys Tyr Leu Gly Cys Lys Gln Asp Asn Ser Ser Ser Pro | | | | | | | | | | | | | | | | |
| 35 40 45 | | | | | | | | | | | | | | | | |
| aag ccc agc tcc gtg ttc aga aat gga ttc tct ggc att aag aag cct | | | | | | | | | | | | | | | | 192 |
| Lys Pro Ser Ser Val Phe Arg Asn Gly Phe Ser Gly Ile Lys Lys Pro | | | | | | | | | | | | | | | | |
| 50 55 60 | | | | | | | | | | | | | | | | |
| tgg cac aga tgt cac gtc tgc aac cac cac ttc cag ttc aaa cag cac | | | | | | | | | | | | | | | | 240 |
| Trp His Arg Cys His Val Cys Asn His His Phe Gln Phe Lys Gln His | | | | | | | | | | | | | | | | |
| 65 70 75 80 | | | | | | | | | | | | | | | | |
| ctt cga gac cac atg aat aca cac acc aac aga cgc cct tac agt tgt | | | | | | | | | | | | | | | | 288 |
| Leu Arg Asp His Met Asn Thr His Thr Asn Arg Arg Pro Tyr Ser Cys | | | | | | | | | | | | | | | | |
| 85 90 95 | | | | | | | | | | | | | | | | |
| cgg att tgt cgc aag tcc tat gta cgt cct ggc agc ctg agc aca cac | | | | | | | | | | | | | | | | 336 |
| Arg Ile Cys Arg Lys Ser Tyr Val Arg Pro Gly Ser Leu Ser Thr His | | | | | | | | | | | | | | | | |
| 100 105 110 | | | | | | | | | | | | | | | | |
| atg aaa ctt cat cat ggt gag aac cgt ctg aag aaa ctc atg tgt tgt | | | | | | | | | | | | | | | | 384 |

180

| | |
|---|-----|
| Met Lys Leu His His Gly Glu Asn Arg Leu Lys Lys Leu Met Cys Cys | |
| 115 120 125 | |
| gag ttt tgt gca aaa gtg ttt ggc cac atc cga gtc tat ttt ggc cat | 432 |
| Glu Phe Cys Ala Lys Val Phe Gly His Ile Arg Val Tyr Phe Gly His | |
| 130 135 140 | |
| ctg aaa gaa gtg cat agg gtt gtg atc agc act gag cct gcg ccc agt | 480 |
| Leu Lys Glu Val His Arg Val Val Ile Ser Thr Glu Pro Ala Pro Ser | |
| 145 150 155 160 | |
| gaa ctg cag cca gga gac ata cca aag aac aga gac atg agt gtg cga | 528 |
| Glu Leu Gln Pro Gly Asp Ile Pro Lys Asn Arg Asp Met Ser Val Arg | |
| 165 170 175 | |
| ggc atg gag gga tca ttg gag agg gaa aac aag tcc aac ctg gaa gaa | 576 |
| Gly Met Glu Gly Ser Leu Glu Arg Glu Asn Lys Ser Asn Leu Glu Glu | |
| 180 185 190 | |
| gac ttc ctt cta aac cag gca gac gaa gtc aaa tta caa atc aaa tgt | 624 |
| Asp Phe Leu Leu Asn Gln Ala Asp Glu Val Lys Leu Gln Ile Lys Cys | |
| 195 200 205 | |
| ggc cnt tgt cag att act gct cag tct ttt gcg gaa ata aaa ttt cat | 672 |
| Gly Xaa Cys Gln Ile Thr Ala Gln Ser Phe Ala Glu Ile Lys Phe His | |
| 210 215 220 | |
| tta ctt gat gtt cat gga gag gaa att gag ggc agg cta caa gaa ggg | 720 |
| Leu Leu Asp Val His Gly Glu Glu Ile Glu Gly Arg Leu Gln Glu Gly | |
| 225 230 235 240 | |
| acc ttc cca gga agc aag ggg act cag gaa gag ttg gtg cag cac gct | 768 |
| Thr Phe Pro Gly Ser Lys Gly Thr Gln Glu Glu Leu Val Gln His Ala | |
| 245 250 255 | |
| agc ccc gac tgg aaa agg cat cct gag aga ggg aag ccg gag aag gtt | 816 |
| Ser Pro Asp Trp Lys Arg His Pro Glu Arg Gly Lys Pro Glu Lys Val | |
| 260 265 270 | |
| cat tcc tcc tcc gag gaa tca cat gca tgt cca aga ctg aaa agg cag | 864 |
| His Ser Ser Ser Glu Glu Ser His Ala Cys Pro Arg Leu Lys Arg Gln | |
| 275 280 285 | |
| ctc cac ctt cat cag aat ggc gtg gaa atg ctc atg gaa aat gaa gga | 912 |

181

Leu His Leu His Gln Asn Gly Val Glu Met Leu Met Glu Asn Glu Gly
 290 295 300
 ccc cag tca gga acc aac aag cca agg gaa acc tgc cag ggc cct gag 960
 Pro Gln Ser Gly Thr Asn Lys Pro Arg Glu Thr Cys Gln Gly Pro Glu
 305 310 315 320
 tgt cct ggc ctc cac acg ttt ctc ttg tgg tcc cat tca ggc ttt aac 1008
 Cys Pro Gly Leu His Thr Phe Leu Leu Trp Ser His Ser Gly Phe Asn
 325 330 335
 tgc ctg ctt tgt gca gag atg ctg gga cgg aaa gag gac ctc ctc cac 1056
 Cys Leu Leu Cys Ala Glu Met Leu Gly Arg Lys Glu Asp Leu Leu His
 340 345 350
 cac tgg aag cac cag cat aac tgt gag gac cct tcc aaa ctg tgg gct 1104
 His Trp Lys His Gln His Asn Cys Glu Asp Pro Ser Lys Leu Trp Ala
 355 360 365
 att tta aat acg gtc tcc aac cag gga gtg atc gaa ctt tcc agt gaa 1152
 Ile Leu Asn Thr Val Ser Asn Gln Gly Val Ile Glu Leu Ser Ser Glu
 370 375 380
 gct gag aaa tga 1164
 Ala Glu Lys *
 385

<210> 128
 <211> 387
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(387)
 <223> Xaa = Any Amino Acid

<400> 128
 Met Val Ile Pro Thr Leu Ala Ser Leu Ala Ser Pro Thr Thr Leu Gln
 1 5 10 15
 Ser Gln Met Leu Gly Gly Leu Gly Gln Asp Val Leu Leu Asn Asn Ser
 20 25 30
 Leu Thr Pro Lys Tyr Leu Gly Cys Lys Gln Asp Asn Ser Ser Ser Pro

182

35 40 45
 Lys Pro Ser Ser Val Phe Arg Asn Gly Phe Ser Gly Ile Lys Lys Pro
 50 55 60
 Trp His Arg Cys His Val Cys Asn His His Phe Gln Phe Lys Gln His
 65 70 75 80
 Leu Arg Asp His Met Asn Thr His Thr Asn Arg Arg Pro Tyr Ser Cys
 85 90 95
 Arg Ile Cys Arg Lys Ser Tyr Val Arg Pro Gly Ser Leu Ser Thr His
 100 105 110
 Met Lys Leu His His Gly Glu Asn Arg Leu Lys Lys Leu Met Cys Cys
 115 120 125
 Glu Phe Cys Ala Lys Val Phe Gly His Ile Arg Val Tyr Phe Gly His
 130 135 140
 Leu Lys Glu Val His Arg Val Val Ile Ser Thr Glu Pro Ala Pro Ser
 145 150 155 160
 Glu Leu Gln Pro Gly Asp Ile Pro Lys Asn Arg Asp Met Ser Val Arg
 165 170 175
 Gly Met Glu Gly Ser Leu Glu Arg Glu Asn Lys Ser Asn Leu Glu Glu
 180 185 190
 Asp Phe Leu Leu Asn Gln Ala Asp Glu Val Lys Leu Gln Ile Lys Cys
 195 200 205
 Gly Xaa Cys Gln Ile Thr Ala Gln Ser Phe Ala Glu Ile Lys Phe His
 210 215 220
 Leu Leu Asp Val His Gly Glu Glu Ile Glu Gly Arg Leu Gln Glu Gly
 225 230 235 240
 Thr Phe Pro Gly Ser Lys Gly Thr Gln Glu Glu Leu Val Gln His Ala
 245 250 255
 Ser Pro Asp Trp Lys Arg His Pro Glu Arg Gly Lys Pro Glu Lys Val
 260 265 270
 His Ser Ser Ser Glu Glu Ser His Ala Cys Pro Arg Leu Lys Arg Gln
 275 280 285
 Leu His Leu His Gln Asn Gly Val Glu Met Leu Met Glu Asn Glu Gly
 290 295 300
 Pro Gln Ser Gly Thr Asn Lys Pro Arg Glu Thr Cys Gln Gly Pro Glu
 305 310 315 320
 Cys Pro Gly Leu His Thr Phe Leu Leu Trp Ser His Ser Gly Phe Asn
 325 330 335
 Cys Leu Leu Cys Ala Glu Met Leu Gly Arg Lys Glu Asp Leu Leu His
 340 345 350
 His Trp Lys His Gln His Asn Cys Glu Asp Pro Ser Lys Leu Trp Ala
 355 360 365
 Ile Leu Asn Thr Val Ser Asn Gln Gly Val Ile Glu Leu Ser Ser Glu
 370 375 380
 Ala Glu Lys

385

```
<210> 129
<211> 2022
<212> DNA
<213> Homo sapiens
```

<220>
<221> CDS
<222> (1)...(2022)

```
<221> misc_feature
<222> (1)...(2022)
<223> n = A,T,C or G
```

<400> 129

atg aag aag gac tgc agt ctt cct ctt act gtc ctt acc tgt gct aaa 48
Met Lys Lys Asp Cys Ser Leu Pro Leu Thr Val Leu Thr Cys Ala Lys
1 5 10 15

gca tgt cca cac atg gct act tgt gga aat gtt ctg ttt gag gga aga 96
Ala Cys Pro His Met Ala Thr Cys Gly Asn Val Leu Phe Glu Gly Arg
20 25 30

aca gtt cag cta ggg aag ctt tgc tgc act gga gtt gaa act gaa gat 144
Thr Val Gln Leu Gly Lys Leu Cys Cys Thr Gly Val Glu Thr Glu Asp
35 40 45

gat gaa gat act gag tca aat tca tcg gta gaa caa gca tcg gtt gaa 192
Asp Glu Asp Thr Glu Ser Asn Ser Ser Val Glu Gln Ala Ser Val Glu
50 55 60

gta cct gat gga cca aca ctc cat gac cca gac ctc tat att gag att 240
Val Pro Asp Gly Pro Thr Leu His Asp Pro Asp Leu Tyr Ile Glu Ile
65 70 75 80

gtg aaa aat acg aag tct gtc cca gaa tat tca gag gtg gct tat ccc 288
Val Lys Asn Thr Lys Ser Val Pro Glu Tyr Ser Glu Val Ala Tyr Pro
85 90 95

gat tat ttt ggt cac att ccg cct cca ttc aaa gag cct att tta gaa 336
Asp Tyr Phe Gly His Ile Pro Pro Pro Phe Lys Glu Pro Ile Leu Glu
100 105 110

184

| | |
|---|-----|
| agg cct tat ggt gta caa agg aca aaa att gct caa gat att gaa agg Arg Pro Tyr Gly Val Gln Arg Thr Lys Ile Ala Gln Asp Ile Glu Arg 115 120 125 | 384 |
| cta ata cat cag agt gat atc ata gat cgt gtg gta tat gac ttg gat Leu Ile His Gln Ser Asp Ile Ile Asp Arg Val Val Tyr Asp Leu Asp 130 135 140 | 432 |
| aac cca aat tac acc att cca gaa gag gga gat att ttg aaa ttt aac Asn Pro Asn Tyr Thr Ile Pro Glu Glu Gly Asp Ile Leu Lys Phe Asn 145 150 155 160 | 480 |
| tcc aaa ttt gag tct ggg aat ctg cgc ana gta att caa att aga aaa Ser Lys Phe Glu Ser Gly Asn Leu Arg Xaa Val Ile Gln Ile Arg Lys 165 170 175 | 528 |
| aat gaa tat gat ctt att ctg aac tca gac ata aac agc aat cat tat Asn Glu Tyr Asp Leu Ile Leu Asn Ser Asp Ile Asn Ser Asn His Tyr 180 185 190 | 576 |
| cat cag tgg ttt tac ttt gaa gtc agt gga atg cga cca ggt gtt gct His Gln Trp Phe Tyr Phe Glu Val Ser Gly Met Arg Pro Gly Val Ala 195 200 205 | 624 |
| tac agg ttt aac atc att aac tgt gaa aag tcc aac agt cag ttt aat Tyr Arg Phe Asn Ile Ile Asn Cys Glu Lys Ser Asn Ser Gln Phe Asn 210 215 220 | 672 |
| tat ggt atg caa cca ctc atg tat tcg gtt cag gaa gca tta aat gcc Tyr Gly Met Gln Pro Leu Met Tyr Ser Val Gln Glu Ala Leu Asn Ala 225 230 235 240 | 720 |
| aga cca tgg tgg att cgt atg ggg act gac att tgt tac tat aaa aat Arg Pro Trp Trp Ile Arg Met Gly Thr Asp Ile Cys Tyr Tyr Lys Asn 245 250 255 | 768 |
| cat ttc tca aga agt tca gtt gct gca ggt ggg caa aag gga aaa tcc His Phe Ser Arg Ser Ser Val Ala Ala Gly Gly Gln Lys Gly Lys Ser 260 265 270 | 816 |
| tac tat aca att aca ttt act gtc aat ttt cca cat aaa gat gat gtt Tyr Tyr Thr Ile Thr Phe Thr Val Asn Phe Pro His Lys Asp Asp Val 275 280 285 | 864 |

185

| | |
|---|------|
| tgc tac ttt gct tat cac tat cca tat acg tat tca act tta cag atg Cys Tyr Phe Ala Tyr His Tyr Pro Tyr Thr Tyr Ser Thr Leu Gln Met 290 295 300 | 912 |
| cat ctt caa aaa ttg gaa tca gca cac aat cct cag caa atc tat ttt His Leu Gln Lys Leu Glu Ser Ala His Asn Pro Gln Gln Ile Tyr Phe 305 310 315 320 | 960 |
| cgg aaa gat gtg tta tgt gaa acc ctg tct gga aac agc tgc ccc ttg Arg Lys Asp Val Leu Cys Glu Thr Leu Ser Gly Asn Ser Cys Pro Leu 325 330 335 | 1008 |
| gtg act ata aca gca atg cca gag tct aat tat tat gaa cat atc tgc Val Thr Ile Thr Ala Met Pro Glu Ser Asn Tyr Tyr Glu His Ile Cys 340 345 350 | 1056 |
| cat ttc aga aat cgc cct tac gtt ttc ttg tct gct cgg gta cat cct His Phe Arg Asn Arg Pro Tyr Val Phe Leu Ser Ala Arg Val His Pro 355 360 365 | 1104 |
| gga gaa act aat gca agt tgg gtt atg aaa gga acg ttg gaa tat ctc Gly Glu Thr Asn Ala Ser Trp Val Met Lys Gly Thr Leu Glu Tyr Leu 370 375 380 | 1152 |
| atg agc aat aac ccc act gct cag agc tta cga gaa tct tat att ttt Met Ser Asn Asn Pro Thr Ala Gln Ser Leu Arg Glu Ser Tyr Ile Phe 385 390 395 400 | 1200 |
| aaa att gtc cct atg tta aat cca gat ggt gtc atc aat gga aat cat Lys Ile Val Pro Met Leu Asn Pro Asp Gly Val Ile Asn Gly Asn His 405 410 415 | 1248 |
| cgc tgt tct tta agt gga gag gat ttg aat agg cag tgg caa agt cca Arg Cys Ser Leu Ser Gly Glu Asp Leu Asn Arg Gln Trp Gln Ser Pro 420 425 430 | 1296 |
| agt ccg gat tta cat cct aca att tac cat gct aag ggg ctg ttg caa Ser Pro Asp Leu His Pro Thr Ile Tyr His Ala Lys Gly Leu Leu Gln 435 440 445 | 1344 |
| tac ttg gct gca gtg aag cgt tta ccc ttg gtt tat tgt gat tat cat Tyr Leu Ala Ala Val Lys Arg Leu Pro Leu Val Tyr Cys Asp Tyr His 450 455 460 | 1392 |

| | |
|---|------|
| ggc cat tcc cga aag aag aat gta ttt atg tat ggt tgc agc atc aaa | 1440 |
| Gly His Ser Arg Lys Lys Asn Val Phe Met Tyr Gly Cys Ser Ile Lys | |
| 465 470 475 480 | |
| gag aca gtg tgg cat acc aat gat aat gca act tca tgt gat gtt gtg | 1488 |
| Glu Thr Val Trp His Thr Asn Asp Asn Ala Thr Ser Cys Asp Val Val | |
| 485 490 495 | |
| gag gat acg gga tac agg aca ttg cct aag ata ctg agc cat atc gcc | 1536 |
| Glu Asp Thr Gly Tyr Arg Thr Leu Pro Lys Ile Leu Ser His Ile Ala | |
| 500 505 510 | |
| cca gca ttt tgc atg agc agc tgt agc ttc gta gtg gaa aaa tct aaa | 1584 |
| Pro Ala Phe Cys Met Ser Ser Cys Ser Phe Val Val Glu Lys Ser Lys | |
| 515 520 525 | |
| gaa tcc aca gca cgt gtt gta gtt tgg agg gaa ata gga gta caa aga | 1632 |
| Glu Ser Thr Ala Arg Val Val Val Trp Arg Glu Ile Gly Val Gln Arg | |
| 530 535 540 | |
| agt tat acc atg gag agt act tta tgt ggc tgt gat cag gga aaa tac | 1680 |
| Ser Tyr Thr Met Glu Ser Thr Leu Cys Gly Cys Asp Gln Gly Lys Tyr | |
| 545 550 555 560 | |
| aag ggt tta cag att ggt acc cga gaa ctg gaa gag atg gga gca aaa | 1728 |
| Lys Gly Leu Gln Ile Gly Thr Arg Glu Leu Glu Glu Met Gly Ala Lys | |
| 565 570 575 | |
| ttt tgt gtt ggt ctt tta cgt ttg aaa aga ctg acc tct cca ttg gag | 1776 |
| Phe Cys Val Gly Leu Leu Arg Leu Lys Arg Leu Thr Ser Pro Leu Glu | |
| 580 585 590 | |
| tat aat ctg cct tcc agc ctg ctt gac ttt gaa aat gat tta att gaa | 1824 |
| Tyr Asn Leu Pro Ser Ser Leu Leu Asp Phe Glu Asn Asp Leu Ile Glu | |
| 595 600 605 | |
| tca agc tgc aaa gta act agc cct acc act tat gtc ttg gat gaa gat | 1872 |
| Ser Ser Cys Lys Val Thr Ser Pro Thr Thr Tyr Val Leu Asp Glu Asp | |
| 610 615 620 | |
| gaa cct cga ttc ctt gaa gaa gtt gat tac agt gca gaa agt aat gat | 1920 |
| Glu Pro Arg Phe Leu Glu Glu Val Asp Tyr Ser Ala Glu Ser Asn Asp | |
| 625 630 635 640 | |

187

gag tta gat att gag ttg gct gaa aat gta gga gat tat gaa cct tct 1968
 Glu Leu Asp Ile Glu Leu Ala Glu Asn Val Gly Asp Tyr Glu Pro Ser
 645 650 655

gct caa gaa gaa gta ctt tct gac tct gaa tta tca aga aca tac cta 2016
 Ala Gln Glu Glu Val Leu Ser Asp Ser Glu Leu Ser Arg Thr Tyr Leu
 660 665 670

cct tga 2022
 Pro *

<210> 130
 <211> 673
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(673)
 <223> Xaa = Any Amino Acid

<400> 130
 Met Lys Lys Asp Cys Ser Leu Pro Leu Thr Val Leu Thr Cys Ala Lys
 1 5 10 15
 Ala Cys Pro His Met Ala Thr Cys Gly Asn Val Leu Phe Glu Gly Arg
 20 25 30
 Thr Val Gln Leu Gly Lys Leu Cys Cys Thr Gly Val Glu Thr Glu Asp
 35 40 45
 Asp Glu Asp Thr Glu Ser Asn Ser Ser Val Glu Gln Ala Ser Val Glu
 50 55 60
 Val Pro Asp Gly Pro Thr Leu His Asp Pro Asp Leu Tyr Ile Glu Ile
 65 70 75 80
 Val Lys Asn Thr Lys Ser Val Pro Glu Tyr Ser Glu Val Ala Tyr Pro
 85 90 95
 Asp Tyr Phe Gly His Ile Pro Pro Pro Phe Lys Glu Pro Ile Leu Glu
 100 105 110
 Arg Pro Tyr Gly Val Gln Arg Thr Lys Ile Ala Gln Asp Ile Glu Arg
 115 120 125
 Leu Ile His Gln Ser Asp Ile Ile Asp Arg Val Val Tyr Asp Leu Asp
 130 135 140
 Asn Pro Asn Tyr Thr Ile Pro Glu Glu Gly Asp Ile Leu Lys Phe Asn
 145 150 155 160

188

Ser Lys Phe Glu Ser Gly Asn Leu Arg Xaa Val Ile Gln Ile Arg Lys
 165 170 175
 Asn Glu Tyr Asp Leu Ile Leu Asn Ser Asp Ile Asn Ser Asn His Tyr
 180 185 190
 His Gln Trp Phe Tyr Phe Glu Val Ser Gly Met Arg Pro Gly Val Ala
 195 200 205
 Tyr Arg Phe Asn Ile Ile Asn Cys Glu Lys Ser Asn Ser Gln Phe Asn
 210 215 220
 Tyr Gly Met Gln Pro Leu Met Tyr Ser Val Gln Glu Ala Leu Asn Ala
 225 230 235 240
 Arg Pro Trp Trp Ile Arg Met Gly Thr Asp Ile Cys Tyr Tyr Lys Asn
 245 250 255
 His Phe Ser Arg Ser Ser Val Ala Ala Gly Gly Gln Lys Gly Lys Ser
 260 265 270
 Tyr Tyr Thr Ile Thr Phe Thr Val Asn Phe Pro His Lys Asp Asp Val
 275 280 285
 Cys Tyr Phe Ala Tyr His Tyr Pro Tyr Thr Tyr Ser Thr Leu Gln Met
 290 295 300
 His Leu Gln Lys Leu Glu Ser Ala His Asn Pro Gln Gln Ile Tyr Phe
 305 310 315 320
 Arg Lys Asp Val Leu Cys Glu Thr Leu Ser Gly Asn Ser Cys Pro Leu
 325 330 335
 Val Thr Ile Thr Ala Met Pro Glu Ser Asn Tyr Tyr Glu His Ile Cys
 340 345 350
 His Phe Arg Asn Arg Pro Tyr Val Phe Leu Ser Ala Arg Val His Pro
 355 360 365
 Gly Glu Thr Asn Ala Ser Trp Val Met Lys Gly Thr Leu Glu Tyr Leu
 370 375 380
 Met Ser Asn Asn Pro Thr Ala Gln Ser Leu Arg Glu Ser Tyr Ile Phe
 385 390 395 400
 Lys Ile Val Pro Met Leu Asn Pro Asp Gly Val Ile Asn Gly Asn His
 405 410 415
 Arg Cys Ser Leu Ser Gly Glu Asp Leu Asn Arg Gln Trp Gln Ser Pro
 420 425 430
 Ser Pro Asp Leu His Pro Thr Ile Tyr His Ala Lys Gly Leu Leu Gln
 435 440 445
 Tyr Leu Ala Ala Val Lys Arg Leu Pro Leu Val Tyr Cys Asp Tyr His
 450 455 460
 Gly His Ser Arg Lys Lys Asn Val Phe Met Tyr Gly Cys Ser Ile Lys
 465 470 475 480
 Glu Thr Val Trp His Thr Asn Asp Asn Ala Thr Ser Cys Asp Val Val
 485 490 495
 Glu Asp Thr Gly Tyr Arg Thr Leu Pro Lys Ile Leu Ser His Ile Ala
 500 505 510

[illegible]

<210> 131
<211> 375
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(375)

| | | | | | | | | | | | | | | | | |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> 131 | | | | | | | | | | | | | | | | |
| atg | att | gga | cct | gca | gta | ttc | ctg | gta | gct | gct | ggc | ttc | att | ggc | tgt | 48 |
| Met | Ile | Gly | Pro | Ala | Val | Phe | Leu | Val | Ala | Ala | Gly | Phe | Ile | Gly | Cys | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| | | | | | | | | | | | | | | | | |
| gat | tat | tct | ttg | gcc | gtt | gct | ttc | cta | act | ata | tca | aca | aca | ctg | gga | 96 |
| Asp | Tyr | Ser | Leu | Ala | Val | Ala | Phe | Leu | Thr | Ile | Ser | Thr | Thr | Leu | Gly | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| | | | | | | | | | | | | | | | | |
| ggc | ttt | tgc | tct | tct | gga | ttt | agc | atc | aac | cat | ctg | gat | att | gct | cct | 144 |
| Gly | Phe | Cys | Ser | Ser | Gly | Phe | Ser | Ile | Asn | His | Leu | Asp | Ile | Ala | Pro | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |

190

| | |
|---|-----|
| tcg tat gct ggt atc ctc ctg ggc atc aca aat aca ttt gcc act att | 192 |
| Ser Tyr Ala Gly Ile Leu Leu Gly Ile Thr Asn Thr Phe Ala Thr Ile | |
| 50 55 60 | |
| cca gga atg gtt ggg ccc gtc att gct aaa agt ctg acc cct gat aac | 240 |
| Pro Gly Met Val Gly Pro Val Ile Ala Lys Ser Leu Thr Pro Asp Asn | |
| 65 70 75 80 | |
| act gtt gga gaa tgg caa acc gtg ttc tat att gct gct gct att aat | 288 |
| Thr Val Gly Glu Trp Gln Thr Val Phe Tyr Ile Ala Ala Ala Ile Asn | |
| 85 90 95 | |
| gtt ttt ggt gcc att ttc ttt aca cta ttc gcc aaa ggt gaa gta caa | 336 |
| Val Phe Gly Ala Ile Phe Phe Thr Leu Phe Ala Lys Gly Glu Val Gln | |
| 100 105 110 | |
| aac tgg gct ctc aat gat cac cat gga cac aga cac tga | 375 |
| Asn Trp Ala Leu Asn Asp His His Gly His Arg His * | |
| 115 120 | |

<210> 132

<211> 124

<212> PRT

<213> Homo sapiens

<400> 132

| | |
|---|--|
| Met Ile Gly Pro Ala Val Phe Leu Val Ala Ala Gly Phe Ile Gly Cys | |
| 1 5 10 15 | |
| Asp Tyr Ser Leu Ala Val Ala Phe Leu Thr Ile Ser Thr Thr Leu Gly | |
| 20 25 30 | |
| Gly Phe Cys Ser Ser Gly Phe Ser Ile Asn His Leu Asp Ile Ala Pro | |
| 35 40 45 | |
| Ser Tyr Ala Gly Ile Leu Leu Gly Ile Thr Asn Thr Phe Ala Thr Ile | |
| 50 55 60 | |
| Pro Gly Met Val Gly Pro Val Ile Ala Lys Ser Leu Thr Pro Asp Asn | |
| 65 70 75 80 | |
| Thr Val Gly Glu Trp Gln Thr Val Phe Tyr Ile Ala Ala Ala Ile Asn | |
| 85 90 95 | |
| Val Phe Gly Ala Ile Phe Phe Thr Leu Phe Ala Lys Gly Glu Val Gln | |
| 100 105 110 | |
| Asn Trp Ala Leu Asn Asp His His Gly His Arg His | |
| 115 120 | |

191

```
<210> 133
<211> 1485
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> CDS  
<222> (1)...(1485)
```

```
<221> misc_feature
<222> (1)...(1485)
<223> n = A,T,C or G
```

<400> 133

atg ccc gca gag tct gga aag aga ttc aaa ccc agc aag tat gtc ccg 48
Met Pro Ala Glu Ser Gly Lys Arg Phe Lys Pro Ser Lys Tyr Val Pro
1 5 10 15

gtc tct gca gcc gcc atc ttc cta gtg gga gct acg aca ctc ttc ttt 96
Val Ser Ala Ala Ala Ile Phe Leu Val Gly Ala Thr Thr Leu Phe Phe
20 25 30

gcc ttt acg tgt cca gga cta agc ctg tat gtg tca cct gca gtg ccc 144
Ala Phe Thr Cys Pro Gly Leu Ser Leu Tyr Val Ser Pro Ala Val Pro
35 40 45

atc tac aat gca att atg ttt ctc ttt gtg ttg gcc aac ttc agc atg 192
Ile Tyr Asn Ala Ile Met Phe Leu Phe Val Leu Ala Asn Phe Ser Met
50 55 60

gcc acc ttc atg gac cca ggg att ttc cct cga gct gag gag gat gag 240
Ala Thr Phe Met Asp Pro Gly Ile Phe Pro Arg Ala Glu Glu Asp Glu
65 70 75 80

gac aag gaa gat gat ttc cga gct ccc ctt tac aaa aca gtg gag ata 288
Asp Lys Glu Asp Asp Phe Arg Ala Pro Leu Tyr Lys Thr Val Glu Ile
85 90 95

aag ggc atc cag gtg cgc atg aaa tgg tgt gcc acc tgc cgc ttt tac 336
Lys Gly Ile Gln Val Arg Met Lys Trp Cys Ala Thr Cys Arg Phe Tyr
100 105 110

cgt ccc cct cga tgt tcc cac tgc agt gtc tgt gac aac tgt gtg gag 384

192

| | |
|---|-----|
| Arg Pro Pro Arg Cys Ser His Cys Ser Val Cys Asp Asn Cys Val Glu | |
| 115 120 125 | |
| gaa ttt gat cat cac tgc ccc tgg gtg aat aac tgt att ggt cgc cgg | 432 |
| Glu Phe Asp His His Cys Pro Trp Val Asn Asn Cys Ile Gly Arg Arg | |
| 130 135 140 | |
| aac tac cgt tat ttt ttc ctt ttc ctc ctt tcc ctg aca gcc cac att | 480 |
| Asn Tyr Arg Tyr Phe Phe Leu Phe Leu Leu Ser Leu Thr Ala His Ile | |
| 145 150 155 160 | |
| atg ggt gtg ttt ggc ttt ggc ctc ctt tat gtc ctc tac cac ata gag | 528 |
| Met Gly Val Phe Gly Phe Gly Leu Leu Tyr Val Leu Tyr His Ile Glu | |
| 165 170 175 | |
| gaa ctc tca ggg gtc cgc acg gct gtc aca atg gca gta atg tgt gtg | 576 |
| Glu Leu Ser Gly Val Arg Thr Ala Val Thr Met Ala Val Met Cys Val | |
| 180 185 190 | |
| gct ggc tta ttc ttc atc cct gta gct ggc ctc acg gga ttt cac gtg | 624 |
| Ala Gly Leu Phe Phe Ile Pro Val Ala Gly Leu Thr Gly Phe His Val | |
| 195 200 205 | |
| gtt ctg gtg gcc agg gga cgc aca acc aat gaa cag gtt acg ggt aaa | 672 |
| Val Leu Val Ala Arg Gly Arg Thr Thr Asn Glu Gln Val Thr Gly Lys | |
| 210 215 220 | |
| ttc cgg gga ggt gtg aac ccc ttc acc aat ggc tgc tgt aac aat gtc | 720 |
| Phe Arg Gly Gly Val Asn Pro Phe Thr Asn Gly Cys Cys Asn Asn Val | |
| 225 230 235 240 | |
| agc cgt gtt ctc tgc agt tct cca gca ccc agg tat ttg ggg aga cca | 768 |
| Ser Arg Val Leu Cys Ser Ser Pro Ala Pro Arg Tyr Leu Gly Arg Pro | |
| 245 250 255 | |
| aag aaa gag aag aca att gta atc aga cct ccc ttc ctt cga cca gaa | 816 |
| Lys Lys Glu Lys Thr Ile Val Ile Arg Pro Pro Phe Leu Arg Pro Glu | |
| 260 265 270 | |
| gtt tca gat ggg cag ata act gtg aag atc atg gat aat ggc atc cag | 864 |
| Val Ser Asp Gly Gln Ile Thr Val Lys Ile Met Asp Asn Gly Ile Gln | |
| 275 280 285 | |
| gga gag ctg agg aga aca aag tct aag gga agc ctg gag ata aca gag | 912 |

193

| | |
|---|------|
| Gly Glu Leu Arg Arg Thr Lys Ser Lys Gly Ser Leu Glu Ile Thr Glu | |
| 290 295 300 | |
| agc cag tct gca gat gct gaa cct cca cct cct cct aag cca gac ctg | 960 |
| Ser Gln Ser Ala Asp Ala Glu Pro Pro Pro Pro Lys Pro Asp Leu | |
| 305 310 315 320 | |
| agc cgt tac aca ggg ttg cga aca cac ctc ggc ttg gct act aat gag | 1008 |
| Ser Arg Tyr Thr Gly Leu Arg Thr His Leu Gly Leu Ala Thr Asn Glu | |
| 325 330 335 | |
| gat agt agc tta ttg gcc aag gac agc ccc ccg aca cct acc atg tac | 1056 |
| Asp Ser Ser Leu Leu Ala Lys Asp Ser Pro Pro Thr Pro Thr Met Tyr | |
| 340 345 350 | |
| aag tat cgg ccg ggt tac agt agc agc agt acg tca gct gcc atg ccg | 1104 |
| Lys Tyr Arg Pro Gly Tyr Ser Ser Ser Thr Ser Ala Ala Met Pro | |
| 355 360 365 | |
| cat tcc tcc agc gcc aag ttg agt cgt ggg gac agc ttg aag gag cca | 1152 |
| His Ser Ser Ser Ala Lys Leu Ser Arg Gly Asp Ser Leu Lys Glu Pro | |
| 370 375 380 | |
| acc tca att gca gag agc agc cgt cac ccc agc tac cgc tca gag ccc | 1200 |
| Thr Ser Ile Ala Glu Ser Ser Arg His Pro Ser Tyr Arg Ser Glu Pro | |
| 385 390 395 400 | |
| agc ttg gaa cca gag agc ttc cgt tct cct acc ttt ggc aaa agt ttt | 1248 |
| Ser Leu Glu Pro Glu Ser Phe Arg Ser Pro Thr Phe Gly Lys Ser Phe | |
| 405 410 415 | |
| cac ttc gat cca cta tcc agt ggc tca cgc tcc tcc agc ctc aag tca | 1296 |
| His Phe Asp Pro Leu Ser Ser Gly Ser Arg Ser Ser Ser Leu Lys Ser | |
| 420 425 430 | |
| ncc cag ggc aca ggc ttt gag ctg ggc cag ttg caa tcc att cgt tca | 1344 |
| Xaa Gln Gly Thr Gly Phe Glu Leu Gly Gln Leu Gln Ser Ile Arg Ser | |
| 435 440 445 | |
| gag ggc acc acc tcc acc tcc tat aag agc ctg gcc aac cag aca cgc | 1392 |
| Glu Gly Thr Thr Ser Thr Ser Tyr Lys Ser Leu Ala Asn Gln Thr Arg | |
| 450 455 460 | |
| aat gga agc cta tct tat gac agc ttg ctc aca cct tca gac agc cct | 1440 |

194

Asn Gly Ser Leu Ser Tyr Asp Ser Leu Leu Thr Pro Ser Asp Ser Pro
 465 470 475 480

gat ttt gag tca gtg cag gca ggg ctg agc cag acc cac ctt tag 1485
 Asp Phe Glu Ser Val Gln Ala Gly Leu Ser Gln Thr His Leu *
 485 490

<210> 134

<211> 494

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(494)

<223> Xaa = Any Amino Acid

<400> 134

Met Pro Ala Glu Ser Gly Lys Arg Phe Lys Pro Ser Lys Tyr Val Pro
 1 5 10 15
 Val Ser Ala Ala Ala Ile Phe Leu Val Gly Ala Thr Thr Leu Phe Phe
 20 25 30
 Ala Phe Thr Cys Pro Gly Leu Ser Leu Tyr Val Ser Pro Ala Val Pro
 35 40 45
 Ile Tyr Asn Ala Ile Met Phe Leu Phe Val Leu Ala Asn Phe Ser Met
 50 55 60
 Ala Thr Phe Met Asp Pro Gly Ile Phe Pro Arg Ala Glu Glu Asp Glu
 65 70 75 80
 Asp Lys Glu Asp Asp Phe Arg Ala Pro Leu Tyr Lys Thr Val Glu Ile
 85 90 95
 Lys Gly Ile Gln Val Arg Met Lys Trp Cys Ala Thr Cys Arg Phe Tyr
 100 105 110
 Arg Pro Pro Arg Cys Ser His Cys Ser Val Cys Asp Asn Cys Val Glu
 115 120 125
 Glu Phe Asp His His Cys Pro Trp Val Asn Asn Cys Ile Gly Arg Arg
 130 135 140
 Asn Tyr Arg Tyr Phe Phe Leu Phe Leu Leu Ser Leu Thr Ala His Ile
 145 150 155 160
 Met Gly Val Phe Gly Phe Gly Leu Leu Tyr Val Leu Tyr His Ile Glu
 165 170 175
 Glu Leu Ser Gly Val Arg Thr Ala Val Thr Met Ala Val Met Cys Val
 180 185 190
 Ala Gly Leu Phe Phe Ile Pro Val Ala Gly Leu Thr Gly Phe His Val

195

| | | |
|---|-----|-----|
| 195 | 200 | 205 |
| Val Leu Val Ala Arg Gly Arg Thr Thr Asn Glu Gln Val Thr Gly Lys | | |
| 210 | 215 | 220 |
| Phe Arg Gly Gly Val Asn Pro Phe Thr Asn Gly Cys Cys Asn Asn Val | | |
| 225 | 230 | 235 |
| Ser Arg Val Leu Cys Ser Ser Pro Ala Pro Arg Tyr Leu Gly Arg Pro | | 240 |
| | 245 | 250 |
| Lys Lys Glu Lys Thr Ile Val Ile Arg Pro Pro Phe Leu Arg Pro Glu | | 255 |
| | 260 | 265 |
| Val Ser Asp Gly Gln Ile Thr Val Lys Ile Met Asp Asn Gly Ile Gln | | 270 |
| | 275 | 280 |
| Gly Glu Leu Arg Arg Thr Lys Ser Lys Gly Ser Leu Glu Ile Thr Glu | | 285 |
| | 290 | 295 |
| Ser Gln Ser Ala Asp Ala Glu Pro Pro Pro Pro Pro Lys Pro Asp Leu | | 300 |
| 305 | 310 | 315 |
| Ser Arg Tyr Thr Gly Leu Arg Thr His Leu Gly Leu Ala Thr Asn Glu | | 320 |
| | 325 | 330 |
| Asp Ser Ser Leu Leu Ala Lys Asp Ser Pro Pro Thr Pro Thr Met Tyr | | 335 |
| | 340 | 345 |
| Lys Tyr Arg Pro Gly Tyr Ser Ser Ser Ser Thr Ser Ala Ala Met Pro | | 350 |
| | 355 | 360 |
| His Ser Ser Ser Ala Lys Leu Ser Arg Gly Asp Ser Leu Lys Glu Pro | | 365 |
| | 370 | 375 |
| Thr Ser Ile Ala Glu Ser Ser Arg His Pro Ser Tyr Arg Ser Glu Pro | | 380 |
| 385 | 390 | 395 |
| Ser Leu Glu Pro Glu Ser Phe Arg Ser Pro Thr Phe Gly Lys Ser Phe | | 400 |
| | 405 | 410 |
| His Phe Asp Pro Leu Ser Ser Gly Ser Arg Ser Ser Ser Leu Lys Ser | | 415 |
| | 420 | 425 |
| Xaa Gln Gly Thr Gly Phe Glu Leu Gly Gln Leu Gln Ser Ile Arg Ser | | 430 |
| | 435 | 440 |
| Glu Gly Thr Thr Ser Thr Ser Tyr Lys Ser Leu Ala Asn Gln Thr Arg | | 445 |
| | 450 | 455 |
| Asn Gly Ser Leu Ser Tyr Asp Ser Leu Leu Thr Pro Ser Asp Ser Pro | | 460 |
| 465 | 470 | 475 |
| Asp Phe Glu Ser Val Gln Ala Gly Leu Ser Gln Thr His Leu | | 480 |
| | 485 | 490 |

<210> 135

<211> 246

<212> DNA

<213> Homo sapiens

<220>

196

<221> CDS

<222> (1)...(246)

<400> 135

| | |
|--|----|
| atg gtt ggg ggg gac gca gat gcc agg tcc aag gcc ttg ctg gga gtc | 48 |
| Met Val Gly Gly Asp Ala Asp Ala Arg Ser Lys Ala Leu Leu Gly Val | |
| 1 5 10 15 | |

| | |
|---|----|
| tgc gtc ggg tca ggc acg gaa gcc tat gtc ctg gta ttg gac cct cac | 96 |
| Cys Val Gly Ser Gly Thr Glu Ala Tyr Val Leu Val Leu Asp Pro His | |
| 20 25 30 | |

| | |
|---|-----|
| tac tgg ggc act cca aaa agc ccc agt gaa cta cag gct gct ggg tgg | 144 |
| Tyr Trp Gly Thr Pro Lys Ser Pro Ser Glu Leu Gln Ala Ala Gly Trp | |
| 35 40 45 | |

| | |
|---|-----|
| gtg ggc tgg caa gag gtg agt gca gcc ttt gac ccc aac tcc ttc tac | 192 |
| Val Gly Trp Gln Glu Val Ser Ala Ala Phe Asp Pro Asn Ser Phe Tyr | |
| 50 55 60 | |

| | |
|--|-----|
| aac ctg tgc ttg acc agc ctt agc tcc caa cag cag cag cgc acc ttg | 240 |
| Asn Leu Cys Leu Thr Ser Leu Ser Ser Gln Gln Gln Gln Arg Thr Leu | |
| 65 70 75 80 | |

| | |
|---------|-----|
| gac tga | 246 |
| Asp * | |

<210> 136

<211> 81

<212> PRT

<213> Homo sapiens

<400> 136

| |
|--|
| Met Val Gly Gly Asp Ala Asp Ala Arg Ser Lys Ala Leu Leu Gly Val |
| 1 5 10 15 |

| |
|---|
| Cys Val Gly Ser Gly Thr Glu Ala Tyr Val Leu Val Leu Asp Pro His |
| 20 25 30 |

| |
|---|
| Tyr Trp Gly Thr Pro Lys Ser Pro Ser Glu Leu Gln Ala Ala Gly Trp |
| 35 40 45 |

| |
|---|
| Val Gly Trp Gln Glu Val Ser Ala Ala Phe Asp Pro Asn Ser Phe Tyr |
| 50 55 60 |

| |
|---|
| Asn Leu Cys Leu Thr Ser Leu Ser Ser Gln Gln Gln Gln Arg Thr Leu |
|---|

197

65
Asp

70

75

80

<210> 137

<211> 552

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(552)

<400> 137

| | |
|--|----|
| atg gaa cag cgg tta gct gag ttt cgg gcg gcg cgg aaa cgg gcg ggt | 48 |
| Met Glu Gln Arg Leu Ala Glu Phe Arg Ala Ala Arg Lys Arg Ala Gly | |
| 1 5 10 15 | |

| | |
|---|----|
| ctg gcg gcc caa ccc cct gct gcc agt cag ggc gca caa acc cca gga | 96 |
| Leu Ala Ala Gln Pro Pro Ala Ala Ser Gln Gly Ala Gln Thr Pro Gly | |
| 20 25 30 | |

| | |
|---|-----|
| gag aag gcg gaa gca gca gcg act cta aag gca gcc cca ggc tgg cta | 144 |
| Glu Lys Ala Glu Ala Ala Ala Thr Leu Lys Ala Ala Pro Gly Trp Leu | |
| 35 40 45 | |

| | |
|---|-----|
| aag cgg ttc ctg gta tgg aaa cct agg ccc gcg agt gcc cgg gcc cag | 192 |
| Lys Arg Phe Leu Val Trp Lys Pro Arg Pro Ala Ser Ala Arg Ala Gln | |
| 50 55 60 | |

| | |
|--|-----|
| ccc ggc cta gtt cag gaa gcg gct cag ccc cag ggc agc aca tca gag | 240 |
| Pro Gly Leu Val Gln Glu Ala Ala Gln Pro Gln Gly Ser Thr Ser Glu | |
| 65 70 75 80 | |

| | |
|---|-----|
| aca cca tgg aac aca gcc att cct ctg ccg tcg tgc tgg gac cag tct | 288 |
| Thr Pro Trp Asn Thr Ala Ile Pro Leu Pro Ser Cys Trp Asp Gln Ser | |
| 85 90 95 | |

| | |
|---|-----|
| ttc ctg acc aat atc acc ttc ttg aag gtt ctt ctc tgg ttg gtc ctg | 336 |
| Phe Leu Thr Asn Ile Thr Phe Leu Lys Val Leu Leu Trp Leu Val Leu | |
| 100 105 110 | |

| | |
|---|-----|
| ctg gga ctg ttt gtg gaa ctg gaa ttt ggc ctg gca tat ttt gtc ctg | 384 |
| Leu Gly Leu Phe Val Glu Leu Glu Phe Gly Leu Ala Tyr Phe Val Leu | |

198

| 115 | 120 | 125 | |
|---|-----|-----|-----|
| tcc ttg ttc tat tgg atg tac gtc ggg aca cga ggc cct gaa gag aag | | | 432 |
| Ser Leu Phe Tyr Trp Met Tyr Val Gly Thr Arg Gly Pro Glu Glu Lys | | | |
| 130 | 135 | 140 | |
| aaa gag gga gag aag agc gcc tac tct gtg ttc aat cca ggc tgt gaa | | | 480 |
| Lys Glu Gly Glu Lys Ser Ala Tyr Ser Val Phe Asn Pro Gly Cys Glu | | | |
| 145 | 150 | 155 | 160 |
| gcc atc cag ggc acc ctg act gca gag cag ttg gag cgc gag tta cag | | | 528 |
| Ala Ile Gln Gly Thr Leu Thr Ala Glu Gln Leu Glu Arg Glu Leu Gln | | | |
| 165 | 170 | 175 | |
| ttg aga ccc ctg gca ggg aga tag | | | 552 |
| Leu Arg Pro Leu Ala Gly Arg * | | | |
| 180 | | | |

<210> 138

<211> 183

<212> PRT

<213> Homo sapiens

<400> 138

| | | | |
|---|-----|-----|----|
| Met Glu Gln Arg Leu Ala Glu Phe Arg Ala Ala Arg Lys Arg Ala Gly | | | |
| 1 | 5 | 10 | 15 |
| Leu Ala Ala Gln Pro Pro Ala Ala Ser Gln Gly Ala Gln Thr Pro Gly | | | |
| 20 | 25 | 30 | |
| Glu Lys Ala Glu Ala Ala Ala Thr Leu Lys Ala Ala Pro Gly Trp Leu | | | |
| 35 | 40 | 45 | |
| Lys Arg Phe Leu Val Trp Lys Pro Arg Pro Ala Ser Ala Arg Ala Gln | | | |
| 50 | 55 | 60 | |
| Pro Gly Leu Val Gln Glu Ala Ala Gln Pro Gln Gly Ser Thr Ser Glu | | | |
| 65 | 70 | 75 | 80 |
| Thr Pro Trp Asn Thr Ala Ile Pro Leu Pro Ser Cys Trp Asp Gln Ser | | | |
| 85 | 90 | 95 | |
| Phe Leu Thr Asn Ile Thr Phe Leu Lys Val Leu Leu Trp Leu Val Leu | | | |
| 100 | 105 | 110 | |
| Leu Gly Leu Phe Val Glu Leu Glu Phe Gly Leu Ala Tyr Phe Val Leu | | | |
| 115 | 120 | 125 | |
| Ser Leu Phe Tyr Trp Met Tyr Val Gly Thr Arg Gly Pro Glu Glu Lys | | | |
| 130 | 135 | 140 | |
| Lys Glu Gly Glu Lys Ser Ala Tyr Ser Val Phe Asn Pro Gly Cys Glu | | | |

Ala Ile Gln Gly Thr Leu Thr Ala Glu Gln Leu Glu Arg Glu Leu Gln
Leu Arg Pro Leu Ala Gly Arg

<220>
<221> CDS
<222> (1)...(912)

| | | | | | | | | | | | | | | | | | | |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|--|
| <400> 139 | | | | | | | | | | | | | | | | | | |
| atg | gcg | gcg | gcg | gca | ttg | ggc | agc | tcc | tca | ggc | tcg | gcg | tcc | ccg | gcc | | 48 | |
| Met | Ala | Ala | Ala | Ala | Leu | Gly | Ser | Ser | Ser | Gly | Ser | Ala | Ser | Pro | Ala | | | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | | | |
| | | | | | | | | | | | | | | | | | | |
| gtg | gct | gag | ctc | tgc | cag | aac | acc | ccg | gag | acc | ttt | ttg | gag | gcc | tcc | | 96 | |
| Val | Ala | Glu | Leu | Cys | Gln | Asn | Thr | Pro | Glu | Thr | Phe | Leu | Glu | Ala | Ser | | | |
| | | | 20 | | | | | 25 | | | | | 30 | | | | | |
| | | | | | | | | | | | | | | | | | | |
| aag | ctg | ctg | ctc | acc | tat | gct | gac | aac | atc | ctc | aga | aac | cct | aat | gat | | 144 | |
| Lys | Leu | Leu | Leu | Thr | Tyr | Ala | Asp | Asn | Ile | Leu | Arg | Asn | Pro | Asn | Asp | | | |
| | | | 35 | | | | 40 | | | | | 45 | | | | | | |
| | | | | | | | | | | | | | | | | | | |
| gaa | aaa | tat | aga | tcc | atc | cgg | att | gga | aac | aca | gcc | ttt | tct | act | aga | | 192 | |
| Glu | Lys | Tyr | Arg | Ser | Ile | Arg | Ile | Gly | Asn | Thr | Ala | Phe | Ser | Thr | Arg | | | |
| | 50 | | | | | 55 | | | | | 60 | | | | | | | |
| | | | | | | | | | | | | | | | | | | |
| ctc | ttg | cct | gtc | aga | gga | gct | gtt | gaa | tgt | tta | ttt | gaa | atg | ggc | ttt | | 240 | |
| Leu | Leu | Pro | Val | Arg | Gly | Ala | Val | Glu | Cys | Leu | Phe | Glu | Met | Gly | Phe | | | |
| 65 | | | | | 70 | | | | | 75 | | | | 80 | | | | |
| | | | | | | | | | | | | | | | | | | |
| gaa | gag | gga | gaa | aca | cat | ctc | atc | ttt | cct | aaa | aaa | gct | tca | gtg | gag | | 288 | |
| Glu | Glu | Gly | Glu | Thr | His | Leu | Ile | Phe | Pro | Lys | Lys | Ala | Ser | Val | Glu | | | |
| | | | | 85 | | | | | 90 | | | | | 95 | | | | |
| | | | | | | | | | | | | | | | | | | |
| cag | ctg | caa | aaa | att | cgt | gac | ctg | att | gcc | ata | gag | aga | agt | agc | aga | | 336 | |
| Gln | Leu | Gln | Lys | Ile | Arg | Asp | Leu | Ile | Ala | Ile | Glu | Arg | Ser | Ser | Arg | | | |
| | | | 100 | | | | | 105 | | | | | | 110 | | | | |

200

| | |
|---|-----|
| ctg gat ggc tca aat aag agc cac aaa gta aag tca tct cag caa cct Leu Asp Gly Ser Asn Lys Ser His Lys Val Lys Ser Ser Gln Gln Pro 115 120 125 | 384 |
| gca gcc agt acc cag ctt cct aca aca cca tct tca aat ccc agt ggg Ala Ala Ser Thr Gln Leu Pro Thr Thr Pro Ser Ser Asn Pro Ser Gly 130 135 140 | 432 |
| tta aac cag cac aca agg aac cgt caa ggg cag tca tca gat cca cca Leu Asn Gln His Thr Arg Asn Arg Gln Gly Gln Ser Ser Asp Pro Pro 145 150 155 160 | 480 |
| tct gct tca acg gtt gct gct gac tca gcc att cta gaa gtt ctt cag Ser Ala Ser Thr Val Ala Ala Asp Ser Ala Ile Leu Glu Val Leu Gln 165 170 175 | 528 |
| tcc aac att cag cat gtg ctg gtc tat gaa aat cct gct ctt cag gag Ser Asn Ile Gln His Val Leu Val Tyr Glu Asn Pro Ala Leu Gln Glu 180 185 190 | 576 |
| aaa gcg ttg gct tgt att ccg gtc caa gaa cta aaa agg aaa tca caa Lys Ala Leu Ala Cys Ile Pro Val Gln Glu Leu Lys Arg Lys Ser Gln 195 200 205 | 624 |
| gaa aag tta tcg aga gct aga aaa ttg gat aaa ggt atc aat ata agt Glu Lys Leu Ser Arg Ala Arg Lys Leu Asp Lys Gly Ile Asn Ile Ser 210 215 220 | 672 |
| gat gag gat ttt ctt ttg ctg gag ctt ttg cac tgg ttt aag gaa gaa Asp Glu Asp Phe Leu Leu Leu Glu Leu Leu His Trp Phe Lys Glu Glu 225 230 235 240 | 720 |
| ttt ttt cac tgg gtg aat aac gtt ttg tgc agc aaa tgt ggt gga cag Phe Phe His Trp Val Asn Asn Val Leu Cys Ser Lys Cys Gly Gly Gln 245 250 255 | 768 |
| act agg tct aga gat aga tca tta ctg ccc agt gat gat gag ctg aag Thr Arg Ser Arg Asp Arg Ser Leu Leu Pro Ser Asp Asp Glu Leu Lys 260 265 270 | 816 |
| tgg ggt gca aag gaa gtg gaa gat cat tac tgt gat gcc tgc cag ttc Trp Gly Ala Lys Glu Val Glu Asp His Tyr Cys Asp Ala Cys Gln Phe 275 280 285 | 864 |

201

agc aat cga ttc cca aga tgg gtg ccc tgg atg gta aaa tca gaa taa 912
 Ser Asn Arg Phe Pro Arg Trp Val Pro Trp Met Val Lys Ser Glu *
 290 295 300

<210> 140

<211> 303

<212> PRT

<213> Homo sapiens

<400> 140

Met Ala Ala Ala Ala Leu Gly Ser Ser Ser Gly Ser Ala Ser Pro Ala
 1 5 10 15
 Val Ala Glu Leu Cys Gln Asn Thr Pro Glu Thr Phe Leu Glu Ala Ser
 20 25 30
 Lys Leu Leu Leu Thr Tyr Ala Asp Asn Ile Leu Arg Asn Pro Asn Asp
 35 40 45
 Glu Lys Tyr Arg Ser Ile Arg Ile Gly Asn Thr Ala Phe Ser Thr Arg
 50 55 60
 Leu Leu Pro Val Arg Gly Ala Val Glu Cys Leu Phe Glu Met Gly Phe
 65 70 75 80
 Glu Glu Gly Glu Thr His Leu Ile Phe Pro Lys Lys Ala Ser Val Glu
 85 90 95
 Gln Leu Gln Lys Ile Arg Asp Leu Ile Ala Ile Glu Arg Ser Ser Arg
 100 105 110
 Leu Asp Gly Ser Asn Lys Ser His Lys Val Lys Ser Ser Gln Gln Pro
 115 120 125
 Ala Ala Ser Thr Gln Leu Pro Thr Thr Pro Ser Ser Asn Pro Ser Gly
 130 135 140
 Leu Asn Gln His Thr Arg Asn Arg Gln Gly Gln Ser Ser Asp Pro Pro
 145 150 155 160
 Ser Ala Ser Thr Val Ala Ala Asp Ser Ala Ile Leu Glu Val Leu Gln
 165 170 175
 Ser Asn Ile Gln His Val Leu Val Tyr Glu Asn Pro Ala Leu Gln Glu
 180 185 190
 Lys Ala Leu Ala Cys Ile Pro Val Gln Glu Leu Lys Arg Lys Ser Gln
 195 200 205
 Glu Lys Leu Ser Arg Ala Arg Lys Leu Asp Lys Gly Ile Asn Ile Ser
 210 215 220
 Asp Glu Asp Phe Leu Leu Leu Glu Leu Leu His Trp Phe Lys Glu Glu
 225 230 235 240
 Phe Phe His Trp Val Asn Asn Val Leu Cys Ser Lys Cys Gly Gly Gln
 245 250 255
 Thr Arg Ser Arg Asp Arg Ser Leu Leu Pro Ser Asp Asp Glu Leu Lys

260 265 270
 Trp Gly Ala Lys Glu Val Glu Asp His Tyr Cys Asp Ala Cys Gln Phe
 275 280 285
 Ser Asn Arg Phe Pro Arg Trp Val Pro Trp Met Val Lys Ser Glu
 290 295 300

```
<220>
<221> CDS
<222> (1)...(750)
```

| | | | | | | | | | | | | | | | |
|---|----|--|--|--|--|--|--|--|--|--|--|--|--|--|-----|
| <400> 141 | | | | | | | | | | | | | | | |
| atg ggt ggc ccc cgg ggc gcg ggc tgg gtg gcg gcg ggc ctg ctg ctc | 48 | | | | | | | | | | | | | | |
| Met Gly Gly Pro Arg Gly Ala Gly Trp Val Ala Ala Gly Leu Leu Leu | | | | | | | | | | | | | | | |
| 1 5 10 15 | | | | | | | | | | | | | | | |
| ggc gcg ggc gcc tgc tac tgc att tac agg ctg acc cgg ggt cgg cgg | | | | | | | | | | | | | | | 96 |
| Gly Ala Gly Ala Cys Tyr Cys Ile Tyr Arg Leu Thr Arg Gly Arg Arg | | | | | | | | | | | | | | | |
| 20 25 30 | | | | | | | | | | | | | | | |
| cgg ggc gac cgc gag ctc ggg ata cgc tct tcg aag tcc gca gaa gac | | | | | | | | | | | | | | | 144 |
| Arg Gly Asp Arg Glu Leu Gly Ile Arg Ser Ser Lys Ser Ala Glu Asp | | | | | | | | | | | | | | | |
| 35 40 45 | | | | | | | | | | | | | | | |
| tta act gat ggt tca tat gat gat gtt cta aat gct gaa caa ctt cag | | | | | | | | | | | | | | | 192 |
| Leu Thr Asp Gly Ser Tyr Asp Asp Val Leu Asn Ala Glu Gln Leu Gln | | | | | | | | | | | | | | | |
| 50 55 60 | | | | | | | | | | | | | | | |
| aaa ctc ctt tac ctg ctg gag tca acg gag gat cct gta att att gaa | | | | | | | | | | | | | | | 240 |
| Lys Leu Leu Tyr Leu Glu Ser Thr Glu Asp Pro Val Ile Ile Glu | | | | | | | | | | | | | | | |
| 65 70 75 80 | | | | | | | | | | | | | | | |
| aga gct ttg att act ttg ggt aac aat gca gcc ttt tca gtt aac caa | | | | | | | | | | | | | | | 288 |
| Arg Ala Leu Ile Thr Leu Gly Asn Asn Ala Ala Phe Ser Val Asn Gln | | | | | | | | | | | | | | | |
| 85 90 95 | | | | | | | | | | | | | | | |
| gct att att cgt gaa ttg ggt ggt att cca att gtt gca aac aaa atc | | | | | | | | | | | | | | | 336 |
| Ala Ile Ile Arg Glu Leu Gly Gly Ile Pro Ile Val Ala Asn Lys Ile | | | | | | | | | | | | | | | |
| 100 105 110 | | | | | | | | | | | | | | | |

203

| | |
|---|-----|
| aac cat tcc aac cag agt att aaa gag aaa gct tta aat gca cta aat Asn His Ser Asn Gln Ser Ile Lys Glu Lys Ala Leu Asn Ala Leu Asn 115 120 125 | 384 |
| aac ctg agt gtg aat gtt gaa aat caa atc aag ata aag gtg caa gtt Asn Leu Ser Val Asn Val Glu Asn Gln Ile Lys Ile Lys Val Gln Val 130 135 140 | 432 |
| ttg aaa ctg ctt ttg aat ttg tct gaa aat cca gcc atg aca gaa gga Leu Lys Leu Leu Leu Asn Leu Ser Glu Asn Pro Ala Met Thr Glu Gly 145 150 155 160 | 480 |
| ctt ctc cgt gcc caa gtg gat tca tca ttc ctt tcc ctt tat gac agc Leu Leu Arg Ala Gln Val Asp Ser Ser Phe Leu Ser Leu Tyr Asp Ser 165 170 175 | 528 |
| cac gta gca aag gag att ctt ctt cga gta ctt acg cta ttt cag aat His Val Ala Lys Glu Ile Leu Leu Arg Val Leu Thr Leu Phe Gln Asn 180 185 190 | 576 |
| ata aag aac tgc ctc aaa ata gaa ggc cat tta gct gtg cag cct act Ile Lys Asn Cys Leu Lys Ile Glu Gly His Leu Ala Val Gln Pro Thr 195 200 205 | 624 |
| ttc act gaa ggt tca ttg ttt ttc ctg tta cat gga gaa gaa tgt gcc Phe Thr Glu Gly Ser Leu Phe Phe Leu Leu His Gly Glu Glu Cys Ala 210 215 220 | 672 |
| cag aaa ata aga gct tta gtt gat cac cat gat gca gag gtg aag gaa Gln Lys Ile Arg Ala Leu Val Asp His His Asp Ala Glu Val Lys Glu 225 230 235 240 | 720 |
| aag gtt gta aca ata ata ccc aaa atc tga Lys Val Val Thr Ile Ile Pro Lys Ile * | 750 |
| 245 | |

<210> 142

<211> 249

<212> PRT

<213> Homo sapiens

<400> 142

Met Gly Gly Pro Arg Gly Ala Gly Trp Val Ala Ala Gly Leu Leu Leu

204

```

      1             5             10             15
Gly Ala Gly Ala Cys Tyr Cys Ile Tyr Arg Leu Thr Arg Gly Arg Arg
      20             25             30
Arg Gly Asp Arg Glu Leu Gly Ile Arg Ser Ser Lys Ser Ala Glu Asp
      35             40             45
Leu Thr Asp Gly Ser Tyr Asp Asp Val Leu Asn Ala Glu Gln Leu Gln
      50             55             60
Lys Leu Leu Tyr Leu Leu Glu Ser Thr Glu Asp Pro Val Ile Ile Glu
      65             70             75             80
Arg Ala Leu Ile Thr Leu Gly Asn Asn Ala Ala Phe Ser Val Asn Gln
      85             90             95
Ala Ile Ile Arg Glu Leu Gly Gly Ile Pro Ile Val Ala Asn Lys Ile
      100            105            110
Asn His Ser Asn Gln Ser Ile Lys Glu Lys Ala Leu Asn Ala Leu Asn
      115            120            125
Asn Leu Ser Val Asn Val Glu Asn Gln Ile Lys Ile Lys Val Gln Val
      130            135            140
Leu Lys Leu Leu Leu Asn Leu Ser Glu Asn Pro Ala Met Thr Glu Gly
      145            150            155            160
Leu Leu Arg Ala Gln Val Asp Ser Ser Phe Leu Ser Leu Tyr Asp Ser
      165            170            175
His Val Ala Lys Glu Ile Leu Leu Arg Val Leu Thr Leu Phe Gln Asn
      180            185            190
Ile Lys Asn Cys Leu Lys Ile Glu Gly His Leu Ala Val Gln Pro Thr
      195            200            205
Phe Thr Glu Gly Ser Leu Phe Phe Leu Leu His Gly Glu Glu Cys Ala
      210            215            220
Gln Lys Ile Arg Ala Leu Val Asp His His Asp Ala Glu Val Lys Glu
      225            230            235            240
Lys Val Val Thr Ile Ile Pro Lys Ile
      245

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<210> 143
 <211> 846
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(846)

<221> misc_feature
 <222> (1)...(846)
 <223> n = A,T,C or G

205

<400> 143

| | |
|---|-----|
| atg ctg ccc aag tcc cgg cga gcc cta act atc cag gng atc gct gcg | 48 |
| Met Leu Pro Lys Ser Arg Arg Ala Leu Thr Ile Gln Xaa Ile Ala Ala | |
| 1 5 10 15 | |
| ctg gcc agg tcc tcc ctg cat ggt att tcc cag gtg gtg aag gac cac | 96 |
| Leu Ala Arg Ser Ser Leu His Gly Ile Ser Gln Val Val Lys Asp His | |
| 20 25 30 | |
| gtg acc aag cct acc gcc atg gcc cag ggc cga gtg gct cac ctc att | 144 |
| Val Thr Lys Pro Thr Ala Met Ala Gln Gly Arg Val Ala His Leu Ile | |
| 35 40 45 | |
| gag tgg aag ggc tgg agc aag ccg agt gac tca cct gct gcc ctg gaa | 192 |
| Glu Trp Lys Gly Trp Ser Lys Pro Ser Asp Ser Pro Ala Ala Leu Glu | |
| 50 55 60 | |
| tca gcc ttt tcc tcc tat tca gac ctc agc gag ggc gaa caa gag gct | 240 |
| Ser Ala Phe Ser Ser Tyr Ser Asp Leu Ser Glu Gly Glu Gln Glu Ala | |
| 65 70 75 80 | |
| cgc ttt gca gca gga gtg gct gag cag ttt gcc atc gcg gaa gcc aag | 288 |
| Arg Phe Ala Ala Gly Val Ala Glu Gln Phe Ala Ile Ala Glu Ala Lys | |
| 85 90 95 | |
| ctc cga gca tgg tct tcg gtg gat ggc gag gac tcc act gat gac tcc | 336 |
| Leu Arg Ala Trp Ser Ser Val Asp Gly Glu Asp Ser Thr Asp Asp Ser | |
| 100 105 110 | |
| tat gat gag gac ttt gct ggg gga atg gac aca gac atg gct ggg cag | 384 |
| Tyr Asp Glu Asp Phe Ala Gly Gly Met Asp Thr Asp Met Ala Gly Gln | |
| 115 120 125 | |
| ctg ccc ctg ggg ccg cac ctc cag gac ctg ttc acc ggc cac cgg ttc | 432 |
| Leu Pro Leu Gly Pro His Leu Gln Asp Leu Phe Thr Gly His Arg Phe | |
| 130 135 140 | |
| tcc cgg cct gtg cgc cag ggc tcc gtg gag cct gag agc gac tgc tca | 480 |
| Ser Arg Pro Val Arg Gln Gly Ser Val Glu Pro Glu Ser Asp Cys Ser | |
| 145 150 155 160 | |
| cag acc gtg tcc cca gac acc ctg tgc tct agt ctg tgc agc ctg gag | 528 |
| Gln Thr Val Ser Pro Asp Thr Leu Cys Ser Ser Leu Cys Ser Leu Glu | |

206

165

170

175

gat ggg ttg ttg ggc tcc ccg gcc cgg ctg gcc tcc cag ctg ctg ggc 576
 Asp Gly Leu Leu Gly Ser Pro Ala Arg Leu Ala Ser Gln Leu Leu Gly
 180 185 190

gat gag ctg ctt ctc gcc aaa ctg ccc ccc agc cgg gaa agt gcc ttc 624
 Asp Glu Leu Leu Leu Ala Lys Leu Pro Pro Ser Arg Glu Ser Ala Phe
 195 200 205

cgc agc ctg ggc cca ctg gag gcc cag gac tca ctc tac aac tcg ccc 672
 Arg Ser Leu Gly Pro Leu Glu Ala Gln Asp Ser Leu Tyr Asn Ser Pro
 210 215 220

ctc aca gag tcc tgc ctt tcc ccc gcg gag gag gag cca gcc ccc tgc 720
 Leu Thr Glu Ser Cys Leu Ser Pro Ala Glu Glu Glu Pro Ala Pro Cys
 225 230 235 240

aag gac tgc cag cca ctc tgc cca cca cta acg ggc agc tgg gaa cgg 768
 Lys Asp Cys Gln Pro Leu Cys Pro Pro Leu Thr Gly Ser Trp Glu Arg
 245 250 255

cag cgg caa gcc tct gac ctg gcc tct tct ggg gtg gtg tcc tta gat 816
 Gln Arg Gln Ala Ser Asp Leu Ala Ser Ser Gly Val Val Ser Leu Asp
 260 265 270

gag gat gag gca gag cca gag gaa cag tga 846
 Glu Asp Glu Ala Glu Pro Glu Glu Gln *
 275 280

<210> 144
 <211> 281
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(281)
 <223> Xaa = Any Amino Acid

<400> 144
 Met Leu Pro Lys Ser Arg Arg Ala Leu Thr Ile Gln Xaa Ile Ala Ala
 1 5 10 15

207

Leu Ala Arg Ser Ser Leu His Gly Ile Ser Gln Val Val Lys Asp His
 20 25 30
 Val Thr Lys Pro Thr Ala Met Ala Gln Gly Arg Val Ala His Leu Ile
 35 40 45
 Glu Trp Lys Gly Trp Ser Lys Pro Ser Asp Ser Pro Ala Ala Leu Glu
 50 55 60
 Ser Ala Phe Ser Ser Tyr Ser Asp Leu Ser Glu Gly Glu Gln Glu Ala
 65 70 75 80
 Arg Phe Ala Ala Gly Val Ala Glu Gln Phe Ala Ile Ala Glu Ala Lys
 85 90 95
 Leu Arg Ala Trp Ser Ser Val Asp Gly Glu Asp Ser Thr Asp Asp Ser
 100 105 110
 Tyr Asp Glu Asp Phe Ala Gly Gly Met Asp Thr Asp Met Ala Gly Gln
 115 120 125
 Leu Pro Leu Gly Pro His Leu Gln Asp Leu Phe Thr Gly His Arg Phe
 130 135 140
 Ser Arg Pro Val Arg Gln Gly Ser Val Glu Pro Glu Ser Asp Cys Ser
 145 150 155 160
 Gln Thr Val Ser Pro Asp Thr Leu Cys Ser Ser Leu Cys Ser Leu Glu
 165 170 175
 Asp Gly Leu Leu Gly Ser Pro Ala Arg Leu Ala Ser Gln Leu Leu Gly
 180 185 190
 Asp Glu Leu Leu Leu Ala Lys Leu Pro Pro Ser Arg Glu Ser Ala Phe
 195 200 205
 Arg Ser Leu Gly Pro Leu Glu Ala Gln Asp Ser Leu Tyr Asn Ser Pro
 210 215 220
 Leu Thr Glu Ser Cys Leu Ser Pro Ala Glu Glu Glu Pro Ala Pro Cys
 225 230 235 240
 Lys Asp Cys Gln Pro Leu Cys Pro Pro Leu Thr Gly Ser Trp Glu Arg
 245 250 255
 Gln Arg Gln Ala Ser Asp Leu Ala Ser Ser Gly Val Val Ser Leu Asp
 260 265 270
 Glu Asp Glu Ala Glu Pro Glu Glu Gln
 275 280

<210> 145
 <211> 1353
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1353)

208

<400> 145

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| atg | ctg | gtg | act | gcc | tac | ctt | gct | ttt | gta | ggc | ctc | ctg | gcc | tcc | tgc | 48 |
| Met | Leu | Val | Thr | Ala | Tyr | Leu | Ala | Phe | Val | Gly | Leu | Leu | Ala | Ser | Cys | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| ctg | ggg | ctg | gaa | ctg | tca | aga | tgc | cgg | gct | aaa | ccc | cct | gga | agg | gcc | 96 |
| Leu | Gly | Leu | Glu | Leu | Ser | Arg | Cys | Arg | Ala | Lys | Pro | Pro | Gly | Arg | Ala | |
| | | 20 | | | | | | 25 | | | | | | 30 | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| tgc | agc | aat | ccc | tcc | ttc | ctt | cgg | ttt | caa | ctg | gac | ttc | tat | cag | gtc | 144 |
| Cys | Ser | Asn | Pro | Ser | Phe | Leu | Arg | Phe | Gln | Leu | Asp | Phe | Tyr | Gln | Val | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| tac | ttc | ctg | gcc | ctg | gca | gct | gat | tgg | ctt | cag | gcc | ccc | tac | ctc | tat | 192 |
| Tyr | Phe | Leu | Ala | Leu | Ala | Ala | Asp | Trp | Leu | Gln | Ala | Pro | Tyr | Leu | Tyr | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| aaa | ctc | tac | cag | cat | tac | tac | ttc | ctg | gaa | ggc | caa | att | gcc | atc | ctc | 240 |
| Lys | Leu | Tyr | Gln | His | Tyr | Tyr | Phe | Leu | Glu | Gly | Gln | Ile | Ala | Ile | Leu | |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| tat | gtc | tgt | ggc | ctt | gcc | tct | aca | gtc | ctc | ttt | ggc | cta | gtg | gcc | tcc | 288 |
| Tyr | Val | Cys | Gly | Leu | Ala | Ser | Thr | Val | Leu | Phe | Gly | Leu | Val | Ala | Ser | |
| | | | 85 | | | | | 90 | | | | | | 95 | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| tcc | ctt | gtg | gat | tgg | ctg | ggc | cgc | aag | aat | tct | tgt | gtc | ctc | ttc | tcc | 336 |
| Ser | Leu | Val | Asp | Trp | Leu | Gly | Arg | Lys | Asn | Ser | Cys | Val | Leu | Phe | Ser | |
| | | 100 | | | | | 105 | | | | | | 110 | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ctg | act | tac | tca | cta | tgc | tgc | tta | acc | aaa | ctc | tct | caa | gac | tac | ttt | 384 |
| Leu | Thr | Tyr | Ser | Leu | Cys | Cys | Leu | Thr | Lys | Leu | Ser | Gln | Asp | Tyr | Phe | |
| | 115 | | | | | | 120 | | | | | 125 | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gtg | ctg | cta | gtg | ggg | cga | gca | ctt | ggc | ggg | ctg | tcc | aca | gcc | ctg | ctc | 432 |
| Val | Leu | Leu | Val | Gly | Arg | Ala | Leu | Gly | Gly | Leu | Ser | Thr | Ala | Leu | Leu | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ttc | tca | gcc | ttc | gag | gcc | tgg | tat | atc | cat | gag | cac | gtg | gaa | cgg | cat | 480 |
| Phe | Ser | Ala | Phe | Glu | Ala | Trp | Tyr | Ile | His | Glu | His | Val | Glu | Arg | His | |
| 145 | | | | 150 | | | | | | 155 | | | | 160 | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gac | ttc | cct | gct | gag | tgg | atc | cca | gct | acc | ttt | gct | cga | gct | gcc | ttc | 528 |
| Asp | Phe | Pro | Ala | Glu | Trp | Ile | Pro | Ala | Thr | Phe | Ala | Arg | Ala | Ala | Phe | |
| | | | 165 | | | | | 170 | | | | | | 175 | | |

209

| | |
|---|------|
| tgg aac cat gtg ctg gct gta gtg gca ggt gtg gca gct gag gct gta Trp Asn His Val Leu Ala Val Val Ala Gly Val Ala Ala Glu Ala Val 180 185 190 | 576 |
| gcc agc tgg ata ggg ctg ggg cct gta gcg ccc ttt gtg gct gcc atc Ala Ser Trp Ile Gly Leu Gly Pro Val Ala Pro Phe Val Ala Ala Ile 195 200 205 | 624 |
| cct ctc ctg gct ctg gca ggg gcc ttg gcc ctt cga aac tgg ggg gag Pro Leu Leu Ala Leu Ala Gly Ala Leu Ala Leu Arg Asn Trp Gly Glu 210 215 220 | 672 |
| aac tat gac cgg cag cgt gcc ttc tca agg acc tgt gct gga ggc ctg Asn Tyr Asp Arg Gln Arg Ala Phe Ser Arg Thr Cys Ala Gly Gly Leu 225 230 235 240 | 720 |
| cgc tgc ctc ctg tcg gac cgc cgc gtg ctg ctg ttg ggc acc ata caa Arg Cys Leu Leu Ser Asp Arg Arg Val Leu Leu Leu Gly Thr Ile Gln 245 250 255 | 768 |
| gct cta ttt gag agt gtc atc ttc atc ttt gtc ttc ctc tgg aca cct Ala Leu Phe Glu Ser Val Ile Phe Ile Phe Val Phe Leu Trp Thr Pro 260 265 270 | 816 |
| gtg ctg gac cca cac ggg gcc cct ctg ggc att atc ttc tcc agc ttc Val Leu Asp Pro His Gly Ala Pro Leu Gly Ile Ile Phe Ser Ser Phe 275 280 285 | 864 |
| atg gca gcc agc ctg ctt ggc tct tcc ctg tac cgt atc gcc acc tcc Met Ala Ala Ser Leu Leu Gly Ser Ser Leu Tyr Arg Ile Ala Thr Ser 290 295 300 | 912 |
| aag agg tac cac ctt cag ccc atg cac ctg ctg tcc ctt gct gtg ctc Lys Arg Tyr His Leu Gln Pro Met His Leu Leu Ser Leu Ala Val Leu 305 310 315 320 | 960 |
| atc gtc gtc ttc tct ctc ttc atg ttg act ttc tct acc agc cca ggc Ile Val Val Phe Ser Leu Phe Met Leu Thr Phe Ser Thr Ser Pro Gly 325 330 335 | 1008 |
| cag gag agt ccg gtg gag tcc ttc ata gcc ttt cta ctt att gag ttg Gln Glu Ser Pro Val Glu Ser Phe Ile Ala Phe Leu Leu Ile Glu Leu 340 345 350 | 1056 |

210

| | |
|---|------|
| gct tgt gga tta tac ttt ccc agc atg agc ttc cta cgg aga aag gtg | 1104 |
| Ala Cys Gly Leu Tyr Phe Pro Ser Met Ser Phe Leu Arg Arg Lys Val | |
| 355 360 365 | |
| atc cct gag aca gag cag gct ggt gta ctc aac tgg ttc cgg gta cct | 1152 |
| Ile Pro Glu Thr Glu Gln Ala Gly Val Leu Asn Trp Phe Arg Val Pro | |
| 370 375 380 | |
| ctg cac tca ctg gct tgc cta ggg ctc ctt gtc ctc cat gac agt gat | 1200 |
| Leu His Ser Leu Ala Cys Leu Gly Leu Leu Val Leu His Asp Ser Asp | |
| 385 390 395 400 | |
| cga aaa aca ggc act cgg aat atg ttc agc att tgc tct gct gtc atg | 1248 |
| Arg Lys Thr Gly Thr Arg Asn Met Phe Ser Ile Cys Ser Ala Val Met | |
| 405 410 415 | |
| gtg atg gct ctg ctg gca gtg gtg gga ctc ttc acc gtg gta agg cat | 1296 |
| Val Met Ala Leu Leu Ala Val Val Gly Leu Phe Thr Val Val Arg His | |
| 420 425 430 | |
| gat gct gag ctg cgg gta cct tca cct act gag gag ccc tat gcc cct | 1344 |
| Asp Ala Glu Leu Arg Val Pro Ser Pro Thr Glu Glu Pro Tyr Ala Pro | |
| 435 440 445 | |
| gag ctg taa | 1353 |
| Glu Leu * | |
| 450 | |

<210> 146

<211> 450

<212> PRT

<213> Homo sapiens

<400> 146

| |
|---|
| Met Leu Val Thr Ala Tyr Leu Ala Phe Val Gly Leu Leu Ala Ser Cys |
| 1 5 10 15 |
| Leu Gly Leu Glu Leu Ser Arg Cys Arg Ala Lys Pro Pro Gly Arg Ala |
| 20 25 30 |
| Cys Ser Asn Pro Ser Phe Leu Arg Phe Gln Leu Asp Phe Tyr Gln Val |
| 35 40 45 |
| Tyr Phe Leu Ala Leu Ala Ala Asp Trp Leu Gln Ala Pro Tyr Leu Tyr |
| 50 55 60 |

211

Lys Leu Tyr Gln His Tyr Tyr Phe Leu Glu Gly Gln Ile Ala Ile Leu
 65 70 75 80
 Tyr Val Cys Gly Leu Ala Ser Thr Val Leu Phe Gly Leu Val Ala Ser
 85 90 95
 Ser Leu Val Asp Trp Leu Gly Arg Lys Asn Ser Cys Val Leu Phe Ser
 100 105 110
 Leu Thr Tyr Ser Leu Cys Cys Leu Thr Lys Leu Ser Gln Asp Tyr Phe
 115 120 125
 Val Leu Leu Val Gly Arg Ala Leu Gly Gly Leu Ser Thr Ala Leu Leu
 130 135 140
 Phe Ser Ala Phe Glu Ala Trp Tyr Ile His Glu His Val Glu Arg His
 145 150 155 160
 Asp Phe Pro Ala Glu Trp Ile Pro Ala Thr Phe Ala Arg Ala Ala Phe
 165 170 175
 Trp Asn His Val Leu Ala Val Val Ala Gly Val Ala Ala Glu Ala Val
 180 185 190
 Ala Ser Trp Ile Gly Leu Gly Pro Val Ala Pro Phe Val Ala Ala Ile
 195 200 205
 Pro Leu Leu Ala Leu Ala Gly Ala Leu Ala Leu Arg Asn Trp Gly Glu
 210 215 220
 Asn Tyr Asp Arg Gln Arg Ala Phe Ser Arg Thr Cys Ala Gly Gly Leu
 225 230 235 240
 Arg Cys Leu Leu Ser Asp Arg Arg Val Leu Leu Leu Gly Thr Ile Gln
 245 250 255
 Ala Leu Phe Glu Ser Val Ile Phe Ile Phe Val Phe Leu Trp Thr Pro
 260 265 270
 Val Leu Asp Pro His Gly Ala Pro Leu Gly Ile Ile Phe Ser Ser Phe
 275 280 285
 Met Ala Ala Ser Leu Leu Gly Ser Ser Leu Tyr Arg Ile Ala Thr Ser
 290 295 300
 Lys Arg Tyr His Leu Gln Pro Met His Leu Leu Ser Leu Ala Val Leu
 305 310 315 320
 Ile Val Val Phe Ser Leu Phe Met Leu Thr Phe Ser Thr Ser Pro Gly
 325 330 335
 Gln Glu Ser Pro Val Glu Ser Phe Ile Ala Phe Leu Leu Ile Glu Leu
 340 345 350
 Ala Cys Gly Leu Tyr Phe Pro Ser Met Ser Phe Leu Arg Arg Lys Val
 355 360 365
 Ile Pro Glu Thr Glu Gln Ala Gly Val Leu Asn Trp Phe Arg Val Pro
 370 375 380
 Leu His Ser Leu Ala Cys Leu Gly Leu Leu Val Leu His Asp Ser Asp
 385 390 395 400
 Arg Lys Thr Gly Thr Arg Asn Met Phe Ser Ile Cys Ser Ala Val Met
 405 410 415

212

Val Met Ala Leu Leu Ala Val Val Gly Leu Phe Thr Val Val Arg His
 420 425 430
 Asp Ala Glu Leu Arg Val Pro Ser Pro Thr Glu Glu Pro Tyr Ala Pro
 435 440 445
 Glu Leu
 450

<210> 147
 <211> 465
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(465)

<221> misc_feature
 <222> (1)...(465)
 <223> n = A,T,C or G

<400> 147
 atg gcg ggg ccg gtg aag gac cgc gag gcc ttc cag agg ctc aac ttc 48
 Met Ala Gly Pro Val Lys Asp Arg Glu Ala Phe Gln Arg Leu Asn Phe
 1 5 10 15
 ctg tac cag gcc gcc cat tgt gtc ctt gcc cag gac ccc gag aac cag 96
 Leu Tyr Gln Ala Ala His Cys Val Leu Ala Gln Asp Pro Glu Asn Gln
 20 25 30
 gcg ctg gcg agg ttt tac tgc tac act gag agg acc att gcg aag ngg 144
 Ala Leu Ala Arg Phe Tyr Cys Tyr Thr Glu Arg Thr Ile Ala Lys Xaa
 35 40 45
 ctc gtc ttg cgg cgg gat ccc tcg gtg aag agg act ctc tgt cga ggc 192
 Leu Val Leu Arg Arg Asp Pro Ser Val Lys Arg Thr Leu Cys Arg Gly
 50 55 60
 tgc tct tcc ctc ctc gtc ccg ggc ctc acc tgc acc cag cgc cag aga 240
 Cys Ser Ser Leu Leu Val Pro Gly Leu Thr Cys Thr Gln Arg Gln Arg
 65 70 75 80
 cgc tgc agg gga cag cgc tgg acc gta cag acc tgc cta aca tgc cag 288
 Arg Cys Arg Gly Gln Arg Trp Thr Val Gln Thr Cys Leu Thr Cys Gln
 85 90 95

213

cgc agc caa cgc ttc ctc aat gat ccc ggg cat tta ctc tgg gga gac 336
 Arg Ser Gln Arg Phe Leu Asn Asp Pro Gly His Leu Leu Trp Gly Asp
 100 105 110

agg cct gag gcc cag ctc ggg agc caa gca gat tcc aaa cca cta caa 384
 Arg Pro Glu Ala Gln Leu Gly Ser Gln Ala Asp Ser Lys Pro Leu Gln
 115 120 125

ccc ttg cca aac aca gcc cac tcc att tca gac cgc ctt cct gag gag 432
 Pro Leu Pro Asn Thr Ala His Ser Ile Ser Asp Arg Leu Pro Glu Glu
 130 135 140

aaa atg cag act cag ggt tcc agt aac cag tga 465
 Lys Met Gln Thr Gln Gly Ser Ser Asn Gln *
 145 150

<210> 148

<211> 154

<212> PRT

<213> Homo sapiens

<400> 148

Met Ala Gly Pro Val Lys Asp Arg Glu Ala Phe Gln Arg Leu Asn Phe
 1 5 10 15
 Leu Tyr Gln Ala Ala His Cys Val Leu Ala Gln Asp Pro Glu Asn Gln
 20 25 30
 Ala Leu Ala Arg Phe Tyr Cys Tyr Thr Glu Arg Thr Ile Ala Lys Xaa
 35 40 45
 Leu Val Leu Arg Arg Asp Pro Ser Val Lys Arg Thr Leu Cys Arg Gly
 50 55 60
 Cys Ser Ser Leu Leu Val Pro Gly Leu Thr Cys Thr Gln Arg Gln Arg
 65 70 75 80
 Arg Cys Arg Gly Gln Arg Trp Thr Val Gln Thr Cys Leu Thr Cys Gln
 85 90 95
 Arg Ser Gln Arg Phe Leu Asn Asp Pro Gly His Leu Leu Trp Gly Asp
 100 105 110
 Arg Pro Glu Ala Gln Leu Gly Ser Gln Ala Asp Ser Lys Pro Leu Gln
 115 120 125
 Pro Leu Pro Asn Thr Ala His Ser Ile Ser Asp Arg Leu Pro Glu Glu
 130 135 140
 Lys Met Gln Thr Gln Gly Ser Ser Asn Gln
 145 150

214

<210> 149
 <211> 390
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(390)

<400> 149

| | |
|---|-----|
| atg atc ccc ctc ctc aga gag agc tta cac ccc atg ctg ctc tcc atc | 48 |
| Met Ile Pro Leu Leu Arg Glu Ser Leu His Pro Met Leu Leu Ser Ile | |
| 1 5 10 15 | |
| atc atc act gtt gca gac aac ctc aac tcc aag aac tca ggg att tac | 96 |
| Ile Ile Thr Val Ala Asp Asn Leu Asn Ser Lys Asn Ser Gly Ile Tyr | |
| 20 25 30 | |
| gct gct gcc gtg gca gtg ctg gtg gcc tca gtt tac ccc cgg aag cct | 144 |
| Ala Ala Ala Val Ala Val Leu Val Ala Ser Val Tyr Pro Arg Lys Pro | |
| 35 40 45 | |
| caa gct gta gag cgg cat gtc ctt ccc atc ctc tgg cac ttc ctg aac | 192 |
| Gln Ala Val Glu Arg His Val Leu Pro Ile Leu Trp His Phe Leu Asn | |
| 50 55 60 | |
| acc gcc acc agg aat ggc acc ctg cct gga ccc agc ggg aac atc cgc | 240 |
| Thr Ala Thr Arg Asn Gly Thr Leu Pro Gly Pro Ser Gly Asn Ile Arg | |
| 65 70 75 80 | |
| ggg gtg gtg tgc cgg ctg tcc agg agc ctc cag gag cac cat ggg ctc | 288 |
| Gly Val Val Cys Arg Leu Ser Arg Ser Leu Gln Glu His His Gly Leu | |
| 85 90 95 | |
| ccg cct gct gga ctt tgc cgc cag cca gcc aaa gca cgt cct caa gac | 336 |
| Pro Pro Ala Gly Leu Cys Arg Gln Pro Ala Lys Ala Arg Pro Gln Asp | |
| 100 105 110 | |
| gct cca gga act ctt aga ctc aga gtc ctt ggg agg cag ccg caa ggc | 384 |
| Ala Pro Gly Thr Leu Arg Leu Arg Val Leu Gly Arg Gln Pro Gln Gly | |
| 115 120 125 | |
| cac tga | 390 |

215

His *

<210> 150
 <211> 129
 <212> PRT
 <213> Homo sapiens

<400> 150
 Met Ile Pro Leu Leu Arg Glu Ser Leu His Pro Met Leu Leu Ser Ile
 1 5 10 15
 Ile Ile Thr Val Ala Asp Asn Leu Asn Ser Lys Asn Ser Gly Ile Tyr
 20 25 30
 Ala Ala Ala Val Ala Val Leu Val Ala Ser Val Tyr Pro Arg Lys Pro
 35 40 45
 Gln Ala Val Glu Arg His Val Leu Pro Ile Leu Trp His Phe Leu Asn
 50 55 60
 Thr Ala Thr Arg Asn Gly Thr Leu Pro Gly Pro Ser Gly Asn Ile Arg
 65 70 75 80
 Gly Val Val Cys Arg Leu Ser Arg Ser Leu Gln Glu His His Gly Leu
 85 90 95
 Pro Pro Ala Gly Leu Cys Arg Gln Pro Ala Lys Ala Arg Pro Gln Asp
 100 105 110
 Ala Pro Gly Thr Leu Arg Leu Arg Val Leu Gly Arg Gln Pro Gln Gly
 115 120 125
 His

<210> 151
 <211> 567
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(567)

<400> 151
 atg gtc cct gcc cct cag cat gtc act gag cta gag ctg ggc atg tac 48
 Met Val Pro Ala Pro Gln His Val Thr Glu Leu Glu Leu Gly Met Tyr
 1 5 10 15
 gcc ctg ctg gga gtc ttc tgc gtg gcc atc ttc atc ttc ttg gtc aat 96

216

| | |
|---|-----|
| Ala Leu Leu Gly Val Phe Cys Val Ala Ile Phe Ile Phe Leu Val Asn | |
| 20 25 30 | |
| ggt gtg gtc ttc gtc ctg cgc tat cag cgc aaa gaa cct ccc gac agt | 144 |
| Gly Val Val Phe Val Leu Arg Tyr Gln Arg Lys Glu Pro Pro Asp Ser | |
| 35 40 45 | |
| gcc act gac ccc acc tcc ccc cag ccc cac aac tgg gtc tgg ctg ggc | 192 |
| Ala Thr Asp Pro Thr Ser Pro Gln Pro His Asn Trp Val Trp Leu Gly | |
| 50 55 60 | |
| act gac cag gag gaa ctg agc cgc cag ctg gac cgg cag tcc cct ggc | 240 |
| Thr Asp Gln Glu Glu Leu Ser Arg Gln Leu Asp Arg Gln Ser Pro Gly | |
| 65 70 75 80 | |
| ccg ccc aag ggg gag ggg agc tgc ccc tgt gag agt ggg gga gga ggg | 288 |
| Pro Pro Lys Gly Glu Gly Ser Cys Pro Cys Glu Ser Gly Gly Gly Gly | |
| 85 90 95 | |
| gag gcc cct acc ctg gcc cct ggc cct cct ggg ggc acc acc agc tcc | 336 |
| Glu Ala Pro Thr Leu Ala Pro Gly Pro Pro Gly Gly Thr Thr Ser Ser | |
| 100 105 110 | |
| tca agc acc ctg gcc cga aag gag gct ggg ggg cgg cgg aag cga gta | 384 |
| Ser Ser Thr Leu Ala Arg Lys Glu Ala Gly Gly Arg Arg Lys Arg Val | |
| 115 120 125 | |
| gag ttt gtg aca ttt gcg cca gcc cct cca gcc cag tca cct gag gag | 432 |
| Glu Phe Val Thr Phe Ala Pro Ala Pro Pro Ala Gln Ser Pro Glu Glu | |
| 130 135 140 | |
| cct gta ggg gcc cct gct gtg cag tcc atc ctt gtg gca ggc gag gag | 480 |
| Pro Val Gly Ala Pro Ala Val Gln Ser Ile Leu Val Ala Gly Glu Glu | |
| 145 150 155 160 | |
| gac atc cgc tgg gtg tgt gag gac atg ggg ctg aag gac cct gag gag | 528 |
| Asp Ile Arg Trp Val Cys Glu Asp Met Gly Leu Lys Asp Pro Glu Glu | |
| 165 170 175 | |
| ctt cgc aac tac atg gag agg atc cgg ggc agc tcc tga | 567 |
| Leu Arg Asn Tyr Met Glu Arg Ile Arg Gly Ser Ser * | |
| 180 185 | |

217

<210> 152
 <211> 188
 <212> PRT
 <213> Homo sapiens

<400> 152

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Met Val Pro Ala Pro Gln His Val Thr Glu Leu Glu Leu Gly Met Tyr
 1           5           10           15
Ala Leu Leu Gly Val Phe Cys Val Ala Ile Phe Ile Phe Leu Val Asn
          20           25           30
Gly Val Val Phe Val Leu Arg Tyr Gln Arg Lys Glu Pro Pro Asp Ser
          35           40           45
Ala Thr Asp Pro Thr Ser Pro Gln Pro His Asn Trp Val Trp Leu Gly
          50           55           60
Thr Asp Gln Glu Glu Leu Ser Arg Gln Leu Asp Arg Gln Ser Pro Gly
          65           70           75           80
Pro Pro Lys Gly Glu Gly Ser Cys Pro Cys Glu Ser Gly Gly Gly Gly
          85           90           95
Glu Ala Pro Thr Leu Ala Pro Gly Pro Pro Gly Gly Thr Thr Ser Ser
          100          105          110
Ser Ser Thr Leu Ala Arg Lys Glu Ala Gly Gly Arg Arg Lys Arg Val
          115          120          125
Glu Phe Val Thr Phe Ala Pro Ala Pro Pro Ala Gln Ser Pro Glu Glu
          130          135          140
Pro Val Gly Ala Pro Ala Val Gln Ser Ile Leu Val Ala Gly Glu Glu
          145          150          155          160
Asp Ile Arg Trp Val Cys Glu Asp Met Gly Leu Lys Asp Pro Glu Glu
          165          170          175
Leu Arg Asn Tyr Met Glu Arg Ile Arg Gly Ser Ser
          180          185

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<210> 153
 <211> 735
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(735)

<400> 153

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atg gct acg gga acg cgc tat gcc ggg aag gtg gtg gtc gtg acc ggg
Met Ala Thr Gly Thr Arg Tyr Ala Gly Lys Val Val Val Val Thr Gly
 1           5           10           15

```

48

218

| | |
|---|-----|
| ggc ggg cgc ggc atc gga gct ggg atc gtg cgc gcc ttc gtg aac agc Gly Gly Arg Gly Ile Gly Ala Gly Ile Val Arg Ala Phe Val Asn Ser 20 25 30 | 96 |
| ggg gcc cga gtg gtt atc tgc gac aag gat gag tct ggg ggc cgg gcc Gly Ala Arg Val Val Ile Cys Asp Lys Asp Glu Ser Gly Gly Arg Ala 35 40 45 | 144 |
| ctg gag cag gag ctc cct gga gct gtc ttt atc ctc tgt gat gtg act Leu Glu Gln Glu Leu Pro Gly Ala Val Phe Ile Leu Cys Asp Val Thr 50 55 60 | 192 |
| cag gaa gat gat gtg aag acc ctg gtt tct gag acc atc cgc cga ttt Gln Glu Asp Asp Val Lys Thr Leu Val Ser Glu Thr Ile Arg Arg Phe 65 70 75 80 | 240 |
| ggc cgc ctg gat tgt gtt gtc aac aac gct ggc cac cac cca ccc cca Gly Arg Leu Asp Cys Val Val Asn Asn Ala Gly His His Pro Pro Pro 85 90 95 | 288 |
| cag agg cct gag gag acc tct gcc cag gga ttc cgc cag ctg ctg gag Gln Arg Pro Glu Glu Thr Ser Ala Gln Gly Phe Arg Gln Leu Leu Glu 100 105 110 | 336 |
| ctg aac cta ctg ggg acg tac acc ttg acc aag ctc gcc ctc ccc tac Leu Asn Leu Leu Gly Thr Tyr Thr Leu Thr Lys Leu Ala Leu Pro Tyr 115 120 125 | 384 |
| ctg cgg aag agt caa ggg aat gtc atc aac atc tcc agc ctg gtg ggg Leu Arg Lys Ser Gln Gly Asn Val Ile Asn Ile Ser Ser Leu Val Gly 130 135 140 | 432 |
| gca atc ggc cag gcc cag gca gtt ccc tat gtg gcc acc aag ggg gca Ala Ile Gly Gln Ala Gln Ala Val Pro Tyr Val Ala Thr Lys Gly Ala 145 150 155 160 | 480 |
| gta aca gcc atg acc aaa gct ttg gcc ctg gat gaa agt cca tat ggt Val Thr Ala Met Thr Lys Ala Leu Ala Leu Asp Glu Ser Pro Tyr Gly 165 170 175 | 528 |
| gtc cga gtc aac tgt atc tcc cca gga aac atc tgg acc ccg ctg tgg Val Arg Val Asn Cys Ile Ser Pro Gly Asn Ile Trp Thr Pro Leu Trp 180 185 190 | 576 |

219

gag gag ctg gca gcc tta atg cca gac cct agg gcc aca atc cga gag 624
 Glu Glu Leu Ala Ala Leu Met Pro Asp Pro Arg Ala Thr Ile Arg Glu
 195 200 205

ggc atg ctg ccc agc cac tgg gcc gca tgg gcc agc ccg ctg agg tcg 672
 Gly Met Leu Pro Ser His Trp Ala Ala Trp Ala Ser Pro Leu Arg Ser
 210 215 220

ggg ctg cgg cag tgt tcc tgg cct ccg aag cca act tct gca cgg gca 720
 Gly Leu Arg Gln Cys Ser Trp Pro Pro Lys Pro Thr Ser Ala Arg Ala
 225 230 235 240

ttg aac tgc tcg tga 735
 Leu Asn Cys Ser *

<210> 154
 <211> 244
 <212> PRT
 <213> Homo sapiens

<400> 154
 Met Ala Thr Gly Thr Arg Tyr Ala Gly Lys Val Val Val Val Thr Gly
 1 5 10 15
 Gly Gly Arg Gly Ile Gly Ala Gly Ile Val Arg Ala Phe Val Asn Ser
 20 25 30
 Gly Ala Arg Val Val Ile Cys Asp Lys Asp Glu Ser Gly Gly Arg Ala
 35 40 45
 Leu Glu Gln Glu Leu Pro Gly Ala Val Phe Ile Leu Cys Asp Val Thr
 50 55 60
 Gln Glu Asp Asp Val Lys Thr Leu Val Ser Glu Thr Ile Arg Arg Phe
 65 70 75 80
 Gly Arg Leu Asp Cys Val Val Asn Asn Ala Gly His His Pro Pro Pro
 85 90 95
 Gln Arg Pro Glu Glu Thr Ser Ala Gln Gly Phe Arg Gln Leu Leu Glu
 100 105 110
 Leu Asn Leu Leu Gly Thr Tyr Thr Leu Thr Lys Leu Ala Leu Pro Tyr
 115 120 125
 Leu Arg Lys Ser Gln Gly Asn Val Ile Asn Ile Ser Ser Leu Val Gly
 130 135 140
 Ala Ile Gly Gln Ala Gln Ala Val Pro Tyr Val Ala Thr Lys Gly Ala
 145 150 155 160

220

Val Thr Ala Met Thr Lys Ala Leu Ala Leu Asp Glu Ser Pro Tyr Gly
 165 170 175
 Val Arg Val Asn Cys Ile Ser Pro Gly Asn Ile Trp Thr Pro Leu Trp
 180 185 190
 Glu Glu Leu Ala Ala Leu Met Pro Asp Pro Arg Ala Thr Ile Arg Glu
 195 200 205
 Gly Met Leu Pro Ser His Trp Ala Ala Trp Ala Ser Pro Leu Arg Ser
 210 215 220
 Gly Leu Arg Gln Cys Ser Trp Pro Pro Lys Pro Thr Ser Ala Arg Ala
 225 230 235 240
 Leu Asn Cys Ser

<210> 155

<211> 975

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(975)

<221> misc_feature

<222> (1)...(975)

<223> n = A,T,C or G

<400> 155

atg atg ctg gca cag ggc ctt ctg ctg cat tnc ntn ccn nna gac tgg 48
 Met Met Leu Ala Gln Gly Leu Leu Leu His Xaa Xaa Xaa Xaa Asp Trp
 1 5 10 15

aca tgg gcc gag ggc atg ggc ctg ggc ccc cct gag ctg tca ggg tca 96
 Thr Trp Ala Glu Gly Met Gly Leu Gly Pro Pro Glu Leu Ser Gly Ser
 20 25 30

gcc tct ccc agc cgg tac cat ggg cct gcc cgc tgg atg ccc cca cgc 144
 Ala Ser Pro Ser Arg Tyr His Gly Pro Ala Arg Trp Met Pro Pro Arg
 35 40 45

tgg gcc cag ggt gcc cct gag ctg gag cag gaa cgc cgg cac cgg cag 192
 Trp Ala Gln Gly Ala Pro Glu Leu Glu Gln Glu Arg Arg His Arg Gln
 50 55 60

att gtg tcc tgg ttc gcc gac cac ccc cgg gcc ccc ttt ggc cta cac 240

| | | | | |
|---|---|-----|-----|-----|
| Ile Val Ser Trp Phe | Ala Asp His Pro Arg Ala Pro Phe Gly Leu His | | | |
| 65 | 70 | 75 | 80 | |
| cgg ctg gtg gag ctt ggg cag agc tca ggc aag aag gca ggt gac tgg | | | 288 | |
| Arg Leu Val Glu Leu Gly Gln Ser Ser Gly Lys Lys Ala Gly Asp Trp | | | | |
| | 85 | 90 | 95 | |
| tat ggg cca tcg cta gtg gca cac atc ctc agg aaa gcc gtg gag agc | | | 336 | |
| Tyr Gly Pro Ser Leu Val Ala His Ile Leu Arg Lys Ala Val Glu Ser | | | | |
| | 100 | 105 | 110 | |
| tgc tcc gac gtc acc cgc ctg gtg gtg tac gtt tct cag gac tgc aca | | | 384 | |
| Cys Ser Asp Val Thr Arg Leu Val Val Tyr Val Ser Gln Asp Cys Thr | | | | |
| | 115 | 120 | 125 | |
| gtg tac aag gcg gat gtg gca cgc ctg gtg gcc agg cca gac ccc aca | | | 432 | |
| Val Tyr Lys Ala Asp Val Ala Arg Leu Val Ala Arg Pro Asp Pro Thr | | | | |
| | 130 | 135 | 140 | |
| gcc gag tgg aag tct gtg gtc atc ctg gtg ccc gtg cga ctg ggt ggc | | | 480 | |
| Ala Glu Trp Lys Ser Val Val Ile Leu Val Pro Val Arg Leu Gly Gly | | | | |
| | 145 | 150 | 155 | 160 |
| gag act ctc aac ccc gtg tat gtg ccc tgc gtg aag gaa ctc ctg cgt | | | 528 | |
| Glu Thr Leu Asn Pro Val Tyr Val Pro Cys Val Lys Glu Leu Leu Arg | | | | |
| | 165 | 170 | 175 | |
| tgc gag ctg tgc ctg ggc atc atg ggt ggg aaa ccg cga cac tca ctg | | | 576 | |
| Cys Glu Leu Cys Leu Gly Ile Met Gly Gly Lys Pro Arg His Ser Leu | | | | |
| | 180 | 185 | 190 | |
| tac ttc att ggc tac caa gat gac ttc ctg ctg tac ctg gac cct cac | | | 624 | |
| Tyr Phe Ile Gly Tyr Gln Asp Asp Phe Leu Leu Tyr Leu Asp Pro His | | | | |
| | 195 | 200 | 205 | |
| tac tgc cag ccc act gtg gat gtc agc cag gcc gac ttc ccc ctg gag | | | 672 | |
| Tyr Cys Gln Pro Thr Val Asp Val Ser Gln Ala Asp Phe Pro Leu Glu | | | | |
| | 210 | 215 | 220 | |
| tcc ttc cac tgc acc tcg ccc cgc aag atg gcc ttt gcc aag atg gac | | | 720 | |
| Ser Phe His Cys Thr Ser Pro Arg Lys Met Ala Phe Ala Lys Met Asp | | | | |
| | 225 | 230 | 235 | 240 |
| cca agc tgt acc gtg ggc ttc tat gct gga gac agg aag gag ttt gac | | | 768 | |

222

Pro Ser Cys Thr Val Gly Phe Tyr Ala Gly Asp Arg Lys Glu Phe Glu
 245 250 255

aca ctc tgc tca gag ctg acc agg gtc ctc agc tcc tcc tca gcc aca 816
 Thr Leu Cys Ser Glu Leu Thr Arg Val Leu Ser Ser Ser Ala Thr
 260 265 270

gag cgg tac ccc atg ttc acc ctg gcc gag ggc cat gct cag gac cac 864
 Glu Arg Tyr Pro Met Phe Thr Leu Ala Glu Gly His Ala Gln Asp His
 275 280 285

agc ctg gac gac ctc tgc tcc cag ctc gcc cag ccc aca ctc cgg ctc 912
 Ser Leu Asp Asp Leu Cys Ser Gln Leu Ala Gln Pro Thr Leu Arg Leu
 290 295 300

cct cgc aca ggg cgg ctc ctc agg gcc aaa cgc ccc agc tct gag gac 960
 Pro Arg Thr Gly Arg Leu Leu Arg Ala Lys Arg Pro Ser Ser Glu Asp
 305 310 315 320

ttt gtg ttt tta taa 975
 Phe Val Phe Leu *

<210> 156
 <211> 324
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(324)
 <223> Xaa = Any Amino Acid

<400> 156

Met Met Leu Ala Gln Gly Leu Leu Leu His Xaa Xaa Xaa Xaa Asp Trp
 1 5 10 15

Thr Trp Ala Glu Gly Met Gly Leu Gly Pro Pro Glu Leu Ser Gly Ser
 20 25 30

Ala Ser Pro Ser Arg Tyr His Gly Pro Ala Arg Trp Met Pro Pro Arg
 35 40 45

Trp Ala Gln Gly Ala Pro Glu Leu Gly Gln Glu Arg Arg His Arg Gln
 50 55 60

Ile Val Ser Trp Phe Ala Asp His Pro Arg Ala Pro Phe Gly Leu His

223

65 70 75 80
 Arg Leu Val Glu Leu Gly Gln Ser Ser Gly Lys Lys Ala Gly Asp Trp
 85 90 95
 Tyr Gly Pro Ser Leu Val Ala His Ile Leu Arg Lys Ala Val Glu Ser
 100 105 110
 Cys Ser Asp Val Thr Arg Leu Val Val Tyr Val Ser Gln Asp Cys Thr
 115 120 125
 Val Tyr Lys Ala Asp Val Ala Arg Leu Val Ala Arg Pro Asp Pro Thr
 130 135 140
 Ala Glu Trp Lys Ser Val Val Ile Leu Val Pro Val Arg Leu Gly Gly
 145 150 155 160
 Glu Thr Leu Asn Pro Val Tyr Val Pro Cys Val Lys Glu Leu Leu Arg
 165 170 175
 Cys Glu Leu Cys Leu Gly Ile Met Gly Gly Lys Pro Arg His Ser Leu
 180 185 190
 Tyr Phe Ile Gly Tyr Gln Asp Asp Phe Leu Leu Tyr Leu Asp Pro His
 195 200 205
 Tyr Cys Gln Pro Thr Val Asp Val Ser Gln Ala Asp Phe Pro Leu Glu
 210 215 220
 Ser Phe His Cys Thr Ser Pro Arg Lys Met Ala Phe Ala Lys Met Asp
 225 230 235 240
 Pro Ser Cys Thr Val Gly Phe Tyr Ala Gly Asp Arg Lys Glu Phe Glu
 245 250 255
 Thr Leu Cys Ser Glu Leu Thr Arg Val Leu Ser Ser Ser Ser Ala Thr
 260 265 270
 Glu Arg Tyr Pro Met Phe Thr Leu Ala Glu Gly His Ala Gln Asp His
 275 280 285
 Ser Leu Asp Asp Leu Cys Ser Gln Leu Ala Gln Pro Thr Leu Arg Leu
 290 295 300
 Pro Arg Thr Gly Arg Leu Leu Arg Ala Lys Arg Pro Ser Ser Glu Asp
 305 310 315 320
 Phe Val Phe Leu

<210> 157

<211> 669

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(669)

<400> 157

| | |
|---|-----|
| atg atc ctt gta gga ctc tgg tta att cag tgg ctg ctc tta aaa tac | 48 |
| Met Ile Leu Val Gly Leu Trp Leu Ile Gln Trp Leu Leu Leu Lys Tyr | |
| 1 5 10 15 | |
| aag tct att att agc aga aga ttt ttc tgc ata gtt ggc acg ctg tac | 96 |
| Lys Ser Ile Ile Ser Arg Arg Phe Phe Cys Ile Val Gly Thr Leu Tyr | |
| 20 25 30 | |
| ctg tat cgg tgt att aca atg tat gta act aca ctc cca gta cct ggt | 144 |
| Leu Tyr Arg Cys Ile Thr Met Tyr Val Thr Thr Leu Pro Val Pro Gly | |
| 35 40 45 | |
| atg cat ttc aac tgt tct ccg aag ctt ttc gga gac tgg gaa gcc caa | 192 |
| Met His Phe Asn Cys Ser Pro Lys Leu Phe Gly Asp Trp Glu Ala Gln | |
| 50 55 60 | |
| ctg cga aga ata atg aag ctc att gct gga ggt ggc ttg tct atc act | 240 |
| Leu Arg Arg Ile Met Lys Leu Ile Ala Gly Gly Gly Leu Ser Ile Thr | |
| 65 70 75 80 | |
| ggc tct cac aac atg tgt ggg gac tat ctg tac agc ggc cac acg gtc | 288 |
| Gly Ser His Asn Met Cys Gly Asp Tyr Leu Tyr Ser Gly His Thr Val | |
| 85 90 95 | |
| atg cta aca ctt acc tac tta ttt atc aaa gag tat tcc cct cgg cga | 336 |
| Met Leu Thr Leu Thr Tyr Leu Phe Ile Lys Glu Tyr Ser Pro Arg Arg | |
| 100 105 110 | |
| ctc tgg tgg tat cac tgg att tgc tgg ctt ctc agc gta gtt gga atc | 384 |
| Leu Trp Trp Tyr His Trp Ile Cys Trp Leu Leu Ser Val Val Gly Ile | |
| 115 120 125 | |
| ttc tgt att ctc tta gcg cat gac cac tac act gtg gac gtg gtg gtg | 432 |
| Phe Cys Ile Leu Leu Ala His Asp His Tyr Thr Val Asp Val Val Val | |
| 130 135 140 | |
| gca tat tac atc acc acg aga ctc ttc tgg tgg tat cac act atg gcc | 480 |
| Ala Tyr Tyr Ile Thr Thr Arg Leu Phe Trp Trp Tyr His Thr Met Ala | |
| 145 150 155 160 | |
| aat cag caa gtg cta aag gaa gct tcc cag atg aac ctc ctg gcc agg | 528 |
| Asn Gln Gln Val Leu Lys Glu Ala Ser Gln Met Asn Leu Leu Ala Arg | |
| 165 170 175 | |

225

gtg tgg tgg tac agg cca ttt cag tac ttt gaa aag aat gtc caa gga 576
 Val Trp Trp Tyr Arg Pro Phe Gln Tyr Phe Glu Lys Asn Val Gln Gly
 180 185 190

att gta cct cga tct tac cat tgg cct ttc ccc tgg cca gta gtc cac 624
 Ile Val Pro Arg Ser Tyr His Trp Pro Phe Pro Trp Pro Val Val His
 195 200 205

ctc agt agg caa gtt aaa tac agc cgg ctg gtg aat gac aca taa 669
 Leu Ser Arg Gln Val Lys Tyr Ser Arg Leu Val Asn Asp Thr *
 210 215 220

<210> 158

<211> 222

<212> PRT

<213> Homo sapiens

<400> 158

Met Ile Leu Val Gly Leu Trp Leu Ile Gln Trp Leu Leu Leu Lys Tyr
 1 5 10 15
 Lys Ser Ile Ile Ser Arg Arg Phe Phe Cys Ile Val Gly Thr Leu Tyr
 20 25 30
 Leu Tyr Arg Cys Ile Thr Met Tyr Val Thr Thr Leu Pro Val Pro Gly
 35 40 45
 Met His Phe Asn Cys Ser Pro Lys Leu Phe Gly Asp Trp Glu Ala Gln
 50 55 60
 Leu Arg Arg Ile Met Lys Leu Ile Ala Gly Gly Gly Leu Ser Ile Thr
 65 70 75 80
 Gly Ser His Asn Met Cys Gly Asp Tyr Leu Tyr Ser Gly His Thr Val
 85 90 95
 Met Leu Thr Leu Thr Tyr Leu Phe Ile Lys Glu Tyr Ser Pro Arg Arg
 100 105 110
 Leu Trp Trp Tyr His Trp Ile Cys Trp Leu Leu Ser Val Val Gly Ile
 115 120 125
 Phe Cys Ile Leu Leu Ala His Asp His Tyr Thr Val Asp Val Val Val
 130 135 140
 Ala Tyr Tyr Ile Thr Thr Arg Leu Phe Trp Trp Tyr His Thr Met Ala
 145 150 155 160
 Asn Gln Gln Val Leu Lys Glu Ala Ser Gln Met Asn Leu Leu Ala Arg
 165 170 175
 Val Trp Trp Tyr Arg Pro Phe Gln Tyr Phe Glu Lys Asn Val Gln Gly
 180 185 190
 Ile Val Pro Arg Ser Tyr His Trp Pro Phe Pro Trp Pro Val Val His

226

195 200 205
 Leu Ser Arg Gln Val Lys Tyr Ser Arg Leu Val Asn Asp Thr
 210 215 220

<210> 159

<211> 540

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(540)

<221> misc_feature

<222> (1)...(540)

<223> n = A,T,C or G

<400> 159

atg gcc gct ccc cgc ngc agg gcc gcg ccc tgg acg acg gcc ctg ctg 48
 Met Ala Ala Pro Arg Xaa Arg Ala Ala Pro Trp Thr Thr Ala Leu Leu
 1 5 10 15

ctg ctc cta gcc tcg cag gtc ctg tct ccg gga agc tgc gcg gac gag 96
 Leu Leu Leu Ala Ser Gln Val Leu Ser Pro Gly Ser Cys Ala Asp Glu
 20 25 30

gag gag gtc ccc gag gag tgg gtg ctc ctg cac gtc gtc cag gcc cag 144
 Glu Glu Val Pro Glu Glu Trp Val Leu Leu His Val Val Gln Gly Gln
 35 40 45

ata ggc gcc ggg aac tac agc tac ctg cgg ctg aac cac gag gcc aag 192
 Ile Gly Ala Gly Asn Tyr Ser Tyr Leu Arg Leu Asn His Glu Gly Lys
 50 55 60

ata gtc ctc agg atg cgc acc tnc aag gga gat gcg gat ctg tac gtc 240
 Ile Val Leu Arg Met Arg Thr Xaa Lys Gly Asp Ala Asp Leu Tyr Val
 65 70 75 80

tcc gcc agc agc ctg cac ccc agc ttc gac gac tac gag ctg caa tcg 288
 Ser Ala Ser Ser Leu His Pro Ser Phe Asp Asp Tyr Glu Leu Gln Ser
 85 90 95

gcc acc tgn cgg ccc gga cgc cgt gtc cat ccc cgc gca ctt ccg gcg 336
 Ala Thr Xaa Arg Pro Gly Arg Arg Val His Pro Arg Ala Leu Pro Ala

227

| 100 | 105 | 110 | |
|---|-----|-----|-----|
| ccc agt ggg cat cgg cgt cta tgg aca ccc ctc cca cct gga gag cga | | | 384 |
| Pro Ser Gly His Arg Arg Leu Trp Thr Pro Leu Pro Pro Gly Glu Arg | | | |
| 115 | 120 | 125 | |
| ggt cga gat gaa ggt gta cta cga cgg cac ggt ncg agc agc acc cgt | | | 432 |
| Val Arg Asp Glu Gly Val Leu Arg Arg His Gly Xaa Ser Ser Thr Arg | | | |
| 130 | 135 | 140 | |
| tcg gcg agg ccg cct acc ccg ccg acg gcg cag atg ccg gcc aga agc | | | 480 |
| Ser Ala Arg Pro Pro Thr Pro Pro Thr Ala Gln Met Pro Ala Arg Ser | | | |
| 145 | 150 | 155 | 160 |
| acg ctg gtg ccc cgg aag acg cct cgc aag agg agg aat ctg ttc tct | | | 528 |
| Thr Leu Val Pro Arg Lys Thr Pro Arg Lys Arg Arg Asn Leu Phe Ser | | | |
| 165 | 170 | 175 | |
| gga cga tat taa | | | 540 |
| Gly Arg Tyr * | | | |

<210> 160
 <211> 179
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(179)
 <223> Xaa = Any Amino Acid

<400> 160

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Pro | Arg | Xaa | Arg | Ala | Ala | Pro | Trp | Thr | Thr | Ala | Leu | Leu |
| 1 | | | 5 | | | | | | 10 | | | | | 15 | |
| Leu | Leu | Leu | Ala | Ser | Gln | Val | Leu | Ser | Pro | Gly | Ser | Cys | Ala | Asp | Glu |
| | | | 20 | | | | | | 25 | | | | 30 | | |
| Glu | Glu | Val | Pro | Glu | Glu | Trp | Val | Leu | Leu | His | Val | Val | Gln | Gly | Gln |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ile | Gly | Ala | Gly | Asn | Tyr | Ser | Tyr | Leu | Arg | Leu | Asn | His | Glu | Gly | Lys |
| | 50 | | | 55 | | | | | | 60 | | | | | |
| Ile | Val | Leu | Arg | Met | Arg | Thr | Xaa | Lys | Gly | Asp | Ala | Asp | Leu | Tyr | Val |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | |

Ser Ala Ser Ser Leu His Pro Ser Phe Asp Asp Tyr Glu Leu Gln Ser
85 90 95
Ala Thr Xaa Arg Pro Gly Arg Arg Val His Pro Arg Ala Leu Pro Ala
100 105 110
Pro Ser Gly His Arg Arg Leu Trp Thr Pro Leu Pro Pro Gly Glu Arg
115 120 125
Val Arg Asp Glu Gly Val Leu Arg Arg His Gly Xaa Ser Ser Thr Arg
130 135 140
Ser Ala Arg Pro Pro Thr Pro Pro Thr Ala Gln Met Pro Ala Arg Ser
145 150 155 160
Thr Leu Val Pro Arg Lys Thr Pro Arg Lys Arg Arg Asn Leu Phe Ser
165 170 175
Gly Arg Tyr

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<220>
<221> CDS
<222> (1)...(1290)
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| | | | | | | | | | | | | | | | | | |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| <400> 161 | | | | | | | | | | | | | | | | | |
| atg | act | gct | gct | ctg | gcc | gtc | gtc | acg | acg | tcg | ggt | ttg | gaa | gat | ggg | 48 | |
| Met | Thr | Ala | Ala | Leu | Ala | Val | Val | Thr | Thr | Ser | Gly | Leu | Glu | Asp | Gly | | |
| | | | | 5 | | | | | 10 | | | | | | | 15 | |
| | | | | | | | | | | | | | | | | | |
| gtg | cct | agg | tcc | cgt | ggc | gaa | ggg | acc | ggg | gaa | gtg | gtc | ttg | gag | cgg | 96 | |
| Val | Pro | Arg | Ser | Arg | Gly | Glu | Gly | Thr | Gly | Glu | Val | Val | Leu | Glu | Arg | | |
| | | | | 20 | | | | | 25 | | | | | | | 30 | |
| | | | | | | | | | | | | | | | | | |
| ggg | ccc | ggc | gcg | gcc | tac | cac | atg | ttc | gtg | gtg | atg | gag | gac | ttg | gtg | 144 | |
| Gly | Pro | Gly | Ala | Ala | Tyr | His | Met | Phe | Val | Val | Met | Glu | Asp | Leu | Val | | |
| | | | | 35 | | | | | 40 | | | | | | | 45 | |
| | | | | | | | | | | | | | | | | | |
| gag | aag | ctg | aag | ctg | ctc | cgc | tac | gag | gag | gag | ttc | ctc | cgg | aag | agc | 192 | |
| Glu | Lys | Leu | Lys | Leu | Leu | Arg | Tyr | Glu | Glu | Glu | Phe | Leu | Arg | Lys | Ser | | |
| | | | | 50 | | | | | 55 | | | | | | | 60 | |
| | | | | | | | | | | | | | | | | | |
| aac | ctg | aag | gcc | ccg | tcc | aga | cac | tat | ttt | gca | ctg | cct | acc | aac | cct | 240 | |
| Asn | Leu | Lys | Ala | Pro | Ser | Arg | His | Tyr | Phe | Ala | Leu | Pro | Thr | Asn | Pro | | |
| | | | | 65 | | | | | 70 | | | | | | | 75 | 80 |

229

| | |
|---|-----|
| ggc gaa cag ttc tac atg ttt tgt act ctt gct gct tgg ttg att aat | 288 |
| Gly Glu Gln Phe Tyr Met Phe Cys Thr Leu Ala Ala Trp Leu Ile Asn | |
| 85 90 95 | |
| aaa gcg gga cgt ccc ttt gag cag cct caa gaa tat gat gac cct aat | 336 |
| Lys Ala Gly Arg Pro Phe Glu Gln Pro Gln Glu Tyr Asp Asp Pro Asn | |
| 100 105 110 | |
| gca aca ata tct aac ata cta tcc gag ctt cgg tca ttt gga aga act | 384 |
| Ala Thr Ile Ser Asn Ile Leu Ser Glu Leu Arg Ser Phe Gly Arg Thr | |
| 115 120 125 | |
| gca gat ttt cct cct tca aaa tta aag tca ggt tat gga gaa cat gta | 432 |
| Ala Asp Phe Pro Pro Ser Lys Leu Lys Ser Gly Tyr Gly Glu His Val | |
| 130 135 140 | |
| tgc tat gtt ctt gat tgc ttc gct gaa gaa gca ttg aaa tat att ggt | 480 |
| Cys Tyr Val Leu Asp Cys Phe Ala Glu Glu Ala Leu Lys Tyr Ile Gly | |
| 145 150 155 160 | |
| ttc acc tgg aaa agg cca ata tac cca gta gaa gaa tta gaa gaa gaa | 528 |
| Phe Thr Trp Lys Arg Pro Ile Tyr Pro Val Glu Glu Leu Glu Glu Glu | |
| 165 170 175 | |
| agc gtt gca gaa gat gat gca gaa tta aca tta aat aaa gtg gat gaa | 576 |
| Ser Val Ala Glu Asp Asp Ala Glu Leu Thr Leu Asn Lys Val Asp Glu | |
| 180 185 190 | |
| gaa ttt gtg gaa gaa gag aca gat aat gaa gaa aac ttt att gat ctc | 624 |
| Glu Phe Val Glu Glu Glu Thr Asp Asn Glu Glu Asn Phe Ile Asp Leu | |
| 195 200 205 | |
| aac gtt tta aag gcc cag aca tat cac ttg gat atg aac gag act gcc | 672 |
| Asn Val Leu Lys Ala Gln Thr Tyr His Leu Asp Met Asn Glu Thr Ala | |
| 210 215 220 | |
| aaa caa gaa gat att ttg gaa tcc aca aca gat gct gca gaa tgg agc | 720 |
| Lys Gln Glu Asp Ile Leu Glu Ser Thr Thr Asp Ala Ala Glu Trp Ser | |
| 225 230 235 240 | |
| cta gaa gtg gaa cgt gta cta ccg caa ctg aaa gtc acg att agg act | 768 |
| Leu Glu Val Glu Arg Val Leu Pro Gln Leu Lys Val Thr Ile Arg Thr | |
| 245 250 255 | |

230

| | |
|---|------|
| gac aat aag gat tgg aga atc cat gtt gac caa atg cac cag cac aga Asp Asn Lys Asp Trp Arg Ile His Val Asp Gln Met His Gln His Arg 260 265 270 | 816 |
| agt gga att gaa tct gct cta aag gag acc aag gga ttt ttg gac aaa Ser Gly Ile Glu Ser Ala Leu Lys Glu Thr Lys Gly Phe Leu Asp Lys 275 280 285 | 864 |
| ctc cat aat gaa att act agg act ttg gaa aag atc agc agc cga gaa Leu His Asn Glu Ile Thr Arg Thr Leu Glu Lys Ile Ser Ser Arg Glu 290 295 300 | 912 |
| aag tac atc aac aat cag ctt gag aat ttg gtt caa gaa tat cgt gca Lys Tyr Ile Asn Asn Gln Leu Glu Asn Leu Val Gln Glu Tyr Arg Ala 305 310 315 320 | 960 |
| gct caa gcc cag ctg agt gag gca aag gag cga tac cag cag gga aat Ala Gln Ala Gln Leu Ser Glu Ala Lys Glu Arg Tyr Gln Gln Gly Asn 325 330 335 | 1008 |
| gga gga gtg acg gaa aga acc aga ctc ctc tct gag gtt atg gaa gaa Gly Gly Val Thr Glu Arg Thr Arg Leu Leu Ser Glu Val Met Glu Glu 340 345 350 | 1056 |
| tta gaa aag gta aaa caa gaa atg gaa gaa aag ggc agc agc atg act Leu Glu Lys Val Lys Gln Glu Met Glu Glu Lys Gly Ser Ser Met Thr 355 360 365 | 1104 |
| gat ggt gct cct ttg gtg aag att aaa cag agc tta aca aaa ctg aag Asp Gly Ala Pro Leu Val Lys Ile Lys Gln Ser Leu Thr Lys Leu Lys 370 375 380 | 1152 |
| caa gaa act gta gag atg gac att aga att ggc att gtg gaa cac aca Gln Glu Thr Val Glu Met Asp Ile Arg Ile Gly Ile Val Glu His Thr 385 390 395 400 | 1200 |
| cta ctc caa tca aag ctg aag gag aag tcc aac atg act agg aac atg Leu Leu Gln Ser Lys Leu Lys Glu Lys Ser Asn Met Thr Arg Asn Met 405 410 415 | 1248 |
| cat gcc aca gtt att cca gaa cca gca aca ggc ttt tat taa His Ala Thr Val Ile Pro Glu Pro Ala Thr Gly Phe Tyr * | 1290 |
| 420 425 | |

231

<210> 162

<211> 429

<212> PRT

<213> Homo sapiens

<400> 162

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Met Thr Ala Ala Leu Ala Val Val Thr Thr Ser Gly Leu Glu Asp Gly
 1           5           10           15
Val Pro Arg Ser Arg Gly Glu Gly Thr Gly Glu Val Val Leu Glu Arg
          20           25           30
Gly Pro Gly Ala Ala Tyr His Met Phe Val Val Met Glu Asp Leu Val
          35           40           45
Glu Lys Leu Lys Leu Leu Arg Tyr Glu Glu Glu Phe Leu Arg Lys Ser
          50           55           60
Asn Leu Lys Ala Pro Ser Arg His Tyr Phe Ala Leu Pro Thr Asn Pro
65           70           75           80
Gly Glu Gln Phe Tyr Met Phe Cys Thr Leu Ala Ala Trp Leu Ile Asn
          85           90           95
Lys Ala Gly Arg Pro Phe Glu Gln Pro Gln Glu Tyr Asp Asp Pro Asn
          100          105          110
Ala Thr Ile Ser Asn Ile Leu Ser Glu Leu Arg Ser Phe Gly Arg Thr
          115          120          125
Ala Asp Phe Pro Pro Ser Lys Leu Lys Ser Gly Tyr Gly Glu His Val
          130          135          140
Cys Tyr Val Leu Asp Cys Phe Ala Glu Glu Ala Leu Lys Tyr Ile Gly
145          150          155          160
Phe Thr Trp Lys Arg Pro Ile Tyr Pro Val Glu Glu Leu Glu Glu Glu
          165          170          175
Ser Val Ala Glu Asp Asp Ala Glu Leu Thr Leu Asn Lys Val Asp Glu
          180          185          190
Glu Phe Val Glu Glu Glu Thr Asp Asn Glu Glu Asn Phe Ile Asp Leu
          195          200          205
Asn Val Leu Lys Ala Gln Thr Tyr His Leu Asp Met Asn Glu Thr Ala
          210          215          220
Lys Gln Glu Asp Ile Leu Glu Ser Thr Thr Asp Ala Ala Glu Trp Ser
225          230          235          240
Leu Glu Val Glu Arg Val Leu Pro Gln Leu Lys Val Thr Ile Arg Thr
          245          250          255
Asp Asn Lys Asp Trp Arg Ile His Val Asp Gln Met His Gln His Arg
          260          265          270
Ser Gly Ile Glu Ser Ala Leu Lys Glu Thr Lys Gly Phe Leu Asp Lys
          275          280          285

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232

Leu His Asn Glu Ile Thr Arg Thr Leu Glu Lys Ile Ser Ser Arg Glu
 290 295 300
 Lys Tyr Ile Asn Asn Gln Leu Glu Asn Leu Val Gln Glu Tyr Arg Ala
 305 310 315 320
 Ala Gln Ala Gln Leu Ser Glu Ala Lys Glu Arg Tyr Gln Gln Gly Asn
 325 330 335
 Gly Gly Val Thr Glu Arg Thr Arg Leu Leu Ser Glu Val Met Glu Glu
 340 345 350
 Leu Glu Lys Val Lys Gln Glu Met Glu Glu Lys Gly Ser Ser Met Thr
 355 360 365
 Asp Gly Ala Pro Leu Val Lys Ile Lys Gln Ser Leu Thr Lys Leu Lys
 370 375 380
 Gln Glu Thr Val Glu Met Asp Ile Arg Ile Gly Ile Val Glu His Thr
 385 390 395 400
 Leu Leu Gln Ser Lys Leu Lys Glu Lys Ser Asn Met Thr Arg Asn Met
 405 410 415
 His Ala Thr Val Ile Pro Glu Pro Ala Thr Gly Phe Tyr
 420 425

<210> 163

<211> 456

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(456)

<400> 163

| | |
|---|-----|
| atg gaa gga cag cgg caa gaa agc cac gca acc cta aca ctc gcc cag | 48 |
| Met Glu Gly Gln Arg Gln Glu Ser His Ala Thr Leu Thr Leu Ala Gln | |
| 1 5 10 15 | |
| gct cat ttc aac aat gga gag tac gcg gag gcc gag gca ctg tac tcc | 96 |
| Ala His Phe Asn Asn Gly Glu Tyr Ala Glu Ala Glu Ala Leu Tyr Ser | |
| 20 25 30 | |
| gct tac att cgc cgg tgc gct tgc gcg gcc tcc agc gac gag agt ccc | 144 |
| Ala Tyr Ile Arg Arg Cys Ala Cys Ala Ala Ser Ser Asp Glu Ser Pro | |
| 35 40 45 | |
| ggg agc aaa tgc agc cct gag gat ttg gct act gca tat aac aac agg | 192 |
| Gly Ser Lys Cys Ser Pro Glu Asp Leu Ala Thr Ala Tyr Asn Asn Arg | |
| 50 55 60 | |

233

ggg caa atc aag tac ttc agg gtt gat ttt tat gaa gcc atg gat gac 240
 Gly Gln Ile Lys Tyr Phe Arg Val Asp Phe Tyr Glu Ala Met Asp Asp
 65 70 75 80
 tac aca tct gcc ata gaa gtc caa ccc aat ttt gaa gtt cca tat tac 288
 Tyr Thr Ser Ala Ile Glu Val Gln Pro Asn Phe Glu Val Pro Tyr Tyr
 85 90 95
 aac aga ggg ttg ata ctg tat agg ctg gga tat ttt gat gat gct ttg 336
 Asn Arg Gly Leu Ile Leu Tyr Arg Leu Gly Tyr Phe Asp Asp Ala Leu
 100 105 110
 gaa gat ttc aag aag gtc tta gac tta aat cct gga ttt caa gat gct 384
 Glu Asp Phe Lys Lys Val Leu Asp Leu Asn Pro Gly Phe Gln Asp Ala
 115 120 125
 act ttg agc tta aaa cag act att cta gac aaa gaa gaa aaa caa aga 432
 Thr Leu Ser Leu Lys Gln Thr Ile Leu Asp Lys Glu Glu Lys Gln Arg
 130 135 140
 aga aat gtt gca aaa aat tat tga 456
 Arg Asn Val Ala Lys Asn Tyr *
 145 150

<210> 164
 <211> 151
 <212> PRT
 <213> Homo sapiens

<400> 164
 Met Glu Gly Gln Arg Gln Glu Ser His Ala Thr Leu Thr Leu Ala Gln
 1 5 10 15
 Ala His Phe Asn Asn Gly Glu Tyr Ala Glu Ala Glu Ala Leu Tyr Ser
 20 25 30
 Ala Tyr Ile Arg Arg Cys Ala Cys Ala Ala Ser Ser Asp Glu Ser Pro
 35 40 45
 Gly Ser Lys Cys Ser Pro Glu Asp Leu Ala Thr Ala Tyr Asn Asn Arg
 50 55 60
 Gly Gln Ile Lys Tyr Phe Arg Val Asp Phe Tyr Glu Ala Met Asp Asp
 65 70 75 80
 Tyr Thr Ser Ala Ile Glu Val Gln Pro Asn Phe Glu Val Pro Tyr Tyr
 85 90 95

234

Asn Arg Gly Leu Ile Leu Tyr Arg Leu Gly Tyr Phe Asp Asp Ala Leu
 100 105 110
 Glu Asp Phe Lys Lys Val Leu Asp Leu Asn Pro Gly Phe Gln Asp Ala
 115 120 125
 Thr Leu Ser Leu Lys Gln Thr Ile Leu Asp Lys Glu Glu Lys Gln Arg
 130 135 140
 Arg Asn Val Ala Lys Asn Tyr
 145 150

<210> 165

<211> 1032

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1032)

<400> 165

atg atg ctg ctg ctc tat gaa gaa ggc ctc cgg gtt gtc ata cac acc 48
 Met Met Leu Leu Leu Tyr Glu Glu Gly Leu Arg Val Val Ile His Thr
 1 5 10 15

tcc aac ctc atc cat gct gac tgg cac cag aaa act caa gga ata tgg 96
 Ser Asn Leu Ile His Ala Asp Trp His Gln Lys Thr Gln Gly Ile Trp
 20 25 30

ttg agc ccc tta tac cca cga att gct gat gga acc cac aaa tct gga 144
 Leu Ser Pro Leu Tyr Pro Arg Ile Ala Asp Gly Thr His Lys Ser Gly
 35 40 45

gag tcg cca aca cat ttt aaa gct gat ctc atc agt tac ttg atg gct 192
 Glu Ser Pro Thr His Phe Lys Ala Asp Leu Ile Ser Tyr Leu Met Ala
 50 55 60

tat aat gcc cct tct ctc aag gag tgg ata gat gtc att cac aag cac 240
 Tyr Asn Ala Pro Ser Leu Lys Glu Trp Ile Asp Val Ile His Lys His
 65 70 75 80

gat ctc tct gaa aca aat gtt tat ctt att ggt tca acc cca gga cgc 288
 Asp Leu Ser Glu Thr Asn Val Tyr Leu Ile Gly Ser Thr Pro Gly Arg
 85 90 95

ttt caa gga agt caa aaa gat aat tgg gga cat ttt aga ctt aag aag 336

235

| | |
|---|-----|
| Phe Gln Gly Ser Gln Lys Asp Asn Trp Gly His Phe Arg Leu Lys Lys | |
| 100 105 110 | |
| ctt ctg aaa gac cat gcc tca tcc atg cct aac gca gag tcc tgg cct | 384 |
| Leu Leu Lys Asp His Ala Ser Ser Met Pro Asn Ala Glu Ser Trp Pro | |
| 115 120 125 | |
| gtc gta ggt cag ttt tca agc gtt ggc tcc ttg gga gcc gat gaa tca | 432 |
| Val Val Gly Gln Phe Ser Ser Val Gly Ser Leu Gly Ala Asp Glu Ser | |
| 130 135 140 | |
| aag tgg tta tgt tct gag ttt aaa gag agc atg ctg aca ctg ggg aag | 480 |
| Lys Trp Leu Cys Ser Glu Phe Lys Glu Ser Met Leu Thr Leu Gly Lys | |
| 145 150 155 160 | |
| gaa agc aag act cca gga aaa agc tct gtt cct ctt tac ttg atc tat | 528 |
| Glu Ser Lys Thr Pro Gly Lys Ser Ser Val Pro Leu Tyr Leu Ile Tyr | |
| 165 170 175 | |
| cct tct gtg gaa aat gtg cgg acc agt tta gaa gga tat cct gct ggg | 576 |
| Pro Ser Val Glu Asn Val Arg Thr Ser Leu Glu Gly Tyr Pro Ala Gly | |
| 180 185 190 | |
| ggc tct ctt ccc tat agc atc cag aca gct gaa aaa cag aat tgg ctg | 624 |
| Gly Ser Leu Pro Tyr Ser Ile Gln Thr Ala Glu Lys Gln Asn Trp Leu | |
| 195 200 205 | |
| cat tcc tat ttt cac aaa tgg tca gct gag act tct ggc cgc agc aat | 672 |
| His Ser Tyr Phe His Lys Trp Ser Ala Glu Thr Ser Gly Arg Ser Asn | |
| 210 215 220 | |
| gcc atg cca cat att aag aca tat atg agg cct tct cca gac ttc agt | 720 |
| Ala Met Pro His Ile Lys Thr Tyr Met Arg Pro Ser Pro Asp Phe Ser | |
| 225 230 235 240 | |
| aaa att gct tgg ttc ctt gtc aca agc gca aat ctg tcc aag gct gcc | 768 |
| Lys Ile Ala Trp Phe Leu Val Thr Ser Ala Asn Leu Ser Lys Ala Ala | |
| 245 250 255 | |
| tgg gga gca ttg gag aag aat ggc acc cag ctg atg atc cgc tcc tac | 816 |
| Trp Gly Ala Leu Glu Lys Asn Gly Thr Gln Leu Met Ile Arg Ser Tyr | |
| 260 265 270 | |
| gag ctc ggg gtc ctt ttc ctc cct tca gca ttt ggt cta gac agt ttc | 864 |

236

Glu Leu Gly Val Leu Phe Leu Pro Ser Ala Phe Gly Leu Asp Ser Phe
 275 280 285
 aaa gtg aaa cag aag ttc ttc gct ggc agc cag gag cca atg gcc acc 912
 Lys Val Lys Gln Lys Phe Phe Ala Gly Ser Gln Glu Pro Met Ala Thr
 290 295 300
 ttt cct gtg cca tat gat ttg cct cca gaa ctg tat gga agt aaa gat 960
 Phe Pro Val Pro Tyr Asp Leu Pro Pro Glu Leu Tyr Gly Ser Lys Asp
 305 310 315 320
 cgg cca tgg ata tgg aac att cct tat gtc aaa gca ccg gat acg cat 1008
 Arg Pro Trp Ile Trp Asn Ile Pro Tyr Val Lys Ala Pro Asp Thr His
 325 330 335
 ggg aac atg tgg gtg ccc tcc tga 1032
 Gly Asn Met Trp Val Pro Ser *
 340

<210> 166
 <211> 343
 <212> PRT
 <213> Homo sapiens

<400> 166
 Met Met Leu Leu Leu Tyr Glu Glu Gly Leu Arg Val Val Ile His Thr
 1 5 10 15
 Ser Asn Leu Ile His Ala Asp Trp His Gln Lys Thr Gln Gly Ile Trp
 20 25 30
 Leu Ser Pro Leu Tyr Pro Arg Ile Ala Asp Gly Thr His Lys Ser Gly
 35 40 45
 Glu Ser Pro Thr His Phe Lys Ala Asp Leu Ile Ser Tyr Leu Met Ala
 50 55 60
 Tyr Asn Ala Pro Ser Leu Lys Glu Trp Ile Asp Val Ile His Lys His
 65 70 75 80
 Asp Leu Ser Glu Thr Asn Val Tyr Leu Ile Gly Ser Thr Pro Gly Arg
 85 90 95
 Phe Gln Gly Ser Gln Lys Asp Asn Trp Gly His Phe Arg Leu Lys Lys
 100 105 110
 Leu Leu Lys Asp His Ala Ser Ser Met Pro Asn Ala Glu Ser Trp Pro
 115 120 125
 Val Val Gly Gln Phe Ser Ser Val Gly Ser Leu Gly Ala Asp Glu Ser
 130 135 140

237

Lys Trp Leu Cys Ser Glu Phe Lys Glu Ser Met Leu Thr Leu Gly Lys
 145 150 155 160
 Glu Ser Lys Thr Pro Gly Lys Ser Ser Val Pro Leu Tyr Leu Ile Tyr
 165 170 175
 Pro Ser Val Glu Asn Val Arg Thr Ser Leu Glu Gly Tyr Pro Ala Gly
 180 185 190
 Gly Ser Leu Pro Tyr Ser Ile Gln Thr Ala Glu Lys Gln Asn Trp Leu
 195 200 205
 His Ser Tyr Phe His Lys Trp Ser Ala Glu Thr Ser Gly Arg Ser Asn
 210 215 220
 Ala Met Pro His Ile Lys Thr Tyr Met Arg Pro Ser Pro Asp Phe Ser
 225 230 235 240
 Lys Ile Ala Trp Phe Leu Val Thr Ser Ala Asn Leu Ser Lys Ala Ala
 245 250 255
 Trp Gly Ala Leu Glu Lys Asn Gly Thr Gln Leu Met Ile Arg Ser Tyr
 260 265 270
 Glu Leu Gly Val Leu Phe Leu Pro Ser Ala Phe Gly Leu Asp Ser Phe
 275 280 285
 Lys Val Lys Gln Lys Phe Phe Ala Gly Ser Gln Glu Pro Met Ala Thr
 290 295 300
 Phe Pro Val Pro Tyr Asp Leu Pro Pro Glu Leu Tyr Gly Ser Lys Asp
 305 310 315 320
 Arg Pro Trp Ile Trp Asn Ile Pro Tyr Val Lys Ala Pro Asp Thr His
 325 330 335
 Gly Asn Met Trp Val Pro Ser
 340

<210> 167

<211> 594

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(594)

<400> 167

atg cca ccc gcg ggg ctc cgc cgg gcc gcg ccg ctc acc gca atc gct 48
 Met Pro Pro Ala Gly Leu Arg Arg Ala Ala Pro Leu Thr Ala Ile Ala
 1 5 10 15

ctg ttg gtg ctg ggg gct ccc cta gtg ctg gcc ggc gag gac tgc ctg 96
 Leu Leu Val Leu Gly Ala Pro Leu Val Leu Ala Gly Glu Asp Cys Leu
 20 25 30

238

| | |
|---|-----|
| tgg tac ctg gac cgg aat ggc tcc tgg cat ccg ggg ttt aac tgc gag Trp Tyr Leu Asp Arg Asn Gly Ser Trp His Pro Gly Phe Asn Cys Glu 35 40 45 | 144 |
| ttc ttc acc ttc tgc tgc ggg acc tgc tac cat cgg tac tgc tgc agg Phe Phe Thr Phe Cys Cys Gly Thr Cys Tyr His Arg Tyr Cys Cys Arg 50 55 60 | 192 |
| gac ctg acc ttg ctt atc acc gag agg cag cag aag cac tgc ctg gcc Asp Leu Thr Leu Leu Ile Thr Glu Arg Gln Gln Lys His Cys Leu Ala 65 70 75 80 | 240 |
| ttc agc ccc aag acc ata gca ggc atc gcc tca gct gtg atc ctc ttt Phe Ser Pro Lys Thr Ile Ala Gly Ile Ala Ser Ala Val Ile Leu Phe 85 90 95 | 288 |
| gtt gct gtg gtt gcc acc acc atc tgc tgc ttc ctc tgt tcc tgt tgc Val Ala Val Val Ala Thr Thr Ile Cys Cys Phe Leu Cys Ser Cys Cys 100 105 110 | 336 |
| tac ctg tac cgc cgg cgc cag cag ctc cag agc cca ttt gaa ggc cag Tyr Leu Tyr Arg Arg Arg Gln Gln Leu Gln Ser Pro Phe Glu Gly Gln 115 120 125 | 384 |
| gag att cca atg aca ggc atc cca gtg cag cca gta tac cca tac ccc Glu Ile Pro Met Thr Gly Ile Pro Val Gln Pro Val Tyr Pro Tyr Pro 130 135 140 | 432 |
| cag gac ccc aaa gct ggc cct gca ccc cca cag cct ggc ttc atg tac Gln Asp Pro Lys Ala Gly Pro Ala Pro Pro Gln Pro Gly Phe Met Tyr 145 150 155 160 | 480 |
| cca cct agt ggt cct gct ccc caa tat cca ctc tac cca gct ggg ccc Pro Pro Ser Gly Pro Ala Pro Gln Tyr Pro Leu Tyr Pro Ala Gly Pro 165 170 175 | 528 |
| cca gtc tac aac cct gca gct cct cct ccc tat atg cca cca cag ccc Pro Val Tyr Asn Pro Ala Ala Pro Pro Pro Tyr Met Pro Pro Gln Pro 180 185 190 | 576 |
| tct tac ccg gga gcc tga Ser Tyr Pro Gly Ala * | 594 |
| 195 | |

<210> 168

<211> 197

<212> PRT

<213> Homo sapiens

<400> 168

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Met Pro Pro Ala Gly Leu Arg Arg Ala Ala Pro Leu Thr Ala Ile Ala
 1           5           10           15
Leu Leu Val Leu Gly Ala Pro Leu Val Leu Ala Gly Glu Asp Cys Leu
      20           25           30
Trp Tyr Leu Asp Arg Asn Gly Ser Trp His Pro Gly Phe Asn Cys Glu
      35           40           45
Phe Phe Thr Phe Cys Cys Gly Thr Cys Tyr His Arg Tyr Cys Cys Arg
 50           55           60
Asp Leu Thr Leu Leu Ile Thr Glu Arg Gln Gln Lys His Cys Leu Ala
65           70           75           80
Phe Ser Pro Lys Thr Ile Ala Gly Ile Ala Ser Ala Val Ile Leu Phe
      85           90           95
Val Ala Val Val Ala Thr Thr Ile Cys Cys Phe Leu Cys Ser Cys Cys
      100          105          110
Tyr Leu Tyr Arg Arg Arg Gln Gln Leu Gln Ser Pro Phe Glu Gly Gln
      115          120          125
Glu Ile Pro Met Thr Gly Ile Pro Val Gln Pro Val Tyr Pro Tyr Pro
      130          135          140
Gln Asp Pro Lys Ala Gly Pro Ala Pro Pro Gln Pro Gly Phe Met Tyr
      145          150          155          160
Pro Pro Ser Gly Pro Ala Pro Gln Tyr Pro Leu Tyr Pro Ala Gly Pro
      165          170          175
Pro Val Tyr Asn Pro Ala Ala Pro Pro Tyr Met Pro Pro Gln Pro
      180          185          190
Ser Tyr Pro Gly Ala
      195

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<210> 169

<211> 669

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(669)

240

<400> 169

| | |
|---|-----|
| atg cgt gtg ggc ctc gcg ctg atc ttg gtg ggc cac gtg aac ctg ctg | 48 |
| Met Arg Val Gly Leu Ala Leu Ile Leu Val Gly His Val Asn Leu Leu | |
| 1 5 10 15 | |
| ctg ggg gcc gtg ctg cat ggc acc gtc ctg cgg cac gtg gcc aat ccc | 96 |
| Leu Gly Ala Val Leu His Gly Thr Val Leu Arg His Val Ala Asn Pro | |
| 20 25 30 | |
| cgc ggc gct gtc acg ccg gag tac acc gta gcc aat gtc atc tct gtc | 144 |
| Arg Gly Ala Val Thr Pro Glu Tyr Thr Val Ala Asn Val Ile Ser Val | |
| 35 40 45 | |
| ggc tcg ggg ctg ctg agc gtt tcc gtg gga ctt gtg gcc ctc ctg gcg | 192 |
| Gly Ser Gly Leu Leu Ser Val Ser Val Gly Leu Val Ala Leu Leu Ala | |
| 50 55 60 | |
| tcc agg aac ctt ctt cgc cct cca ctg cac tgg gtc ctg ctg gca cta | 240 |
| Ser Arg Asn Leu Leu Arg Pro Pro Leu His Trp Val Leu Leu Ala Leu | |
| 65 70 75 80 | |
| gct ctg gtg aac ctg ctc ttg tcc gtt gcc tgc tcc ctg ggc ctc ctt | 288 |
| Ala Leu Val Asn Leu Leu Leu Ser Val Ala Cys Ser Leu Gly Leu Leu | |
| 85 90 95 | |
| ctt gct gtg tca ctc act gtg gcc aac ggt ggc cgc cgc ctt att gct | 336 |
| Leu Ala Val Ser Leu Thr Val Ala Asn Gly Gly Arg Arg Leu Ile Ala | |
| 100 105 110 | |
| gac tgc cac cca gga ctg ctg gat cct ctg gta cca ctg gat gag ggg | 384 |
| Asp Cys His Pro Gly Leu Leu Asp Pro Leu Val Pro Leu Asp Glu Gly | |
| 115 120 125 | |
| ccg gga cat act gac tgc ccc ttt gac ccc aca aga atc tat gat aca | 432 |
| Pro Gly His Thr Asp Cys Pro Phe Asp Pro Thr Arg Ile Tyr Asp Thr | |
| 130 135 140 | |
| gcc ttg gct ctc tgg atc cct tct ttg ctc atg tct gca ggg gag gct | 480 |
| Ala Leu Ala Leu Trp Ile Pro Ser Leu Leu Met Ser Ala Gly Glu Ala | |
| 145 150 155 160 | |
| gct cta tct ggt tac tgc tgt gtg gct gca ctc act cta cgt gga gtt | 528 |
| Ala Leu Ser Gly Tyr Cys Cys Val Ala Ala Leu Thr Leu Arg Gly Val | |
| 165 170 175 | |

241

ggg ccc tgc agg aag gac gga ctt cag ggg cag cta gag gaa atg aca 576
 Gly Pro Cys Arg Lys Asp Gly Leu Gln Gly Gln Leu Glu Glu Met Thr
 180 185 190

gag ctt gaa tct cct aaa tgt aaa agg cag gaa aat gag cag cta ctg 624
 Glu Leu Glu Ser Pro Lys Cys Lys Arg Gln Glu Asn Glu Gln Leu Leu
 195 200 205

gat caa aat caa gaa atc cgg gca tca cag aga agt tgg gtt tag 669
 Asp Gln Asn Gln Glu Ile Arg Ala Ser Gln Arg Ser Trp Val *
 210 215 220

<210> 170

<211> 222

<212> PRT

<213> Homo sapiens

<400> 170

Met Arg Val Gly Leu Ala Leu Ile Leu Val Gly His Val Asn Leu Leu
 1 5 10 15
 Leu Gly Ala Val Leu His Gly Thr Val Leu Arg His Val Ala Asn Pro
 20 25 30
 Arg Gly Ala Val Thr Pro Glu Tyr Thr Val Ala Asn Val Ile Ser Val
 35 40 45
 Gly Ser Gly Leu Leu Ser Val Ser Val Gly Leu Val Ala Leu Leu Ala
 50 55 60
 Ser Arg Asn Leu Leu Arg Pro Pro Leu His Trp Val Leu Leu Ala Leu
 65 70 75 80
 Ala Leu Val Asn Leu Leu Ser Val Ala Cys Ser Leu Gly Leu Leu
 85 90 95
 Leu Ala Val Ser Leu Thr Val Ala Asn Gly Gly Arg Arg Leu Ile Ala
 100 105 110
 Asp Cys His Pro Gly Leu Leu Asp Pro Leu Val Pro Leu Asp Glu Gly
 115 120 125
 Pro Gly His Thr Asp Cys Pro Phe Asp Pro Thr Arg Ile Tyr Asp Thr
 130 135 140
 Ala Leu Ala Leu Trp Ile Pro Ser Leu Leu Met Ser Ala Gly Glu Ala
 145 150 155 160
 Ala Leu Ser Gly Tyr Cys Cys Val Ala Ala Leu Thr Leu Arg Gly Val
 165 170 175
 Gly Pro Cys Arg Lys Asp Gly Leu Gln Gly Gln Leu Glu Glu Met Thr
 180 185 190

242

Glu Leu Glu Ser Pro Lys Cys Lys Arg Gln Glu Asn Glu Gln Leu Leu
 195 200 205
 Asp Gln Asn Gln Glu Ile Arg Ala Ser Gln Arg Ser Trp Val
 210 215 220

<210> 171
 <211> 345
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(345)

<400> 171

atg ctg ctg tgg ctt ctt gtc ttc tct gct ctg ggt atc cag gcc tgg 48
 Met Leu Leu Trp Leu Leu Val Phe Ser Ala Leu Gly Ile Gln Ala Trp
 1 5 10 15

ggt gat tcc tcc tgg aac aaa aca caa gct aaa cag gta tca gag ggg 96
 Gly Asp Ser Ser Trp Asn Lys Thr Gln Ala Lys Gln Val Ser Glu Gly
 20 25 30

ctc cag tac cta ttt gag aac atc tcc cag ctc act gaa aaa gat gtc 144
 Leu Gln Tyr Leu Phe Glu Asn Ile Ser Gln Leu Thr Glu Lys Asp Val
 35 40 45

tcc acc acg gtc tct cgc aag gca tgg ggg gca gaa gct gtt ggc tgc 192
 Ser Thr Thr Val Ser Arg Lys Ala Trp Gly Ala Glu Ala Val Gly Cys
 50 55 60

agt att cag ctg acc acg cca gtg aat gtc ctt gtt ata cac cat gtc 240
 Ser Ile Gln Leu Thr Thr Pro Val Asn Val Leu Val Ile His His Val
 65 70 75 80

cct gga ctg gag tgt cac gac cag aca gtc tgc agc cag aga ctg cgg 288
 Pro Gly Leu Glu Cys His Asp Gln Thr Val Cys Ser Gln Arg Leu Arg
 85 90 95

gaa ctg cag gcc cat cat gtc cac aac aac agt ggg tgt gat gtg gcc 336
 Glu Leu Gln Ala His His Val His Asn Asn Ser Gly Cys Asp Val Ala
 100 105 110

tac aag taa 345

243

Tyr Lys *

<210> 172
 <211> 114
 <212> PRT
 <213> Homo sapiens

<400> 172
 Met Leu Leu Trp Leu Leu Val Phe Ser Ala Leu Gly Ile Gln Ala Trp
 1 5 10 15
 Gly Asp Ser Ser Trp Asn Lys Thr Gln Ala Lys Gln Val Ser Glu Gly
 20 25 30
 Leu Gln Tyr Leu Phe Glu Asn Ile Ser Gln Leu Thr Glu Lys Asp Val
 35 40 45
 Ser Thr Thr Val Ser Arg Lys Ala Trp Gly Ala Glu Ala Val Gly Cys
 50 55 60
 Ser Ile Gln Leu Thr Thr Pro Val Asn Val Leu Val Ile His His Val
 65 70 75 80
 Pro Gly Leu Glu Cys His Asp Gln Thr Val Cys Ser Gln Arg Leu Arg
 85 90 95
 Glu Leu Gln Ala His His Val His Asn Asn Ser Gly Cys Asp Val Ala
 100 105 110
 Tyr Lys

<210> 173
 <211> 924
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(924)

<400> 173
 atg gag cag ctg cag gag gcc ctg aag gta cgc aag gat gat gcc cac 48
 Met Glu Gln Leu Gln Glu Ala Leu Lys Val Arg Lys Asp Asp Ala His
 1 5 10 15
 gcc ctc cac ctg ctg gca ctg ctc ttc tct gcc cag aag cac cac cag 96
 Ala Leu His Leu Leu Ala Leu Leu Phe Ser Ala Gln Lys His His Gln
 20 25 30

244

| | |
|---|-----|
| cat gcc ctg gat gtt gtc aac atg gcc atc acc gag cac cct gag aac His Ala Leu Asp Val Val Asn Met Ala Ile Thr Glu His Pro Glu Asn 35 40 45 | 144 |
| ttc aac ctg atg ttc acc aag gtg aag ctg gag cag gtg ctg aaa ggc Phe Asn Leu Met Phe Thr Lys Val Lys Leu Glu Gln Val Leu Lys Gly 50 55 60 | 192 |
| cca gag gaa gcc ctc gtg acc tgc aga caa gtg ctg agg ctg tgg cag Pro Glu Glu Ala Leu Val Thr Cys Arg Gln Val Leu Arg Leu Trp Gln 65 70 75 80 | 240 |
| acc ctg tac agc ttc tcc cag ctg gga ggc cta gaa aag gat ggc agc Thr Leu Tyr Ser Phe Ser Gln Leu Gly Gly Leu Glu Lys Asp Gly Ser 85 90 95 | 288 |
| ttc ggt gag ggc ctc acc atg aag aag cag agt ggc atg cac ctg act Phe Gly Glu Gly Leu Thr Met Lys Lys Gln Ser Gly Met His Leu Thr 100 105 110 | 336 |
| ttg cct gat gcc cat gat gca gac tct ggc tcc cgg cgg gct tcg tcc Leu Pro Asp Ala His Asp Ala Asp Ser Gly Ser Arg Arg Ala Ser Ser 115 120 125 | 384 |
| atc gcc gcc tcc cgg ctg gag gag gcc atg tca gag ctg act atg ccc Ile Ala Ala Ser Arg Leu Glu Glu Ala Met Ser Glu Leu Thr Met Pro 130 135 140 | 432 |
| tct tcg gtc ctg aag cag ggc ccc atg cag ctg tgg acc acg ctg gaa Ser Ser Val Leu Lys Gln Gly Pro Met Gln Leu Trp Thr Thr Leu Glu 145 150 155 160 | 480 |
| cag atc tgg ctg cag gct gct gag ctg ttc atg gag cag cag cac ctc Gln Ile Trp Leu Gln Ala Ala Glu Leu Phe Met Glu Gln Gln His Leu 165 170 175 | 528 |
| aag gaa gca ggt ttc tgc atc cag gag gcg gcg ggc ctc ttc ccc act Lys Glu Ala Gly Phe Cys Ile Gln Glu Ala Ala Gly Leu Phe Pro Thr 180 185 190 | 576 |
| tct cac tca gta ctc tat atg cgg ggc cgg ctg gct gag gtg aag ggc Ser His Ser Val Leu Tyr Met Arg Gly Arg Leu Ala Glu Val Lys Gly 195 200 205 | 624 |

245

| | |
|---|-----|
| aac ctg gag gag gcc aag cag ctg tac aag gag gcg ctc acg gtg aac Asn Leu Glu Glu Ala Lys Gln Leu Tyr Lys Glu Ala Leu Thr Val Asn 210 215 220 | 672 |
| cca gat ggc gtg cgc atc atg cat agc ctg ggt ctg atg ctg agt cgg Pro Asp Gly Val Arg Ile Met His Ser Leu Gly Leu Met Leu Ser Arg 225 230 235 240 | 720 |
| ctg ggc cac aag agc ttg gcc cag aag gtg ctt cgt gat gcc gtg gag Leu Gly His Lys Ser Leu Ala Gln Lys Val Leu Arg Asp Ala Val Glu 245 250 255 | 768 |
| agg cag agt acg tgc cac gag gcg tgg cag ggc ctg ggc gag gtg ctg Arg Gln Ser Thr Cys His Glu Ala Trp Gln Gly Leu Gly Glu Val Leu 260 265 270 | 816 |
| cag gcc cag ggc cag aac gag gct gcc gtt gac tgc ttc ctc acc gcc Gln Ala Gln Gly Gln Asn Glu Ala Ala Val Asp Cys Phe Leu Thr Ala 275 280 285 | 864 |
| ctt gag ctg gag gcc agc agc cct gta ctg ccc ttc tcc atc atc ccc Leu Glu Leu Glu Ala Ser Ser Pro Val Leu Pro Phe Ser Ile Ile Pro 290 295 300 | 912 |
| aga gag ctc tga Arg Glu Leu * 305 | 924 |

<210> 174

<211> 307

<212> PRT

<213> Homo sapiens

<400> 174

| |
|--|
| Met Glu Gln Leu Gln Glu Ala Leu Lys Val Arg Lys Asp Asp Ala His 1 5 10 15 |
| Ala Leu His Leu Leu Ala Leu Leu Phe Ser Ala Gln Lys His His Gln 20 25 30 |
| His Ala Leu Asp Val Val Asn Met Ala Ile Thr Glu His Pro Glu Asn 35 40 45 |
| Phe Asn Leu Met Phe Thr Lys Val Lys Leu Glu Gln Val Leu Lys Gly 50 55 60 |

246

Pro Glu Glu Ala Leu Val Thr Cys Arg Gln Val Leu Arg Leu Trp Gln
 65 70 75 80
 Thr Leu Tyr Ser Phe Ser Gln Leu Gly Gly Leu Glu Lys Asp Gly Ser
 85 90 95
 Phe Gly Glu Gly Leu Thr Met Lys Lys Gln Ser Gly Met His Leu Thr
 100 105 110
 Leu Pro Asp Ala His Asp Ala Asp Ser Gly Ser Arg Arg Ala Ser Ser
 115 120 125
 Ile Ala Ala Ser Arg Leu Glu Glu Ala Met Ser Glu Leu Thr Met Pro
 130 135 140
 Ser Ser Val Leu Lys Gln Gly Pro Met Gln Leu Trp Thr Thr Leu Glu
 145 150 155 160
 Gln Ile Trp Leu Gln Ala Ala Glu Leu Phe Met Glu Gln Gln His Leu
 165 170 175
 Lys Glu Ala Gly Phe Cys Ile Gln Glu Ala Ala Gly Leu Phe Pro Thr
 180 185 190
 Ser His Ser Val Leu Tyr Met Arg Gly Arg Leu Ala Glu Val Lys Gly
 195 200 205
 Asn Leu Glu Glu Ala Lys Gln Leu Tyr Lys Glu Ala Leu Thr Val Asn
 210 215 220
 Pro Asp Gly Val Arg Ile Met His Ser Leu Gly Leu Met Leu Ser Arg
 225 230 235 240
 Leu Gly His Lys Ser Leu Ala Gln Lys Val Leu Arg Asp Ala Val Glu
 245 250 255
 Arg Gln Ser Thr Cys His Glu Ala Trp Gln Gly Leu Gly Glu Val Leu
 260 265 270
 Gln Ala Gln Gly Gln Asn Glu Ala Ala Val Asp Cys Phe Leu Thr Ala
 275 280 285
 Leu Glu Leu Glu Ala Ser Ser Pro Val Leu Pro Phe Ser Ile Ile Pro
 290 295 300
 Arg Glu Leu
 305

<210> 175
 <211> 627
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(627)

<221> misc_feature
 <222> (1)...(627)

247

<223> n = A,T,C or G

<400> 175

| | |
|--|----|
| atg gga ctc ggc gcg cga ggt gct tgg gcc gcg ctg ctc ctg ggg acg | 48 |
| Met Gly Leu Gly Ala Arg Gly Ala Trp Ala Ala Leu Leu Leu Gly Thr | |
| 1 5 10 15 | |

| | |
|---|----|
| ctg cag gtg cta gcg ctg ctg ggg gcc gcc cat gaa agc gca ncc atg | 96 |
| Leu Gln Val Leu Ala Leu Leu Gly Ala Ala His Glu Ser Ala Xaa Met | |
| 20 25 30 | |

| | |
|---|-----|
| gcg gca tct gca aac ata gag aat tct ggg ctt cca cac aac tcc agt | 144 |
| Ala Ala Ser Ala Asn Ile Glu Asn Ser Gly Leu Pro His Asn Ser Ser | |
| 35 40 45 | |

| | |
|---|-----|
| gct aac tca aca gag act ctc caa cat gtg cct tct gac cat aca aat | 192 |
| Ala Asn Ser Thr Glu Thr Leu Gln His Val Pro Ser Asp His Thr Asn | |
| 50 55 60 | |

| | |
|--|-----|
| gaa act tcc aac agt act gtg aaa cca cca act tca gtt gcc tca gac | 240 |
| Glu Thr Ser Asn Ser Thr Val Lys Pro Pro Thr Ser Val Ala Ser Asp | |
| 65 70 75 80 | |

| | |
|---|-----|
| tcc agt aat aca acg gtc acc acc atg aaa cct aca gcg gca tct aat | 288 |
| Ser Ser Asn Thr Thr Val Thr Thr Met Lys Pro Thr Ala Ala Ser Asn | |
| 85 90 95 | |

| | |
|---|-----|
| aca aca aca cca ggg atg gtc tca aca aat atg act tct acc acc tta | 336 |
| Thr Thr Thr Pro Gly Met Val Ser Thr Asn Met Thr Ser Thr Thr Leu | |
| 100 105 110 | |

| | |
|---|-----|
| aag tct aca ccc aaa aca aca agt gtt tca cag aac aca tct cag ata | 384 |
| Lys Ser Thr Pro Lys Thr Thr Ser Val Ser Gln Asn Thr Ser Gln Ile | |
| 115 120 125 | |

| | |
|---|-----|
| tca aca tcc aca atg acc gta acc cac aat agt tca gtg aca tct gct | 432 |
| Ser Thr Ser Thr Met Thr Val Thr His Asn Ser Ser Val Thr Ser Ala | |
| 130 135 140 | |

| | |
|--|-----|
| gct tca tca gta aca atc aca aca act atg cat tct gaa gca aag aaa | 480 |
| Ala Ser Ser Val Thr Ile Thr Thr Thr Met His Ser Glu Ala Lys Lys | |
| 145 150 155 160 | |

| | |
|---|-----|
| gga tca aaa ttt gat act ggg agc ttt gtt ggt ggt att gta tta acg | 528 |
|---|-----|

248

Gly Ser Lys Phe Asp Thr Gly Ser Phe Val Gly Gly Ile Val Leu Thr
 165 170 175
 ctg gga gtt tta tct att ctt tac att gga tgc aaa atg tat tac tca 576
 Leu Gly Val Leu Ser Ile Leu Tyr Ile Gly Cys Lys Met Tyr Tyr Ser
 180 185 190
 aga aga ggc att cgg tat cga acc ata gat gaa cat gat gcc atc att 624
 Arg Arg Gly Ile Arg Tyr Arg Thr Ile Asp Glu His Asp Ala Ile Ile
 195 200 205
 taa 627
 *

<210> 176

<211> 208

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(208)

<223> Xaa = Any Amino Acid

<400> 176

Met Gly Leu Gly Ala Arg Gly Ala Trp Ala Ala Leu Leu Leu Gly Thr
 1 5 10 15
 Leu Gln Val Leu Ala Leu Leu Gly Ala Ala His Glu Ser Ala Xaa Met
 20 25 30
 Ala Ala Ser Ala Asn Ile Glu Asn Ser Gly Leu Pro His Asn Ser Ser
 35 40 45
 Ala Asn Ser Thr Glu Thr Leu Gln His Val Pro Ser Asp His Thr Asn
 50 55 60
 Glu Thr Ser Asn Ser Thr Val Lys Pro Pro Thr Ser Val Ala Ser Asp
 65 70 75 80
 Ser Ser Asn Thr Thr Val Thr Thr Met Lys Pro Thr Ala Ala Ser Asn
 85 90 95
 Thr Thr Thr Pro Gly Met Val Ser Thr Asn Met Thr Ser Thr Thr Leu
 100 105 110
 Lys Ser Thr Pro Lys Thr Thr Ser Val Ser Gln Asn Thr Ser Gln Ile
 115 120 125
 Ser Thr Ser Thr Met Thr Val Thr His Asn Ser Ser Val Thr Ser Ala

249

| | | |
|---|-----|-----|
| 130 | 135 | 140 |
| Ala Ser Ser Val Thr Ile Thr Thr Thr Met His Ser Glu Ala Lys Lys | | |
| 145 | 150 | 155 |
| Gly Ser Lys Phe Asp Thr Gly Ser Phe Val Gly Gly Ile Val Leu Thr | | 160 |
| | 165 | 170 |
| Leu Gly Val Leu Ser Ile Leu Tyr Ile Gly Cys Lys Met Tyr Tyr Ser | | 175 |
| | 180 | 185 |
| Arg Arg Gly Ile Arg Tyr Arg Thr Ile Asp Glu His Asp Ala Ile Ile | | 190 |
| | 195 | 200 |
| | | 205 |

<210> 177

<211> 1401

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1401)

<221> misc_feature

<222> (1)...(1401)

<223> n = A,T,C or G

<400> 177

| | |
|---|-----|
| atg gtc tgg gcc tct ctg ggg gct gcc tgg gtg gca nat ggt gtt cag | 48 |
| Met Val Trp Ala Ser Leu Gly Ala Ala Trp Val Ala Xaa Gly Val Gln | |
| 1 5 10 15 | |
| tgc gac agg aca gtt gta aac ggc atc atc gca acc gtc gtg gtc agt | 96 |
| Cys Asp Arg Thr Val Val Asn Gly Ile Ile Ala Thr Val Val Val Ser | |
| 20 25 30 | |
| tgg atc atc atc gct gcc aca gtg gtt tcc att atc att gtc ttt gac | 144 |
| Trp Ile Ile Ile Ala Ala Thr Val Val Ser Ile Ile Ile Val Phe Asp | |
| 35 40 45 | |
| cct ctt ggg ggg aaa atg gct cca tat tcc tct gcc ggc ccc agc cac | 192 |
| Pro Leu Gly Gly Lys Met Ala Pro Tyr Ser Ser Ala Gly Pro Ser His | |
| 50 55 60 | |
| ctg gat agt cat gat tca agc cag tta ctt aat ggc ctc aag aca gca | 240 |
| Leu Asp Ser His Asp Ser Ser Gln Leu Leu Asn Gly Leu Lys Thr Ala | |
| 65 70 75 80 | |

250

| | |
|---|-----|
| gct aca agc gtg tgg gaa acc aga atc aag ctc ttg tgc tgt tgc att Ala Thr Ser Val Trp Glu Thr Arg Ile Lys Leu Leu Cys Cys Cys Ile 85 90 95 | 288 |
| ggg aaa gac gac cat act cgg gtt gct ttt tcg agt acg gca gag ctt Gly Lys Asp Asp His Thr Arg Val Ala Phe Ser Ser Thr Ala Glu Leu 100 105 110 | 336 |
| ttc tca acc tac ttt tca gac aca gat ctg gtg ccc agc gac att gcg Phe Ser Thr Tyr Phe Ser Asp Thr Asp Leu Val Pro Ser Asp Ile Ala 115 120 125 | 384 |
| gcg ggc ctc gcc ctg ctt cat cag caa cag gac aat atc agg aac aac Ala Gly Leu Ala Leu Leu His Gln Gln Gln Asp Asn Ile Arg Asn Asn 130 135 140 | 432 |
| caa gag cct gcc cag gtg gtc tgc cat gcc cca ggg agc tcc cag gaa Gln Glu Pro Ala Gln Val Val Cys His Ala Pro Gly Ser Ser Gln Glu 145 150 155 160 | 480 |
| gct gat ctg gat gca gaa tta gaa aac tgc cat cat tac atg cag ttt Ala Asp Leu Asp Ala Glu Leu Glu Asn Cys His His Tyr Met Gln Phe 165 170 175 | 528 |
| gca gca gcg gcc tat ggg tgg ccc ctc tac atc tac aga aac ccc ctc Ala Ala Ala Ala Tyr Gly Trp Pro Leu Tyr Ile Tyr Arg Asn Pro Leu 180 185 190 | 576 |
| acg ggg ctg tgc agg att ggt ggt gac tgc tgc aga agc aga acc aca Thr Gly Leu Cys Arg Ile Gly Gly Asp Cys Cys Arg Ser Arg Thr Thr 195 200 205 | 624 |
| gac tat gac ttg gtc gga ggc gat cag ctc aac tgt cac ttc ggc tcc Asp Tyr Asp Leu Val Gly Gly Asp Gln Leu Asn Cys His Phe Gly Ser 210 215 220 | 672 |
| atc ctg cac acc aca ggg ctg cag tac agg gac ttc atc cac gtc agc Ile Leu His Thr Thr Gly Leu Gln Tyr Arg Asp Phe Ile His Val Ser 225 230 235 240 | 720 |
| ttc cat gac aag gtt tac gag ctg ccg ttt tta gtg gct ctg gat cac Phe His Asp Lys Val Tyr Glu Leu Pro Phe Leu Val Ala Leu Asp His 245 250 255 | 768 |

251

| | |
|---|------|
| agg aaa gag tct gtt gtg gtc gct gtg agg ggg acc atg tct ctg cag Arg Lys Glu Ser Val Val Val Ala Val Arg Gly Thr Met Ser Leu Gln 260 265 270 | 816 |
| gat gtc ctt acg gac ctg tca gcg gag agt gag gtg ctg gac gtg gag Asp Val Leu Thr Asp Leu Ser Ala Glu Ser Glu Val Leu Asp Val Glu 275 280 285 | 864 |
| tgt gag gtg cag gac cgc ctg gca cac aag ggt att tct caa gct gcc Cys Glu Val Gln Asp Arg Leu Ala His Lys Gly Ile Ser Gln Ala Ala 290 295 300 | 912 |
| aga tac gtt tac caa cga ctc atc aac gac ggg att ttg agc caa gcc Arg Tyr Val Tyr Gln Arg Leu Ile Asn Asp Gly Ile Leu Ser Gln Ala 305 310 315 320 | 960 |
| ttc agc att gct cct gag tac cgg ctg gtc ata gtg ggc cac agc ctc Phe Ser Ile Ala Pro Glu Tyr Arg Leu Val Ile Val Gly His Ser Leu 325 330 335 | 1008 |
| ggg ggn ggg gcg gcc gcc ctg ctg gcc acc atg ctc aga gcc gcc tac Gly Xaa Gly Ala Ala Ala Leu Leu Ala Thr Met Leu Arg Ala Ala Tyr 340 345 350 | 1056 |
| ccg cag gtc agg tgc tac gcc ttc tcc cca ccc cgg ggg ctg tgg agc Pro Gln Val Arg Cys Tyr Ala Phe Ser Pro Pro Arg Gly Leu Trp Ser 355 360 365 | 1104 |
| aaa gct ctg cag gaa tat tct cag agc ttc atc gtg tca ctc gtc ctg Lys Ala Leu Gln Glu Tyr Ser Gln Ser Phe Ile Val Ser Leu Val Leu 370 375 380 | 1152 |
| ggg aag gat gtg att ccc agg ctc agt gtg acc aac ttg gaa gat ctg Gly Lys Asp Val Ile Pro Arg Leu Ser Val Thr Asn Leu Glu Asp Leu 385 390 395 400 | 1200 |
| aag aga aga atc ttg cga gtg gtc gcg cac tgc aat aaa ccc aag tac Lys Arg Arg Ile Leu Arg Val Val Ala His Cys Asn Lys Pro Lys Tyr 405 410 415 | 1248 |
| aag atc ttg ctg cac ggt ttg tgg tac gaa ctg ttt gga gga aac ccc Lys Ile Leu Leu His Gly Leu Trp Tyr Glu Leu Phe Gly Gly Asn Pro 420 425 430 | 1296 |

aac aac ttg ccc agc aca agg ggt ctc cag tgt gga cgt ggc ctg acc 1344
Asn Asn Leu Pro Ser Thr Arg Gly Leu Gln Cys Gly Arg Gly Leu Thr
435 440 445

agg gcc act gga aac tgt ccc agg aac gat gga ctc acg ctt ttg tcc 1392
Arg Ala Thr Gly Asn Cys Pro Arg Asn Asp Gly Leu Thr Leu Leu Ser
450 455 460

tta aac tga 1401
Leu Asn *
465

```
<210> 178
<211> 466
<212> PRT
<213> Homo sapiens
```

<220>
<221> VARIANT
<222> (1)...(466)
<223> Xaa = Any Amino Acid

| | | | | | | | | | | | | | | | |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> 178 | | | | | | | | | | | | | | | |
| Met | Val | Trp | Ala | Ser | Leu | Gly | Ala | Ala | Trp | Val | Ala | Xaa | Gly | Val | Gln |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Cys | Asp | Arg | Thr | Val | Val | Asn | Gly | Ile | Ile | Ala | Thr | Val | Val | Val | Ser |
| | | | 20 | | | | | 25 | | | | | | 30 | |
| Trp | Ile | Ile | Ile | Ala | Ala | Thr | Val | Val | Ser | Ile | Ile | Ile | Val | Phe | Asp |
| | | | 35 | | | | | 40 | | | | | | 45 | |
| Pro | Leu | Gly | Gly | Lys | Met | Ala | Pro | Tyr | Ser | Ser | Ala | Gly | Pro | Ser | His |
| | | | | | | | | | | | | | | | |
| Leu | Asp | Ser | His | Asp | Ser | Ser | Gln | Leu | Leu | Asn | Gly | Leu | Lys | Thr | Ala |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Ala | Thr | Ser | Val | Trp | Glu | Thr | Arg | Ile | Lys | Leu | Leu | Cys | Cys | Cys | Ile |
| | | | | 85 | | | | | 90 | | | | | | 95 |
| Gly | Lys | Asp | Asp | His | Thr | Arg | Val | Ala | Phe | Ser | Ser | Thr | Ala | Glu | Leu |
| | | | | 100 | | | | 105 | | | | | | 110 | |
| Phe | Ser | Thr | Tyr | Phe | Ser | Asp | Thr | Asp | Leu | Val | Pro | Ser | Asp | Ile | Ala |
| | | | | 115 | | | | 120 | | | | | | 125 | |
| Ala | Gly | Leu | Ala | Leu | Leu | His | Gln | Gln | Gln | Asp | Asn | Ile | Arg | Asn | Asn |
| | | | | | | | | | | | | | | | |
| Gln | Glu | Pro | Ala | Gln | Val | Val | Cys | His | Ala | Pro | Gly | Ser | Ser | Gln | Glu |
| 145 | | | | | 150 | | | | | | 155 | | | | 160 |

253

Ala Asp Leu Asp Ala Glu Leu Glu Asn Cys His His Tyr Met Gln Phe
 165 170 175
 Ala Ala Ala Ala Tyr Gly Trp Pro Leu Tyr Ile Tyr Arg Asn Pro Leu
 180 185 190
 Thr Gly Leu Cys Arg Ile Gly Gly Asp Cys Cys Arg Ser Arg Thr Thr
 195 200 205
 Asp Tyr Asp Leu Val Gly Gly Asp Gln Leu Asn Cys His Phe Gly Ser
 210 215 220
 Ile Leu His Thr Thr Gly Leu Gln Tyr Arg Asp Phe Ile His Val Ser
 225 230 235 240
 Phe His Asp Lys Val Tyr Glu Leu Pro Phe Leu Val Ala Leu Asp His
 245 250 255
 Arg Lys Glu Ser Val Val Val Ala Val Arg Gly Thr Met Ser Leu Gln
 260 265 270
 Asp Val Leu Thr Asp Leu Ser Ala Glu Ser Glu Val Leu Asp Val Glu
 275 280 285
 Cys Glu Val Gln Asp Arg Leu Ala His Lys Gly Ile Ser Gln Ala Ala
 290 295 300
 Arg Tyr Val Tyr Gln Arg Leu Ile Asn Asp Gly Ile Leu Ser Gln Ala
 305 310 315 320
 Phe Ser Ile Ala Pro Glu Tyr Arg Leu Val Ile Val Gly His Ser Leu
 325 330 335
 Gly Xaa Gly Ala Ala Ala Leu Leu Ala Thr Met Leu Arg Ala Ala Tyr
 340 345 350
 Pro Gln Val Arg Cys Tyr Ala Phe Ser Pro Pro Arg Gly Leu Trp Ser
 355 360 365
 Lys Ala Leu Gln Glu Tyr Ser Gln Ser Phe Ile Val Ser Leu Val Leu
 370 375 380
 Gly Lys Asp Val Ile Pro Arg Leu Ser Val Thr Asn Leu Glu Asp Leu
 385 390 395 400
 Lys Arg Arg Ile Leu Arg Val Val Ala His Cys Asn Lys Pro Lys Tyr
 405 410 415
 Lys Ile Leu Leu His Gly Leu Trp Tyr Glu Leu Phe Gly Gly Asn Pro
 420 425 430
 Asn Asn Leu Pro Ser Thr Arg Gly Leu Gln Cys Gly Arg Gly Leu Thr
 435 440 445
 Arg Ala Thr Gly Asn Cys Pro Arg Asn Asp Gly Leu Thr Leu Leu Ser
 450 455 460
 Leu Asn
 465

<210> 179

<211> 909

<212> DNA

254

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(909)

<221> misc_feature

<222> (1)...(909)

<223> n = A,T,C or G

<400> 179

| | |
|--|----|
| atg tcc cca agg act agg cca cgc agg tcc act ggc tat tct gag gtg | 48 |
| Met Ser Pro Arg Thr Arg Pro Arg Arg Ser Thr Gly Tyr Ser Glu Val | |
| 1 5 10 15 | |

| | |
|---|----|
| ata gtt gtc gtt gga gga tgt gag cga gtt gga gga ttt aat ctt cca | 96 |
| Ile Val Val Val Gly Gly Cys Glu Arg Val Gly Gly Phe Asn Leu Pro | |
| 20 25 30 | |

| | |
|---|-----|
| tac act gag tgc tac gat cct gta aca gga gaa tgg aag tct ttg gct | 144 |
| Tyr Thr Glu Cys Tyr Asp Pro Val Thr Gly Glu Trp Lys Ser Leu Ala | |
| 35 40 45 | |

| | |
|---|-----|
| aag ctt cca gaa ttt acc aaa tca gag tat gca gtc tgt gct cta agg | 192 |
| Lys Leu Pro Glu Phe Thr Lys Ser Glu Tyr Ala Val Cys Ala Leu Arg | |
| 50 55 60 | |

| | |
|--|-----|
| aat gac att ctt gtt tca ggt gga aga atc aac agc cgt gat gtc tgg | 240 |
| Asn Asp Ile Leu Val Ser Gly Gly Arg Ile Asn Ser Arg Asp Val Trp | |
| 65 70 75 80 | |

| | |
|---|-----|
| att tat aac tca cag tta aat att tgg ntc aga gtt gcc tct ctc aat | 288 |
| Ile Tyr Asn Ser Gln Leu Asn Ile Trp Xaa Arg Val Ala Ser Leu Asn | |
| 85 90 95 | |

| | |
|---|-----|
| aaa ggc aga tgg cgt cac aaa atg gct gtc ctc ctt ggt aaa gta tat | 336 |
| Lys Gly Arg Trp Arg His Lys Met Ala Val Leu Leu Gly Lys Val Tyr | |
| 100 105 110 | |

| | |
|---|-----|
| gtt gtc ggt ggc tat gat ggg caa aac aga ctt agc agc gta gaa tgt | 384 |
| Val Val Gly Gly Tyr Asp Gly Gln Asn Arg Leu Ser Ser Val Glu Cys | |
| 115 120 125 | |

| | |
|---|-----|
| tat gat tcc ttt tca aat cga tgg act gaa gtt gct ccc ctt aag gaa | 432 |
|---|-----|

255

| Tyr | Asp | Ser | Phe | Ser | Asn | Arg | Trp | Thr | Glu | Val | Ala | Pro | Leu | Lys | Glu | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 130 | | | | | | 135 | | | | | 140 | | | | | |
| gcc | gtg | agt | tct | cct | gca | gtg | act | agc | tgt | gta | ggc | aaa | ctg | ttt | gtg | 480 |
| Ala | Val | Ser | Ser | Pro | Ala | Val | Thr | Ser | Cys | Val | Gly | Lys | Leu | Phe | Val | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| att | ggc | gga | gga | cct | gat | gat | aat | act | tgt | tct | gat | aag | gtt | caa | tct | 528 |
| Ile | Gly | Gly | Gly | Pro | Asp | Asp | Asn | Thr | Cys | Ser | Asp | Lys | Val | Gln | Ser | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| tat | gat | cca | gaa | acc | aat | tct | tgg | cta | ctt | cgt | gca | gct | atc | cca | att | 576 |
| Tyr | Asp | Pro | Glu | Thr | Asn | Ser | Trp | Leu | Leu | Arg | Ala | Ala | Ile | Pro | Ile | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| gcc | aaa | agg | tgt | ata | aca | gct | gta | tcc | cta | aac | aac | ctg | atc | tat | gtt | 624 |
| Ala | Lys | Arg | Cys | Ile | Thr | Ala | Val | Ser | Leu | Asn | Asn | Leu | Ile | Tyr | Val | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| gcc | ggc | gga | ctg | acc | aag | gca | ata | tac | tgt | tac | gat | cca | gtt | gaa | gat | 672 |
| Ala | Gly | Gly | Leu | Thr | Lys | Ala | Ile | Tyr | Cys | Tyr | Asp | Pro | Val | Glu | Asp | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| tac | tgg | atg | cac | gta | cag | aat | aca | ttc | agc | cgt | cag | gaa | aac | tgt | ggc | 720 |
| Tyr | Trp | Met | His | Val | Gln | Asn | Thr | Phe | Ser | Arg | Gln | Glu | Asn | Cys | Gly | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| atg | tct | gtg | tgt | aat | ggc | aaa | ata | tat | atc | ctg | ggc | gga | aga | cgg | gaa | 768 |
| Met | Ser | Val | Cys | Asn | Gly | Lys | Ile | Tyr | Ile | Leu | Gly | Gly | Arg | Arg | Glu | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| aat | gga | gaa | gcc | aca | gac | act | att | ctc | tgt | tat | gat | cct | gca | aca | agt | 816 |
| Asn | Gly | Glu | Ala | Thr | Asp | Thr | Ile | Leu | Cys | Tyr | Asp | Pro | Ala | Thr | Ser | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| atc | atc | aca | ggg | gta | gct | gca | atg | ccc | agg | cca | gtg | tcc | tat | cat | ggc | 864 |
| Ile | Ile | Thr | Gly | Val | Ala | Ala | Met | Pro | Arg | Pro | Val | Ser | Tyr | His | Gly | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |
| tgt | gtg | act | att | cat | aga | tac | aat | gag | aaa | tgc | ttt | aaa | ctc | tga | | 909 |
| Cys | Val | Thr | Ile | His | Arg | Tyr | Asn | Glu | Lys | Cys | Phe | Lys | Leu | * | | |
| | 290 | | | | | | 295 | | | | 300 | | | | | |

256

<210> 180
 <211> 302
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(302)
 <223> Xaa = Any Amino Acid

<400> 180

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Pro | Arg | Thr | Arg | Pro | Arg | Arg | Ser | Thr | Gly | Tyr | Ser | Glu | Val |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Ile | Val | Val | Val | Gly | Gly | Cys | Glu | Arg | Val | Gly | Gly | Phe | Asn | Leu | Pro |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Tyr | Thr | Glu | Cys | Tyr | Asp | Pro | Val | Thr | Gly | Glu | Trp | Lys | Ser | Leu | Ala |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Lys | Leu | Pro | Glu | Phe | Thr | Lys | Ser | Glu | Tyr | Ala | Val | Cys | Ala | Leu | Arg |
| | 50 | | | | | 55 | | | | 60 | | | | | |
| Asn | Asp | Ile | Leu | Val | Ser | Gly | Gly | Arg | Ile | Asn | Ser | Arg | Asp | Val | Trp |
| 65 | | | | | 70 | | | | 75 | | | | | 80 | |
| Ile | Tyr | Asn | Ser | Gln | Leu | Asn | Ile | Trp | Xaa | Arg | Val | Ala | Ser | Leu | Asn |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Lys | Gly | Arg | Trp | Arg | His | Lys | Met | Ala | Val | Leu | Leu | Gly | Lys | Val | Tyr |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Val | Val | Gly | Gly | Tyr | Asp | Gly | Gln | Asn | Arg | Leu | Ser | Ser | Val | Glu | Cys |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Tyr | Asp | Ser | Phe | Ser | Asn | Arg | Trp | Thr | Glu | Val | Ala | Pro | Leu | Lys | Glu |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Ala | Val | Ser | Ser | Pro | Ala | Val | Thr | Ser | Cys | Val | Gly | Lys | Leu | Phe | Val |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Ile | Gly | Gly | Gly | Pro | Asp | Asp | Asn | Thr | Cys | Ser | Asp | Lys | Val | Gln | Ser |
| | | | 165 | | | | | 170 | | | | | | 175 | |
| Tyr | Asp | Pro | Glu | Thr | Asn | Ser | Trp | Leu | Leu | Arg | Ala | Ala | Ile | Pro | Ile |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Ala | Lys | Arg | Cys | Ile | Thr | Ala | Val | Ser | Leu | Asn | Asn | Leu | Ile | Tyr | Val |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Ala | Gly | Gly | Leu | Thr | Lys | Ala | Ile | Tyr | Cys | Tyr | Asp | Pro | Val | Glu | Asp |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Tyr | Trp | Met | His | Val | Gln | Asn | Thr | Phe | Ser | Arg | Gln | Glu | Asn | Cys | Gly |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Met | Ser | Val | Cys | Asn | Gly | Lys | Ile | Tyr | Ile | Leu | Gly | Gly | Arg | Arg | Glu |
| | | | 245 | | | | | | 250 | | | | | 255 | |
| Asn | Gly | Glu | Ala | Thr | Asp | Thr | Ile | Leu | Cys | Tyr | Asp | Pro | Ala | Thr | Ser |

257

260 265 270
 Ile Ile Thr Gly Val Ala Ala Met Pro Arg Pro Val Ser Tyr His Gly
 275 280 285
 Cys Val Thr Ile His Arg Tyr Asn Glu Lys Cys Phe Lys Leu
 290 295 300

<210> 181
 <211> 405
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(405)
 <221> misc_feature
 <222> (1)...(405)
 <223> n = A,T,C or G

<400> 181
 atg ccg ctc cta cga gga ctg ctg tgg ctc cag gtg ctg tgt gcg ggc 48
 Met Pro Leu Leu Arg Gly Leu Leu Trp Leu Gln Val Leu Cys Ala Gly
 1 5 10 15
 cct ctc cat aca gag gct gtg gta ctt ctg gtt cct tct gat gat ggg 96
 Pro Leu His Thr Glu Ala Val Val Leu Leu Val Pro Ser Asp Asp Gly
 20 25 30
 cgt gct ttt ctg ctg cgg anc ggc ttc ttc atc cgg agg cgc atg tac 144
 Arg Ala Phe Leu Leu Arg Xaa Gly Phe Phe Ile Arg Arg Arg Met Tyr
 35 40 45
 ccc ccg ccg ctg atc gag gag cca gcc ttc aat gtg tcc tac acc agg 192
 Pro Pro Pro Leu Ile Glu Glu Pro Ala Phe Asn Val Ser Tyr Thr Arg
 50 55 60
 cag ccc cca aat ccc ggc cca gga gcc cag cag ccg ggg ccg ccc tat 240
 Gln Pro Pro Asn Pro Gly Pro Gly Ala Gln Gln Pro Gly Pro Pro Tyr
 65 70 75 80
 tac acc gac cca gga gga ccg ggg atg aac cct gtc ggg aat tcc atg 288
 Tyr Thr Asp Pro Gly Gly Pro Gly Met Asn Pro Val Gly Asn Ser Met
 85 90 95

258

gca atg gct ttc cag gtc cca ccc aac tca ccc cag ggg agt gtg gcc 336
 Ala Met Ala Phe Gln Val Pro Pro Asn Ser Pro Gln Gly Ser Val Ala
 100 105 110

tgc ccg ccc cct cca gcc tac tgc aac acg cct ccg ccc ccg tac gaa 384
 Cys Pro Pro Pro Pro Ala Tyr Cys Asn Thr Pro Pro Pro Pro Tyr Glu
 115 120 125

cag gta gtg aag gcc aag tag 405
 Gln Val Val Lys Ala Lys *
 130

<210> 182

<211> 134

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(134)

<223> Xaa = Any Amino Acid

<400> 182

Met Pro Leu Leu Arg Gly Leu Leu Trp Leu Gln Val Leu Cys Ala Gly
 1 5 10 15
 Pro Leu His Thr Glu Ala Val Val Leu Leu Val Pro Ser Asp Asp Gly
 20 25 30
 Arg Ala Phe Leu Leu Arg Xaa Gly Phe Phe Ile Arg Arg Arg Met Tyr
 35 40 45
 Pro Pro Pro Leu Ile Glu Glu Pro Ala Phe Asn Val Ser Tyr Thr Arg
 50 55 60
 Gln Pro Pro Asn Pro Gly Pro Gly Ala Gln Gln Pro Gly Pro Pro Tyr
 65 70 75 80
 Tyr Thr Asp Pro Gly Gly Pro Gly Met Asn Pro Val Gly Asn Ser Met
 85 90 95
 Ala Met Ala Phe Gln Val Pro Pro Asn Ser Pro Gln Gly Ser Val Ala
 100 105 110
 Cys Pro Pro Pro Pro Ala Tyr Cys Asn Thr Pro Pro Pro Pro Tyr Glu
 115 120 125
 Gln Val Val Lys Ala Lys
 130

<210> 183

```
<211> 900
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> CDS  
<222> (1)...(900)
```

```
<221> misc_feature
<222> (1)...(900)
<223> n = A,T,C or G
```

| | | | | | | | | | | | | | | | | | |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| <400> 183 | | | | | | | | | | | | | | | | | |
| atg | gag | aga | gcg | ttc | cag | aca | gct | ctg | tgg | ttg | ctg | cag | ccg | gaa | gtc | 48 | |
| Met | Glu | Arg | Ala | Phe | Gln | Thr | Ala | Leu | Trp | Leu | Leu | Gln | Pro | Glu | Val | | |
| 1 | | | 5 | | | 10 | | | 15 | | | | | | | | |
| | | | | | | | | | | | | | | | | | |
| gtc | ttc | atc | ctg | ggg | gat | atc | ttt | gat | gaa | ggg | aag | tgg | agc | acc | cct | 96 | |
| Val | Phe | Ile | Leu | Gly | Asp | Ile | Phe | Asp | Glu | Gly | Lys | Trp | Ser | Thr | Pro | | |
| | | | 20 | | | 25 | | | 30 | | | | | | | | |
| | | | | | | | | | | | | | | | | | |
| nag | gcc | tgg | gcg | gat | gat | gtg | gag | cgg | ttt | cag | aaa | atg | ttc | aga | cac | 144 | |
| Xaa | Ala | Trp | Ala | Asp | Asp | Val | Glu | Arg | Phe | Gln | Lys | Met | Phe | Arg | His | | |
| 35 | | | 40 | | | 45 | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | |
| cca | agt | cat | gta | cag | ctg | aag | gta | gtt | gct | gga | aac | cat | gac | att | ggc | 192 | |
| Pro | Ser | His | Val | Gln | Leu | Lys | Val | Val | Ala | Gly | Asn | His | Asp | Ile | Gly | | |
| 50 | | | 55 | | | 60 | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | |
| ttc | cat | tat | gag | atg | aac | aca | tac | aaa | gta | gaa | cgc | ttt | gag | aaa | gtg | 240 | |
| Phe | His | Tyr | Glu | Met | Asn | Thr | Tyr | Lys | Val | Glu | Arg | Phe | Glu | Lys | Val | | |
| 65 | | | 70 | | | 75 | | | 80 | | | | | | | | |
| | | | | | | | | | | | | | | | | | |
| ttc | agc | tct | gaa | aga | ctg | ttt | tct | tgg | aaa | ggc | att | aac | ttt | gtg | atg | 288 | |
| Phe | Ser | Ser | Glu | Arg | Leu | Phe | Ser | Trp | Lys | Gly | Ile | Asn | Phe | Val | Met | | |
| | | | 85 | | | 90 | | | 95 | | | | | | | | |
| | | | | | | | | | | | | | | | | | |
| gtc | aac | agc | gtg | gcg | ctg | aac | ggg | gat | ggc | tgt | ggc | atc | tgc | tct | gaa | 336 | |
| Val | Asn | Ser | Val | Ala | Leu | Asn | Gly | Asp | Gly | Cys | Gly | Ile | Cys | Ser | Glu | | |
| 100 | | | 105 | | | 110 | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | |
| aca | gaa | gca | gag | ctc | att | gaa | gtt | tct | cac | aga | ctg | aac | tgc | tcc | cga | 384 | |
| Thr | Glu | Ala | Glu | Leu | Ile | Glu | Val | Ser | His | Arg | Leu | Asn | Cys | Ser | Arg | | |
| 115 | | | 120 | | | 125 | | | | | | | | | | | |

260

| | |
|---|-----|
| gag gca cgt ggc tcc agc cgg tgt gga cct ggg cct ctg ctg ccc acg Glu Ala Arg Gly Ser Ser Arg Cys Gly Pro Gly Pro Leu Leu Pro Thr 130 135 140 | 432 |
| tct gcc cct gtc ctc ctg cag cat tat cct ctg tat cgg aga agt gat Ser Ala Pro Val Leu Leu Gln His Tyr Pro Leu Tyr Arg Arg Ser Asp 145 150 155 160 | 480 |
| gct aac tgt tct ggg gaa gac gct gct cct gca gag gaa agg gac atc Ala Asn Cys Ser Gly Glu Asp Ala Ala Pro Ala Glu Glu Arg Asp Ile 165 170 175 | 528 |
| cca ttt aag gag aac tat gac gtg ctt tca cgg gag gca tca caa aag Pro Phe Lys Glu Asn Tyr Asp Val Leu Ser Arg Glu Ala Ser Gln Lys 180 185 190 | 576 |
| ctg ctg tgg tgg ctc cag ccg cgc ctg gtt ctc agt ggc cac acg cac Leu Leu Trp Trp Leu Gln Pro Arg Leu Val Leu Ser Gly His Thr His 195 200 205 | 624 |
| agc gcc tgc gag gtg cac cac ggg ggc cga gtc ccc gag ctc agc gtc Ser Ala Cys Glu Val His His Gly Gly Arg Val Pro Glu Leu Ser Val 210 215 220 | 672 |
| cca tct ttc agt tgg agg aac aga aac aac ccc agt ttc atc atg ggt Pro Ser Phe Ser Trp Arg Asn Arg Asn Asn Pro Ser Phe Ile Met Gly 225 230 235 240 | 720 |
| agc atc acg ccc aca gac tac acc ctc tcc aag tgc tac ctc cca cgt Ser Ile Thr Pro Thr Asp Tyr Thr Leu Ser Lys Cys Tyr Leu Pro Arg 245 250 255 | 768 |
| gag gat gtg gtt ttg atc atc tac tgt gga gtg gtg ggc ttc ctt gtg Glu Asp Val Val Leu Ile Ile Tyr Cys Gly Val Val Gly Phe Leu Val 260 265 270 | 816 |
| gtc ctc aca ctc act cac ttt ggg ctt cta gcc tca cct ttt ctt tct Val Leu Thr Leu Thr His Phe Gly Leu Leu Ala Ser Pro Phe Leu Ser 275 280 285 | 864 |
| ggt ttg aac ttg ctc gga aag cgt aag aca aga tga Gly Leu Asn Leu Leu Gly Lys Arg Lys Thr Arg * | 900 |
| 290 295 | |

261

<210> 184

<211> 299

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(299)

<223> Xaa = Any Amino Acid

<400> 184.

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Met Glu Arg Ala Phe Gln Thr Ala Leu Trp Leu Leu Gln Pro Glu Val
 1           5           10          15
Val Phe Ile Leu Gly Asp Ile Phe Asp Glu Gly Lys Trp Ser Thr Pro
 20          25          30
Xaa Ala Trp Ala Asp Asp Val Glu Arg Phe Gln Lys Met Phe Arg His
 35          40          45
Pro Ser His Val Gln Leu Lys Val Val Ala Gly Asn His Asp Ile Gly
 50          55          60
Phe His Tyr Glu Met Asn Thr Tyr Lys Val Glu Arg Phe Glu Lys Val
 65          70          75          80
Phe Ser Ser Glu Arg Leu Phe Ser Trp Lys Gly Ile Asn Phe Val Met
 85          90          95
Val Asn Ser Val Ala Leu Asn Gly Asp Gly Cys Gly Ile Cys Ser Glu
 100         105         110
Thr Glu Ala Glu Leu Ile Glu Val Ser His Arg Leu Asn Cys Ser Arg
 115         120         125
Glu Ala Arg Gly Ser Ser Arg Cys Gly Pro Gly Pro Leu Leu Pro Thr
 130         135         140
Ser Ala Pro Val Leu Leu Gln His Tyr Pro Leu Tyr Arg Arg Ser Asp
 145         150         155         160
Ala Asn Cys Ser Gly Glu Asp Ala Ala Pro Ala Glu Glu Arg Asp Ile
 165         170         175
Pro Phe Lys Glu Asn Tyr Asp Val Leu Ser Arg Glu Ala Ser Gln Lys
 180         185         190
Leu Leu Trp Trp Leu Gln Pro Arg Leu Val Leu Ser Gly His Thr His
 195         200         205
Ser Ala Cys Glu Val His His Gly Gly Arg Val Pro Glu Leu Ser Val
 210         215         220
Pro Ser Phe Ser Trp Arg Asn Arg Asn Asn Pro Ser Phe Ile Met Gly
 225         230         235         240
Ser Ile Thr Pro Thr Asp Tyr Thr Leu Ser Lys Cys Tyr Leu Pro Arg

```

262

245 250 255
 Glu Asp Val Val Leu Ile Ile Tyr Cys Gly Val Val Gly Phe Leu Val
 260 265 270
 Val Leu Thr Leu Thr His Phe Gly Leu Leu Ala Ser Pro Phe Leu Ser
 275 280 285
 Gly Leu Asn Leu Leu Gly Lys Arg Lys Thr Arg
 290 295

<210> 185
 <211> 453
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(453)

<400> 185

| | |
|---|-----|
| atg tca gca tgt ttg gca ttg gag cgg gtt gca gct ggc caa ggg ctg | 48 |
| Met Ser Ala Cys Leu Ala Leu Glu Arg Val Ala Ala Gly Gln Gly Leu | |
| 1 5 10 15 | |
| cct act gaa tca ctc ttc tat cgt gct gtt ctt cag gat att att aaa | 96 |
| Pro Thr Glu Ser Leu Phe Tyr Arg Ala Val Leu Gln Asp Ile Ile Lys | |
| 20 25 30 | |
| gat tgt tat ggc atc acc aaa tgt gat cgg cat gtt ggt aaa att tat | 144 |
| Asp Cys Tyr Gly Ile Thr Lys Cys Asp Arg His Val Gly Lys Ile Tyr | |
| 35 40 45 | |
| tcc aaa tgt tct tct ttt ctg gat tat gtc aga cgg tct cta aag aag | 192 |
| Ser Lys Cys Ser Ser Phe Leu Asp Tyr Val Arg Arg Ser Leu Lys Lys | |
| 50 55 60 | |
| ctt gga tta gat gag tcc aag ctg cca gaa aaa att ata atg aac tac | 240 |
| Leu Gly Leu Asp Glu Ser Lys Leu Pro Glu Lys Ile Ile Met Asn Tyr | |
| 65 70 75 80 | |
| tac gag aag tat aag cct cga atg aat gag ctg gaa gct ttt aat atg | 288 |
| Tyr Glu Lys Tyr Lys Pro Arg Met Asn Glu Leu Glu Ala Phe Asn Met | |
| 85 90 95 | |
| ttg aaa gtt gta ctg gct ccc tgt ata gag act ttg att ctt ctg gat | 336 |
| Leu Lys Val Val Leu Ala Pro Cys Ile Glu Thr Leu Ile Leu Leu Asp | |

263

| 100 | 105 | 110 | |
|---|-----|-----|-----|
| cga ctt tgt tac ctg aaa gag cag gaa gat att gca tgg tct gct ctt | | | 384 |
| Arg Leu Cys Tyr Leu Lys Glu Gln Glu Asp Ile Ala Trp Ser Ala Leu | | | |
| 115 | 120 | 125 | |
| gtg aag ttg ttt gat ccc gtg aaa tct ccc aga tgt tat gct gtt att | | | 432 |
| Val Lys Leu Phe Asp Pro Val Lys Ser Pro Arg Cys Tyr Ala Val Ile | | | |
| 130 | 135 | 140 | |
| gcc ctg aag aag cag cag tga | | | 453 |
| Ala Leu Lys Lys Gln Gln * | | | |
| 145 | 150 | | |

<210> 186
 <211> 150
 <212> PRT
 <213> Homo sapiens

<400> 186

| | | | |
|---|-----|-----|----|
| Met Ser Ala Cys Leu Ala Leu Glu Arg Val Ala Ala Gly Gln Gly Leu | | | |
| 1 | 5 | 10 | 15 |
| Pro Thr Glu Ser Leu Phe Tyr Arg Ala Val Leu Gln Asp Ile Ile Lys | | | |
| 20 | 25 | 30 | |
| Asp Cys Tyr Gly Ile Thr Lys Cys Asp Arg His Val Gly Lys Ile Tyr | | | |
| 35 | 40 | 45 | |
| Ser Lys Cys Ser Ser Phe Leu Asp Tyr Val Arg Arg Ser Leu Lys Lys | | | |
| 50 | 55 | 60 | |
| Leu Gly Leu Asp Glu Ser Lys Leu Pro Glu Lys Ile Ile Met Asn Tyr | | | |
| 65 | 70 | 75 | 80 |
| Tyr Glu Lys Tyr Lys Pro Arg Met Asn Glu Leu Glu Ala Phe Asn Met | | | |
| 85 | 90 | 95 | |
| Leu Lys Val Val Leu Ala Pro Cys Ile Glu Thr Leu Ile Leu Leu Asp | | | |
| 100 | 105 | 110 | |
| Arg Leu Cys Tyr Leu Lys Glu Gln Glu Asp Ile Ala Trp Ser Ala Leu | | | |
| 115 | 120 | 125 | |
| Val Lys Leu Phe Asp Pro Val Lys Ser Pro Arg Cys Tyr Ala Val Ile | | | |
| 130 | 135 | 140 | |
| Ala Leu Lys Lys Gln Gln | | | |
| 145 | 150 | | |

<210> 187
 <211> 1491

264

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1491)

<400> 187

atg gcg ctg tgg cgc ggc tcc gcg tac gcg ggc ttc ctg gcg ctg gcc 48
Met Ala Leu Trp Arg Gly Ser Ala Tyr Ala Gly Phe Leu Ala Leu Ala
1 5 10 15

gtg ggc tgc gtc ttc ctg ctg gag cca gag ctg cca ggc tcg gcg ctg 96
Val Gly Cys Val Phe Leu Leu Glu Pro Glu Leu Pro Gly Ser Ala Leu
20 25 30

cgc tct ctc tgg agc tcg ctg tgt ctg ggg ccc gcg cct gcg ccc ccg 144
Arg Ser Leu Trp Ser Ser Leu Cys Leu Gly Pro Ala Pro Ala Pro Pro
35 40 45

gga ccc gtc tcc ccc gag ggc cgg ttg gcg gca gcc tgg gac gcg ctt 192
Gly Pro Val Ser Pro Glu Gly Arg Leu Ala Ala Ala Trp Asp Ala Leu
50 55 60

atc gtg cgg cca gtc cgg cgc tgg cgc cgc gtg gca gtg gga gtc aat 240
Ile Val Arg Pro Val Arg Arg Trp Arg Arg Val Ala Val Gly Val Asn
65 70 75 80

gca tgt gtt gat gtg gtg ctc tca ggg gtg aag ctc ttg cag gca ctt 288
Ala Cys Val Asp Val Val Leu Ser Gly Val Lys Leu Leu Gln Ala Leu
85 90 95

ggc ctt agt cct ggg aat ggg aaa gat cac agc att ctg cat tca agg 336
Gly Leu Ser Pro Gly Asn Gly Lys Asp His Ser Ile Leu His Ser Arg
100 105 110

aat gat ctg gaa gaa gcc ttc att cac ttc atg ggg aag gga gca gct 384
Asn Asp Leu Glu Glu Ala Phe Ile His Phe Met Gly Lys Gly Ala Ala
115 120 125

gct gag cgc ttc ttc agt gat aag gaa act ttt cac gac att gcc cag 432
Ala Glu Arg Phe Phe Ser Asp Lys Glu Thr Phe His Asp Ile Ala Gln
130 135 140

| | |
|---|-----|
| gtt gcg tca gag ttc cca gga gcc cag cac tat gta gga gga aat gca Val Ala Ser Glu Phe Pro Gly Ala Gln His Tyr Val Gly Gly Asn Ala 145 150 155 160 | 480 |
| gct tta att gga cag aaa ttt gca gcc aac tca gat tta aag gtt ctt Ala Leu Ile Gly Gln Lys Phe Ala Ala Asn Ser Asp Leu Lys Val Leu 165 170 175 | 528 |
| ctt tgc ggt cca gtt ggt cca aag cta cat gag ctt ctt gat gac aat Leu Cys Gly Pro Val Gly Pro Lys Leu His Glu Leu Leu Asp Asp Asn 180 185 190 | 576 |
| gtc ttt gtt cca cca gag tca ttg cag gaa gtg gat gag ttc cac ctc Val Phe Val Pro Pro Glu Ser Leu Gln Glu Val Asp Glu Phe His Leu 195 200 205 | 624 |
| att tta gag tat caa gca ggg gag gag tgg ggc cag tta aaa gct ccc Ile Leu Glu Tyr Gln Ala Gly Glu Glu Trp Gly Gln Leu Lys Ala Pro 210 215 220 | 672 |
| cat gcc aac cga ttc atc ttc tct cac gac ctc tcc aac ggg gcc atg His Ala Asn Arg Phe Ile Phe Ser His Asp Leu Ser Asn Gly Ala Met 225 230 235 240 | 720 |
| aat atg ctg gag gtg ttt gtg tct agc ctg gag gag ttt cag cca gac Asn Met Leu Glu Val Phe Val Ser Ser Leu Glu Glu Phe Gln Pro Asp 245 250 255 | 768 |
| ctg gtg gtc ctc tct gga ttg cac atg atg gag gga caa agc aag gag Leu Val Val Leu Ser Gly Leu His Met Met Glu Gly Gln Ser Lys Glu 260 265 270 | 816 |
| ctc cag agg aag aga ctc ttg gag gtt gta acc tcc att tct gac atc Leu Gln Arg Lys Arg Leu Leu Glu Val Val Thr Ser Ile Ser Asp Ile 275 280 285 | 864 |
| ccc act ggt att cca gtt cac cta gag ctg gcc agt atg act aac agg Pro Thr Gly Ile Pro Val His Leu Glu Leu Ala Ser Met Thr Asn Arg 290 295 300 | 912 |
| gag ctc atg agc agc att gtc cat cag gtc ttt ccc gcg gtg act tcc Glu Leu Met Ser Ser Ile Val His Gln Val Phe Pro Ala Val Thr Ser 305 310 315 320 | 960 |

266

| | |
|---|------|
| ctt ggg ctg aat gaa cag gag ctg tta ttt ctc acc cag tca gcc tct Leu Gly Leu Asn Glu Gln Glu Leu Leu Phe Leu Thr Gln Ser Ala Ser 325 330 335 | 1008 |
| gga cct cac tct tct ctc tct tcc tgg aac ggt gtt cct gat gtg ggc Gly Pro His Ser Ser Leu Ser Ser Trp Asn Gly Val Pro Asp Val Gly 340 345 350 | 1056 |
| atg gtc agt gac atc ctc ttc tgg atc ttg aaa gaa cat ggg agg agt Met Val Ser Asp Ile Leu Phe Trp Ile Leu Lys Glu His Gly Arg Ser 355 360 365 | 1104 |
| aaa agc aga gcc tcg gat ctc acc agg atc cat ttc cac acg ctg gtc Lys Ser Arg Ala Ser Asp Leu Thr Arg Ile His Phe His Thr Leu Val 370 375 380 | 1152 |
| tac cac atc ctg gca act gtg gat gga cac tgg gcc aac cag ctg gca Tyr His Ile Leu Ala Thr Val Asp Gly His Trp Ala Asn Gln Leu Ala 385 390 395 400 | 1200 |
| gcc gtg gct gca gga gct cgt gtg gct ggg aca cag gcc tgc gcc aca Ala Val Ala Ala Gly Ala Arg Val Ala Gly Thr Gln Ala Cys Ala Thr 405 410 415 | 1248 |
| gaa acc ata gac acc agc cga gtg tct ctg agg gca ccc caa gag ttc Glu Thr Ile Asp Thr Ser Arg Val Ser Leu Arg Ala Pro Gln Glu Phe 420 425 430 | 1296 |
| atg act tcc cat tcg gag gca ggc tcc agg att gta tta aac cca aac Met Thr Ser His Ser Glu Ala Gly Ser Arg Ile Val Leu Asn Pro Asn 435 440 445 | 1344 |
| aag cca gta gta gaa tgg cac aga gag gga ata tcc ttc cac ttc aca Lys Pro Val Val Glu Trp His Arg Glu Gly Ile Ser Phe His Phe Thr 450 455 460 | 1392 |
| cca gta ttg gtg tgt aaa gac ccc att cga act gta ggc ctt gga gat Pro Val Leu Val Cys Lys Asp Pro Ile Arg Thr Val Gly Leu Gly Asp 465 470 475 480 | 1440 |
| gcc att tca gcc gaa gga ctc ttc tat tcg gaa gta cac cct cac tat Ala Ile Ser Ala Glu Gly Leu Phe Tyr Ser Glu Val His Pro His Tyr 485 490 495 | 1488 |

267

tag
*

1491

<210> 188
 <211> 496
 <212> PRT
 <213> Homo sapiens

<400> 188

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Met Ala Leu Trp Arg Gly Ser Ala Tyr Ala Gly Phe Leu Ala Leu Ala
 1      5      10      15
Val Gly Cys Val Phe Leu Leu Glu Pro Glu Leu Pro Gly Ser Ala Leu
 20     25     30
Arg Ser Leu Trp Ser Ser Leu Cys Leu Gly Pro Ala Pro Ala Pro Pro
 35     40     45
Gly Pro Val Ser Pro Glu Gly Arg Leu Ala Ala Ala Trp Asp Ala Leu
 50     55     60
Ile Val Arg Pro Val Arg Arg Trp Arg Arg Val Ala Val Gly Val Asn
 65     70     75     80
Ala Cys Val Asp Val Val Leu Ser Gly Val Lys Leu Leu Gln Ala Leu
 85     90     95
Gly Leu Ser Pro Gly Asn Gly Lys Asp His Ser Ile Leu His Ser Arg
 100    105    110
Asn Asp Leu Glu Glu Ala Phe Ile His Phe Met Gly Lys Gly Ala Ala
 115    120    125
Ala Glu Arg Phe Phe Ser Asp Lys Glu Thr Phe His Asp Ile Ala Gln
 130    135    140
Val Ala Ser Glu Phe Pro Gly Ala Gln His Tyr Val Gly Gly Asn Ala
 145    150    155    160
Ala Leu Ile Gly Gln Lys Phe Ala Ala Asn Ser Asp Leu Lys Val Leu
 165    170    175
Leu Cys Gly Pro Val Gly Pro Lys Leu His Glu Leu Leu Asp Asp Asn
 180    185    190
Val Phe Val Pro Pro Glu Ser Leu Gln Glu Val Asp Glu Phe His Leu
 195    200    205
Ile Leu Glu Tyr Gln Ala Gly Glu Glu Trp Gly Gln Leu Lys Ala Pro
 210    215    220
His Ala Asn Arg Phe Ile Phe Ser His Asp Leu Ser Asn Gly Ala Met
 225    230    235    240
Asn Met Leu Glu Val Phe Val Ser Ser Leu Glu Glu Phe Gln Pro Asp
 245    250    255
Leu Val Val Leu Ser Gly Leu His Met Met Glu Gly Gln Ser Lys Glu

```

268

260 265 270
 Leu Gln Arg Lys Arg Leu Leu Glu Val Val Thr Ser Ile Ser Asp Ile
 275 280 285
 Pro Thr Gly Ile Pro Val His Leu Glu Leu Ala Ser Met Thr Asn Arg
 290 295 300
 Glu Leu Met Ser Ser Ile Val His Gln Val Phe Pro Ala Val Thr Ser
 305 310 315 320
 Leu Gly Leu Asn Glu Gln Glu Leu Leu Phe Leu Thr Gln Ser Ala Ser
 325 330 335
 Gly Pro His Ser Ser Leu Ser Ser Trp Asn Gly Val Pro Asp Val Gly
 340 345 350
 Met Val Ser Asp Ile Leu Phe Trp Ile Leu Lys Glu His Gly Arg Ser
 355 360 365
 Lys Ser Arg Ala Ser Asp Leu Thr Arg Ile His Phe His Thr Leu Val
 370 375 380
 Tyr His Ile Leu Ala Thr Val Asp Gly His Trp Ala Asn Gln Leu Ala
 385 390 395 400
 Ala Val Ala Ala Gly Ala Arg Val Ala Gly Thr Gln Ala Cys Ala Thr
 405 410 415
 Glu Thr Ile Asp Thr Ser Arg Val Ser Leu Arg Ala Pro Gln Glu Phe
 420 425 430
 Met Thr Ser His Ser Glu Ala Gly Ser Arg Ile Val Leu Asn Pro Asn
 435 440 445
 Lys Pro Val Val Glu Trp His Arg Glu Gly Ile Ser Phe His Phe Thr
 450 455 460
 Pro Val Leu Val Cys Lys Asp Pro Ile Arg Thr Val Gly Leu Gly Asp
 465 470 475 480
 Ala Ile Ser Ala Glu Gly Leu Phe Tyr Ser Glu Val His Pro His Tyr
 485 490 495

<210> 189
 <211> 339
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(339)

<400> 189

atg ggg tct cgg ttg tcc cag cct ttt gag tcc tat atc act gcg cct
 Met Gly Ser Arg Leu Ser Gln Pro Phe Glu Ser Tyr Ile Thr Ala Pro
 1 5 10 15

48

269

ccc ggt acc gcc gcc gcg ccc gcc aaa cct gcg ccc cca gct aca ccc 96
 Pro Gly Thr Ala Ala Pro Ala Lys Pro Ala Pro Pro Ala Thr Pro
 20 25 30

gga gcg ccg acc tcc cca gca gaa cac cgc ctg ttg aag acc tgc tgg 144
 Gly Ala Pro Thr Ser Pro Ala Glu His Arg Leu Leu Lys Thr Cys Trp
 35 40 45

agc tgt cgc gtg ctt tct ggg ttg ggg ctg atg ggg gcg ggc ggg tac 192
 Ser Cys Arg Val Leu Ser Gly Leu Gly Leu Met Gly Ala Gly Gly Tyr
 50 55 60

gtg tac tgg gtg gca cgg aag ccc atg aag atg gga tac ccc ccg agt 240
 Val Tyr Trp Val Ala Arg Lys Pro Met Lys Met Gly Tyr Pro Pro Ser
 65 70 75 80

cca tgg acc att acg cag atg gtc atc ggc ctc agc att gcc acc tgg 288
 Pro Trp Thr Ile Thr Gln Met Val Ile Gly Leu Ser Ile Ala Thr Trp
 85 90 95

ggt atc gtt gtc atg gca gac ccc aaa ggg aag gcc tac cgc gtt gtt 336
 Gly Ile Val Val Met Ala Asp Pro Lys Gly Lys Ala Tyr Arg Val Val
 100 105 110

tga 339
 *

<210> 190
 <211> 112
 <212> PRT
 <213> Homo sapiens

<400> 190
 Met Gly Ser Arg Leu Ser Gln Pro Phe Glu Ser Tyr Ile Thr Ala Pro
 1 5 10 15
 Pro Gly Thr Ala Ala Ala Pro Ala Lys Pro Ala Pro Pro Ala Thr Pro
 20 25 30
 Gly Ala Pro Thr Ser Pro Ala Glu His Arg Leu Leu Lys Thr Cys Trp
 35 40 45
 Ser Cys Arg Val Leu Ser Gly Leu Gly Leu Met Gly Ala Gly Gly Tyr
 50 55 60
 Val Tyr Trp Val Ala Arg Lys Pro Met Lys Met Gly Tyr Pro Pro Ser

270

65 70 75 80
 Pro Trp Thr Ile Thr Gln Met Val Ile Gly Leu Ser Ile Ala Thr Trp
 85 90 95
 Gly Ile Val Val Met Ala Asp Pro Lys Gly Lys Ala Tyr Arg Val Val
 100 105 110

<210> 191
 <211> 630
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(630)

<400> 191

atg gcg gcg gcc atg gca gca tct tcc ctg acg gtc acc tta ggg cgg 48
 Met Ala Ala Ala Met Ala Ala Ser Ser Leu Thr Val Thr Leu Gly Arg
 1 5 10 15

ctg gcg tcc gcg tgc agc cac agc atc ctg aga cct tcg ggg ccc gga 96
 Leu Ala Ser Ala Cys Ser His Ser Ile Leu Arg Pro Ser Gly Pro Gly
 20 25 30

gca gcc tcc ctt tgg tct gct tct cga agg ttc aat tca cag agc act 144
 Ala Ala Ser Leu Trp Ser Ala Ser Arg Arg Phe Asn Ser Gln Ser Thr
 35 40 45

tca tat cta cca gga tat gtt cct aaa aca tcc ctg agt tca cca cct 192
 Ser Tyr Leu Pro Gly Tyr Val Pro Lys Thr Ser Leu Ser Ser Pro Pro
 50 55 60

tgg cca gaa gtt gtt ctg cca gac cca gtt gag gag acc aga cac cat 240
 Trp Pro Glu Val Val Leu Pro Asp Pro Val Glu Glu Thr Arg His His
 65 70 75 80

gca gag gtc gtg aag aag gtg aat gag atg atc gtc acg ggg cag tat 288
 Ala Glu Val Val Lys Lys Val Asn Glu Met Ile Val Thr Gly Gln Tyr
 85 90 95

ggc agg ctc ttt gcc gtg gtg cac ttt gcc agc cgc cag tgg aag gtg 336
 Gly Arg Leu Phe Ala Val Val His Phe Ala Ser Arg Gln Trp Lys Val
 100 105 110

271

| | |
|---|-----|
| acc tct gaa gac ctg atc tta att gga aat gaa cta gac ctt gcg tgt | 384 |
| Thr Ser Glu Asp Leu Ile Leu Ile Gly Asn Glu Leu Asp Leu Ala Cys | |
| 115 120 125 | |
| gga gag aga att cga ctg gag aag gtc ctg ctg gtt ggg gca gac aac | 432 |
| Gly Glu Arg Ile Arg Leu Glu Lys Val Leu Leu Val Gly Ala Asp Asn | |
| 130 135 140 | |
| ttc acg ctg ctt ggc aag cca ctc ctc gga aag gat ctt gtt cga gta | 480 |
| Phe Thr Leu Leu Gly Lys Pro Leu Leu Gly Lys Asp Leu Val Arg Val | |
| 145 150 155 160 | |
| gaa gcc aca gtc att gaa aag aca gaa tca tgg cca aga atc att atg | 528 |
| Glu Ala Thr Val Ile Glu Lys Thr Glu Ser Trp Pro Arg Ile Ile Met | |
| 165 170 175 | |
| aga ttc agg aaa agg aaa aac ttc aag aag aaa aga atc gtc acg acc | 576 |
| Arg Phe Arg Lys Arg Lys Asn Phe Lys Lys Lys Arg Ile Val Thr Thr | |
| 180 185 190 | |
| ccg cag act gtc ctc cgg ata aac agc att gag att gct ccg tgt ttg | 624 |
| Pro Gln Thr Val Leu Arg Ile Asn Ser Ile Glu Ile Ala Pro Cys Leu | |
| 195 200 205 | |
| ttg tga | 630 |
| Leu * | |

<210> 192
 <211> 209
 <212> PRT
 <213> Homo sapiens

<400> 192
 Met Ala Ala Ala Met Ala Ala Ser Ser Leu Thr Val Thr Leu Gly Arg
 1 5 10 15
 Leu Ala Ser Ala Cys Ser His Ser Ile Leu Arg Pro Ser Gly Pro Gly
 20 25 30
 Ala Ala Ser Leu Trp Ser Ala Ser Arg Arg Phe Asn Ser Gln Ser Thr
 35 40 45
 Ser Tyr Leu Pro Gly Tyr Val Pro Lys Thr Ser Leu Ser Ser Pro Pro
 50 55 60
 Trp Pro Glu Val Val Leu Pro Asp Pro Val Glu Glu Thr Arg His His

272

65 70 75 80
 Ala Glu Val Val Lys Lys Val Asn Glu Met Ile Val Thr Gly Gln Tyr
 85 90 95
 Gly Arg Leu Phe Ala Val Val His Phe Ala Ser Arg Gln Trp Lys Val
 100 105 110
 Thr Ser Glu Asp Leu Ile Leu Ile Gly Asn Glu Leu Asp Leu Ala Cys
 115 120 125
 Gly Glu Arg Ile Arg Leu Glu Lys Val Leu Leu Val Gly Ala Asp Asn
 130 135 140
 Phe Thr Leu Leu Gly Lys Pro Leu Leu Gly Lys Asp Leu Val Arg Val
 145 150 155 160
 Glu Ala Thr Val Ile Glu Lys Thr Glu Ser Trp Pro Arg Ile Ile Met
 165 170 175
 Arg Phe Arg Lys Arg Lys Asn Phe Lys Lys Lys Arg Ile Val Thr Thr
 180 185 190
 Pro Gln Thr Val Leu Arg Ile Asn Ser Ile Glu Ile Ala Pro Cys Leu
 195 200 205
 Leu

<210> 193

<211> 351

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(351)

<400> 193

| | |
|--|-----|
| atg ggg tct cgg ttg tcc cag cct ttt gag tcc tat atc act gcg cct | 48 |
| Met Gly Ser Arg Leu Ser Gln Pro Phe Glu Ser Tyr Ile Thr Ala Pro | |
| 1 5 10 15 | |
| ccc ggt acc gcc gcc gcg ccc gcc aaa cct gcg ccc cca gct aca ccc | 96 |
| Pro Gly Thr Ala Ala Ala Pro Ala Lys Pro Ala Pro Pro Ala Thr Pro | |
| 20 25 30 | |
| gga gcg ccg acc tcc cca gca gaa cac cgc ctg ttg aag acc tgc tgg | 144 |
| Gly Ala Pro Thr Ser Pro Ala Glu His Arg Leu Leu Lys Thr Cys Trp | |
| 35 40 45 | |
| agc tgt cgc gtg ctt tct ggg ttg ggg ctg atg ggg gcg ggc ggg tac | 192 |
| Ser Cys Arg Val Leu Ser Gly Leu Gly Leu Met Gly Ala Gly Gly Tyr | |

273

| 50 | 55 | 60 | |
|---|-----|-----|-----|
| gtg tac tgg gtg gca cgg aag ccc atg aag atg gga tac ccc ccg agt | | | 240 |
| Val Tyr Trp Val Ala Arg Lys Pro Met Lys Met Gly Tyr Pro Pro Ser | | | |
| 65 | 70 | 75 | 80 |
| cca tgg acc att acg cag atg gtc atc ggc ctc agt gag aat caa ggc | | | 288 |
| Pro Trp Thr Ile Thr Gln Met Val Ile Gly Leu Ser Glu Asn Gln Gly | | | |
| | 85 | 90 | 95 |
| att gcc acc tgg ggt atc gtt gtc atg gca gac ccc aaa ggg aag gcc | | | 336 |
| Ile Ala Thr Trp Gly Ile Val Val Met Ala Asp Pro Lys Gly Lys Ala | | | |
| 100 | 105 | 110 | |
| tac cgc gtt gtt tga | | | 351 |
| Tyr Arg Val Val * | | | |
| 115 | | | |

<210> 194
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 194
 Met Gly Ser Arg Leu Ser Gln Pro Phe Glu Ser Tyr Ile Thr Ala Pro
 1 5 10 15
 Pro Gly Thr Ala Ala Ala Pro Ala Lys Pro Ala Pro Pro Ala Thr Pro
 20 25 30
 Gly Ala Pro Thr Ser Pro Ala Glu His Arg Leu Leu Lys Thr Cys Trp
 35 40 45
 Ser Cys Arg Val Leu Ser Gly Leu Gly Leu Met Gly Ala Gly Gly Tyr
 50 55 60
 Val Tyr Trp Val Ala Arg Lys Pro Met Lys Met Gly Tyr Pro Pro Ser
 65 70 75 80
 Pro Trp Thr Ile Thr Gln Met Val Ile Gly Leu Ser Glu Asn Gln Gly
 85 90 95
 Ile Ala Thr Trp Gly Ile Val Val Met Ala Asp Pro Lys Gly Lys Ala
 100 105 110
 Tyr Arg Val Val
 115

<210> 195
 <211> 1047

274

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1047)

<400> 195

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| atg | cgg | ctc | ctc | ggc | tgg | tgg | caa | gta | ttg | ctg | tgg | gtg | ctg | gga | ctt | 48 |
| Met | Arg | Leu | Leu | Gly | Trp | Trp | Gln | Val | Leu | Leu | Trp | Val | Leu | Gly | Leu | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| ccc | gtc | cgc | ggc | gtg | gag | gtt | gca | gag | gaa | agt | ggc | cgc | tta | tgg | tca | 96 |
| Pro | Val | Arg | Gly | Val | Glu | Val | Ala | Glu | Glu | Ser | Gly | Arg | Leu | Trp | Ser | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gag | gag | cag | cct | gct | cac | cct | ctc | cag | gtg | ggg | gct | gtg | tac | ctg | ggc | 144 |
| Glu | Glu | Gln | Pro | Ala | His | Pro | Leu | Gln | Val | Gly | Ala | Val | Tyr | Leu | Gly | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gag | gag | gag | ctc | ctg | cat | gac | ccg | atg | ggc | cag | gac | agg | gca | gca | gaa | 192 |
| Glu | Glu | Glu | Leu | Leu | His | Asp | Pro | Met | Gly | Gln | Asp | Arg | Ala | Ala | Glu | |
| | | 50 | | | | | 55 | | | | | 60 | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gag | gcc | aat | gcg | gtg | ctg | ggg | ctg | gac | acc | caa | ggc | gat | cac | atg | gtg | 240 |
| Glu | Ala | Asn | Ala | Val | Leu | Gly | Leu | Asp | Thr | Gln | Gly | Asp | His | Met | Val | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| atg | ctg | tct | gtg | att | cct | ggg | gaa | gct | gag | gac | aaa | gtg | agt | tca | gag | 288 |
| Met | Leu | Ser | Val | Ile | Pro | Gly | Glu | Ala | Glu | Asp | Lys | Val | Ser | Ser | Glu | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| cct | agc | ggc | gtc | acc | tgt | ggt | gct | gga | gga | gcg | gag | gac | tca | agg | tgc | 336 |
| Pro | Ser | Gly | Val | Thr | Cys | Gly | Ala | Gly | Gly | Ala | Glu | Asp | Ser | Arg | Cys | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| aac | gtc | cga | gag | agc | ctt | ttc | tct | ctg | gat | ggc | gct | gga | gca | cac | ttc | 384 |
| Asn | Val | Arg | Glu | Ser | Leu | Phe | Ser | Leu | Asp | Gly | Ala | Gly | Ala | His | Phe | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| cct | gac | aga | gaa | gag | gag | tat | tac | aca | gag | cca | gaa | gtg | gcg | gaa | tct | 432 |
| Pro | Asp | Arg | Glu | Glu | Glu | Tyr | Tyr | Thr | Glu | Pro | Glu | Val | Ala | Glu | Ser | |
| | | 130 | | | | | 135 | | | | | 140 | | | | |

| | |
|---|-----|
| gac gca gcc ccg aca gag gac tcc aat aac act gaa agt ctg aaa tcc | 480 |
| Asp Ala Ala Pro Thr Glu Asp Ser Asn Asn Thr Glu Ser Leu Lys Ser | |
| 145 150 155 160 | |
| cca aag gtg aac tgt gag gag aga aac att aca gga tta gaa aat ttc | 528 |
| Pro Lys Val Asn Cys Glu Glu Arg Asn Ile Thr Gly Leu Glu Asn Phe | |
| 165 170 175 | |
| act ctg aaa att tta aat atg tca cag gac ctt atg gat ttt ctg aac | 576 |
| Thr Leu Lys Ile Leu Asn Met Ser Gln Asp Leu Met Asp Phe Leu Asn | |
| 180 185 190 | |
| cca aac ggt agt gac tgt act cta gtc ctg ttt tac acc ccg tgg tgc | 624 |
| Pro Asn Gly Ser Asp Cys Thr Leu Val Leu Phe Tyr Thr Pro Trp Cys | |
| 195 200 205 | |
| cgc ttt tct gcc agt ttg gcc cct cac ttt aac tct ctg ccc cgg gca | 672 |
| Arg Phe Ser Ala Ser Leu Ala Pro His Phe Asn Ser Leu Pro Arg Ala | |
| 210 215 220 | |
| ttt cca gct ctt cac ttt ttg gca ctg gat gca tct cag cac agc agc | 720 |
| Phe Pro Ala Leu His Phe Leu Ala Leu Asp Ala Ser Gln His Ser Ser | |
| 225 230 235 240 | |
| ctt tct acc agg ttt ggc acc gta gct gtt cct aat att tta tta ttt | 768 |
| Leu Ser Thr Arg Phe Gly Thr Val Ala Val Pro Asn Ile Leu Leu Phe | |
| 245 250 255 | |
| caa gga gct aaa cca atg gcc aga ttt aat cat aca gat cga aca ctg | 816 |
| Gln Gly Ala Lys Pro Met Ala Arg Phe Asn His Thr Asp Arg Thr Leu | |
| 260 265 270 | |
| gaa aca ctg aaa atc ttc att ttt aat cag aca ggt ata gaa gcc aag | 864 |
| Glu Thr Leu Lys Ile Phe Ile Phe Asn Gln Thr Gly Ile Glu Ala Lys | |
| 275 280 285 | |
| aag aat gtg gtg gta act caa gcc gac caa ata ggc cct ctt ccc agc | 912 |
| Lys Asn Val Val Val Thr Gln Ala Asp Gln Ile Gly Pro Leu Pro Ser | |
| 290 295 300 | |
| act ttg ata aaa agt gtg gac tgg ttg ctt gta ttt tcc tta ttc ttt | 960 |
| Thr Leu Ile Lys Ser Val Asp Trp Leu Leu Val Phe Ser Leu Phe Phe | |
| 305 310 315 320 | |

276

tta att agt ttt att atg tat gct acc att cga act gag agt att cgg 1008
 Leu Ile Ser Phe Ile Met Tyr Ala Thr Ile Arg Thr Glu Ser Ile Arg
 325 330 335

tgg cta att cca gga caa gag cag gaa cat gtg gag tag 1047
 Trp Leu Ile Pro Gly Gln Glu Gln Glu His Val Glu *
 340 345

<210> 196

<211> 348

<212> PRT

<213> Homo sapiens

<400> 196

Met Arg Leu Leu Gly Trp Trp Gln Val Leu Leu Trp Val Leu Gly Leu
 1 5 10 15
 Pro Val Arg Gly Val Glu Val Ala Glu Glu Ser Gly Arg Leu Trp Ser
 20 25 30
 Glu Glu Gln Pro Ala His Pro Leu Gln Val Gly Ala Val Tyr Leu Gly
 35 40 45
 Glu Glu Glu Leu Leu His Asp Pro Met Gly Gln Asp Arg Ala Ala Glu
 50 55 60
 Glu Ala Asn Ala Val Leu Gly Leu Asp Thr Gln Gly Asp His Met Val
 65 70 75 80
 Met Leu Ser Val Ile Pro Gly Glu Ala Glu Asp Lys Val Ser Ser Glu
 85 90 95
 Pro Ser Gly Val Thr Cys Gly Ala Gly Gly Ala Glu Asp Ser Arg Cys
 100 105 110
 Asn Val Arg Glu Ser Leu Phe Ser Leu Asp Gly Ala Gly Ala His Phe
 115 120 125
 Pro Asp Arg Glu Glu Glu Tyr Tyr Thr Glu Pro Glu Val Ala Glu Ser
 130 135 140
 Asp Ala Ala Pro Thr Glu Asp Ser Asn Asn Thr Glu Ser Leu Lys Ser
 145 150 155 160
 Pro Lys Val Asn Cys Glu Glu Arg Asn Ile Thr Gly Leu Glu Asn Phe
 165 170 175
 Thr Leu Lys Ile Leu Asn Met Ser Gln Asp Leu Met Asp Phe Leu Asn
 180 185 190
 Pro Asn Gly Ser Asp Cys Thr Leu Val Leu Phe Tyr Thr Pro Trp Cys
 195 200 205
 Arg Phe Ser Ala Ser Leu Ala Pro His Phe Asn Ser Leu Pro Arg Ala
 210 215 220
 Phe Pro Ala Leu His Phe Leu Ala Leu Asp Ala Ser Gln His Ser Ser

278

| 65 | 70 | 75 | 80 | |
|---|-----|-----|-----|-----|
| gtg ata att cac gta gga gca ctg agc ttg aag gag tca cag gaa ctg | | | | 288 |
| Val Ile Ile His Val Gly Ala Leu Ser Leu Lys Glu Ser Gln Glu Leu | | | | |
| | 85 | 90 | 95 | |
| gcc caa cat gca gca gaa ata gga gct gat ggc atc gct gtc att gca | | | | 336 |
| Ala Gln His Ala Ala Glu Ile Gly Ala Asp Gly Ile Ala Val Ile Ala | | | | |
| | 100 | 105 | 110 | |
| ccg ttc ttc ctc aag cca tgg acc aaa gat atc ctg att aat ttc cta | | | | 384 |
| Pro Phe Phe Leu Lys Pro Trp Thr Lys Asp Ile Leu Ile Asn Phe Leu | | | | |
| | 115 | 120 | 125 | |
| aag gaa gtg gct gct gcg ccc ctg ccc tgc cat ttt att act atc aca | | | | 432 |
| Lys Glu Val Ala Ala Ala Pro Leu Pro Cys His Phe Ile Thr Ile Thr | | | | |
| | 130 | 135 | 140 | |
| ttc ctg cct tga | | | | 444 |
| Phe Leu Pro * | | | | |
| 145 | | | | |

<210> 198

<211> 147

<212> PRT

<213> Homo sapiens

<400> 198

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Phe | Pro | Lys | Lys | Lys | Leu | Gln | Gly | Leu | Val | Ala | Ala | Thr | Ile |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Thr | Pro | Met | Thr | Glu | Asn | Gly | Glu | Ile | Asn | Phe | Ser | Val | Ile | Gly | Gln |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Tyr | Val | Asp | Tyr | Leu | Val | Lys | Glu | Gln | Gly | Val | Lys | Asn | Ile | Phe | Val |
| | | 35 | | | | 40 | | | | | 45 | | | | |
| Asn | Gly | Thr | Thr | Gly | Glu | Gly | Leu | Ser | Leu | Ser | Val | Ser | Glu | Arg | Arg |
| | | 50 | | | | 55 | | | | 60 | | | | | |
| Gln | Val | Ala | Glu | Glu | Trp | Val | Thr | Lys | Gly | Lys | Asp | Lys | Leu | Asp | Gln |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| Val | Ile | Ile | His | Val | Gly | Ala | Leu | Ser | Leu | Lys | Glu | Ser | Gln | Glu | Leu |
| | | | 85 | | | | | 90 | | | | | 95 | | |
| Ala | Gln | His | Ala | Ala | Glu | Ile | Gly | Ala | Asp | Gly | Ile | Ala | Val | Ile | Ala |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Pro | Phe | Phe | Leu | Lys | Pro | Trp | Thr | Lys | Asp | Ile | Leu | Ile | Asn | Phe | Leu |

279

115 120 125
 Lys Glu Val Ala Ala Ala Pro Leu Pro Cys His Phe Ile Thr Ile Thr
 130 135 140
 Phe Leu Pro
 145

<210> 199
 <211> 705
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(705)

<221> misc_feature
 <222> (1)...(705)
 <223> n = A,T,C or G

<400> 199
 atg atg tct caa ggt agt cag ttt ttg tat tca act ttt ggc tat acc 48
 Met Met Ser Gln Gly Ser Gln Phe Leu Tyr Ser Thr Phe Gly Tyr Thr
 1 5 10 15

 cta ctg gca gcc ata gta gag aga gct tca gga tgt aaa tat ttg gac 96
 Leu Leu Ala Ala Ile Val Glu Arg Ala Ser Gly Cys Lys Tyr Leu Asp
 20 25 30

 tat atg cag aaa ata ttc cat gac ttg gat atg ctg acg act gtg cag 144
 Tyr Met Gln Lys Ile Phe His Asp Leu Asp Met Leu Thr Thr Val Gln
 35 40 45

 gaa gaa aac gag cca gtg att tac aat aga gca aga ttt tat gtt tac 192
 Glu Glu Asn Glu Pro Val Ile Tyr Asn Arg Ala Arg Phe Tyr Val Tyr
 50 55 60

 aat aaa aag aaa cgt ctt gtc aac aca cct tac gtg gat aac tcc tat 240
 Asn Lys Lys Lys Arg Leu Val Asn Thr Pro Tyr Val Asp Asn Ser Tyr
 65 70 75 80

 aaa tgg gct ggt ggt gga ttt ctg tct aca gtg ggt gac ctt ctg aaa 288
 Lys Trp Ala Gly Gly Gly Phe Leu Ser Thr Val Gly Asp Leu Leu Lys
 85 90 95

280

```

ttt ggg aat gca atg ctt tat ggt tac caa gtt ggg ctg ttt aag aac      336
Phe Gly Asn Ala Met Leu Tyr Gly Tyr Gln Val Gly Leu Phe Lys Asn
      100                      105                      110

tca aat gaa aat ctt tta cct gga tac ctc aaa cca gaa aca atg gtt      384
Ser Asn Glu Asn Leu Leu Pro Gly Tyr Leu Lys Pro Glu Thr Met Val
      115                      120                      125

atg atg tgg acc cca gtc cct aac aca gag atg tct tgg gat aaa gag      432
Met Met Trp Thr Pro Val Pro Asn Thr Glu Met Ser Trp Asp Lys Glu
      130                      135                      140

ggg aaa tat gca atg gcg tgg ggt gtt gtg gaa ang aaa caa acg tat      480
Gly Lys Tyr Ala Met Ala Trp Gly Val Val Glu Xaa Lys Gln Thr Tyr
      145                      150                      155                      160

ggg tcg tgt aga aag caa cgg cat tat gct tca cat act gga ggg gca      528
Gly Ser Cys Arg Lys Gln Arg His Tyr Ala Ser His Thr Gly Gly Ala
      165                      170                      175

gtg ggt gcc agt agt gtc ctg ctg gtc ctt cct gaa gaa ctg gat aca      576
Val Gly Ala Ser Ser Val Leu Leu Val Leu Pro Glu Glu Leu Asp Thr
      180                      185                      190

gag act ata aat aac aag gtt ccc cca aga gga atc att gtt tct atc      624
Glu Thr Ile Asn Asn Lys Val Pro Pro Arg Gly Ile Ile Val Ser Ile
      195                      200                      205

ata tgt aac atg caa tct gtt ggc ctc aat agc acc gct ttg aag att      672
Ile Cys Asn Met Gln Ser Val Gly Leu Asn Ser Thr Ala Leu Lys Ile
      210                      215                      220

gcc ctt gaa ttt gat aaa gac aga tca gac tga      705
Ala Leu Glu Phe Asp Lys Asp Arg Ser Asp *
      225                      230

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<210> 200
 <211> 234
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT

281

<222> (1)...(234)

<223> Xaa = Any Amino Acid

<400> 200

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Met Met Ser Gln Gly Ser Gln Phe Leu Tyr Ser Thr Phe Gly Tyr Thr
 1             5             10             15
Leu Leu Ala Ala Ile Val Glu Arg Ala Ser Gly Cys Lys Tyr Leu Asp
      20             25             30
Tyr Met Gln Lys Ile Phe His Asp Leu Asp Met Leu Thr Thr Val Gln
      35             40             45
Glu Glu Asn Glu Pro Val Ile Tyr Asn Arg Ala Arg Phe Tyr Val Tyr
      50             55             60
Asn Lys Lys Lys Arg Leu Val Asn Thr Pro Tyr Val Asp Asn Ser Tyr
      65             70             75             80
Lys Trp Ala Gly Gly Gly Phe Leu Ser Thr Val Gly Asp Leu Leu Lys
      85             90             95
Phe Gly Asn Ala Met Leu Tyr Gly Tyr Gln Val Gly Leu Phe Lys Asn
      100            105            110
Ser Asn Glu Asn Leu Leu Pro Gly Tyr Leu Lys Pro Glu Thr Met Val
      115            120            125
Met Met Trp Thr Pro Val Pro Asn Thr Glu Met Ser Trp Asp Lys Glu
      130            135            140
Gly Lys Tyr Ala Met Ala Trp Gly Val Val Glu Xaa Lys Gln Thr Tyr
      145            150            155            160
Gly Ser Cys Arg Lys Gln Arg His Tyr Ala Ser His Thr Gly Gly Ala
      165            170            175
Val Gly Ala Ser Ser Val Leu Leu Val Leu Pro Glu Glu Leu Asp Thr
      180            185            190
Glu Thr Ile Asn Asn Lys Val Pro Pro Arg Gly Ile Ile Val Ser Ile
      195            200            205
Ile Cys Asn Met Gln Ser Val Gly Leu Asn Ser Thr Ala Leu Lys Ile
      210            215            220
Ala Leu Glu Phe Asp Lys Asp Arg Ser Asp
      225            230

```

<210> 201

<211> 885

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(885)

282

<221> misc_feature
 <222> (1)...(885)
 <223> n = A,T,C or G

<400> 201

| | |
|---|-----|
| atg ctg gct gtg tca gtg ctg gcc gca gtc cgc ggc ggc gac gag gtg | 48 |
| Met Leu Ala Val Ser Val Leu Ala Ala Val Arg Gly Gly Asp Glu Val | |
| 1 5 10 15 | |
| agg cgc gtc cgc gag agc aac gtc ctc cac gag aag tcc aag ggg aag | 96 |
| Arg Arg Val Arg Glu Ser Asn Val Leu His Glu Lys Ser Lys Gly Lys | |
| 20 25 30 | |
| acg cgc gag gga gcc gag gac aag atg acc agc ggc gac gtg ctg tcc | 144 |
| Thr Arg Glu Gly Ala Glu Asp Lys Met Thr Ser Gly Asp Val Leu Ser | |
| 35 40 45 | |
| aac cgc aag atg ttc tac ctg ctc aag acc gcc ttc ccc agc gtc cag | 192 |
| Asn Arg Lys Met Phe Tyr Leu Leu Lys Thr Ala Phe Pro Ser Val Gln | |
| 50 55 60 | |
| att aat act gag gaa cac gtg gat gca gct gat cag gag gtt atc ttg | 240 |
| Ile Asn Thr Glu Glu His Val Asp Ala Ala Asp Gln Glu Val Ile Leu | |
| 65 70 75 80 | |
| tgg gat cat aag att cct gag gat atc cta aag gaa gta act act cct | 288 |
| Trp Asp His Lys Ile Pro Glu Asp Ile Leu Lys Glu Val Thr Thr Pro | |
| 85 90 95 | |
| aaa gag gta cca gca gaa agt gtt act gtc tgg att gac cca ctt gat | 336 |
| Lys Glu Val Pro Ala Glu Ser Val Thr Val Trp Ile Asp Pro Leu Asp | |
| 100 105 110 | |
| gct aca cag gaa tat aca gag gat ctt cga aag tac gtc act act atg | 384 |
| Ala Thr Gln Glu Tyr Thr Glu Asp Leu Arg Lys Tyr Val Thr Thr Met | |
| 115 120 125 | |
| gtg tgt gtg gct gta aat ggt aaa ccc atg cta gga gtt ata cat aag | 432 |
| Val Cys Val Ala Val Asn Gly Lys Pro Met Leu Gly Val Ile His Lys | |
| 130 135 140 | |
| cca ttt tcc gaa tat aca gct tgg gca atg gta gat ggt ggt tca aat | 480 |
| Pro Phe Ser Glu Tyr Thr Ala Trp Ala Met Val Asp Gly Gly Ser Asn | |
| 145 150 155 160 | |

283

| | |
|---|-----|
| gtg aaa gcc cgc tct tcc tac aat gag aag acc cca agg ntc gtt gtg | 528 |
| Val Lys Ala Arg Ser Ser Tyr Asn Glu Lys Thr Pro Arg Xaa Val Val | |
| 165 170 175 | |
| tct cgt tcc cat tca ggg atg gtc aaa cag gtc gct ctt cag act ttt | 576 |
| Ser Arg Ser His Ser Gly Met Val Lys Gln Val Ala Leu Gln Thr Phe | |
| 180 185 190 | |
| gga aac cag act aca att atc cca gct ggt ggt gct ggt tat aaa gtt | 624 |
| Gly Asn Gln Thr Thr Ile Ile Pro Ala Gly Gly Ala Gly Tyr Lys Val | |
| 195 200 205 | |
| tta gca ctt ttg gat gtg cct gat aag agt caa gaa aaa gct gat tta | 672 |
| Leu Ala Leu Leu Asp Val Pro Asp Lys Ser Gln Glu Lys Ala Asp Leu | |
| 210 215 220 | |
| tac atc cat gtg aca tac atc aaa aag tgg gat ata tgt gct ggt aat | 720 |
| Tyr Ile His Val Thr Tyr Ile Lys Lys Trp Asp Ile Cys Ala Gly Asn | |
| 225 230 235 240 | |
| gcc atc tta aaa gcc cta ggg ggg cat atg act acc ctg agt ggt gaa | 768 |
| Ala Ile Leu Lys Ala Leu Gly Gly His Met Thr Thr Leu Ser Gly Glu | |
| 245 250 255 | |
| gaa atc agt tac act ggt tca gac ggc att gaa ggg gga ctc ctt gct | 816 |
| Glu Ile Ser Tyr Thr Gly Ser Asp Gly Ile Glu Gly Gly Leu Leu Ala | |
| 260 265 270 | |
| agc atc aga atg aac cac cag gcc ctg gtc aga aaa ctc cca gat cta | 864 |
| Ser Ile Arg Met Asn His Gln Ala Leu Val Arg Lys Leu Pro Asp Leu | |
| 275 280 285 | |
| gaa aag aca gga cat aaa tga | 885 |
| Glu Lys Thr Gly His Lys * | |
| 290 | |

<210> 202

<211> 294

<212> PRT

<213> Homo sapiens

<220>

284

<221> VARIANT

<222> (1)...(294)

<223> Xaa = Any Amino Acid

<400> 202

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Met Leu Ala Val Ser Val Leu Ala Ala Val Arg Gly Gly Asp Glu Val
 1             5             10             15
Arg Arg Val Arg Glu Ser Asn Val Leu His Glu Lys Ser Lys Gly Lys
      20             25             30
Thr Arg Glu Gly Ala Glu Asp Lys Met Thr Ser Gly Asp Val Leu Ser
      35             40             45
Asn Arg Lys Met Phe Tyr Leu Leu Lys Thr Ala Phe Pro Ser Val Gln
 50             55             60
Ile Asn Thr Glu Glu His Val Asp Ala Ala Asp Gln Glu Val Ile Leu
65             70             75             80
Trp Asp His Lys Ile Pro Glu Asp Ile Leu Lys Glu Val Thr Thr Pro
      85             90             95
Lys Glu Val Pro Ala Glu Ser Val Thr Val Trp Ile Asp Pro Leu Asp
      100             105             110
Ala Thr Gln Glu Tyr Thr Glu Asp Leu Arg Lys Tyr Val Thr Thr Met
      115             120             125
Val Cys Val Ala Val Asn Gly Lys Pro Met Leu Gly Val Ile His Lys
      130             135             140
Pro Phe Ser Glu Tyr Thr Ala Trp Ala Met Val Asp Gly Gly Ser Asn
145             150             155             160
Val Lys Ala Arg Ser Ser Tyr Asn Glu Lys Thr Pro Arg Xaa Val Val
      165             170             175
Ser Arg Ser His Ser Gly Met Val Lys Gln Val Ala Leu Gln Thr Phe
      180             185             190
Gly Asn Gln Thr Thr Ile Ile Pro Ala Gly Gly Ala Gly Tyr Lys Val
      195             200             205
Leu Ala Leu Leu Asp Val Pro Asp Lys Ser Gln Glu Lys Ala Asp Leu
      210             215             220
Tyr Ile His Val Thr Tyr Ile Lys Lys Trp Asp Ile Cys Ala Gly Asn
225             230             235             240
Ala Ile Leu Lys Ala Leu Gly Gly His Met Thr Thr Leu Ser Gly Glu
      245             250             255
Glu Ile Ser Tyr Thr Gly Ser Asp Gly Ile Glu Gly Gly Leu Leu Ala
      260             265             270
Ser Ile Arg Met Asn His Gln Ala Leu Val Arg Lys Leu Pro Asp Leu
      275             280             285
Glu Lys Thr Gly His Lys
      290

```


285

<210> 203
 <211> 861
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(861)

<400> 203

| | |
|---|-----|
| atg gag gaa aaa aga cgg cga gcc cga gtt cag gga gcc tgg gct gcc | 48 |
| Met Glu Glu Lys Arg Arg Arg Ala Arg Val Gln Gly Ala Trp Ala Ala | |
| 1 5 10 15 | |
| cct gtt aaa agc cag gcc att gct cag cca gct acc act gct aag agc | 96 |
| Pro Val Lys Ser Gln Ala Ile Ala Gln Pro Ala Thr Thr Ala Lys Ser | |
| 20 25 30 | |
| cat ctc cac cag aag cct ggc cag acc tgg aag aac aaa gag cat cat | 144 |
| His Leu His Gln Lys Pro Gly Gln Thr Trp Lys Asn Lys Glu His His | |
| 35 40 45 | |
| ctc tct gac aga gag ttt gtg ttc aaa gaa cct cag cag gta gta cgt | 192 |
| Leu Ser Asp Arg Glu Phe Val Phe Lys Glu Pro Gln Gln Val Val Arg | |
| 50 55 60 | |
| aga gct cct gag cca cga gtg att gac aga gag ggt gtg tat gaa atc | 240 |
| Arg Ala Pro Glu Pro Arg Val Ile Asp Arg Glu Gly Val Tyr Glu Ile | |
| 65 70 75 80 | |
| agc ctg tca ccc aca ggt gta tct agg gtc tgt ttg tat cct ggc ttt | 288 |
| Ser Leu Ser Pro Thr Gly Val Ser Arg Val Cys Leu Tyr Pro Gly Phe | |
| 85 90 95 | |
| gtt gac gtg aaa gaa gct gac tgg ata ttg gaa cag ctt tgt caa gat | 336 |
| Val Asp Val Lys Glu Ala Asp Trp Ile Leu Glu Gln Leu Cys Gln Asp | |
| 100 105 110 | |
| gtt ccc tgg aaa cag agg acc ggc atc aga gag gat ata act tat cag | 384 |
| Val Pro Trp Lys Gln Arg Thr Gly Ile Arg Glu Asp Ile Thr Tyr Gln | |
| 115 120 125 | |
| caa cca aga ctt aca gca tgg tat gga gaa ctt cct tac act tat tca | 432 |
| Gln Pro Arg Leu Thr Ala Trp Tyr Gly Glu Leu Pro Tyr Thr Tyr Ser | |

286

| 130 | 135 | 140 | |
|---|-----|-----|-----|
| aga atc act atg gaa cca aat cct cac tgg cac cct gtg ctg cgc aca | | | 480 |
| Arg Ile Thr Met Glu Pro Asn Pro His Trp His Pro Val Leu Arg Thr | | | |
| 145 | 150 | 155 | 160 |
| cta aag aac cgc att gaa gag aac act ggc cac acc ttc aac tcc tta | | | 528 |
| Leu Lys Asn Arg Ile Glu Glu Asn Thr Gly His Thr Phe Asn Ser Leu | | | |
| 165 | 170 | 175 | |
| ctc tgc aat ctt tat cgc aat gag aag gac agc gtg gac tgg cac agt | | | 576 |
| Leu Cys Asn Leu Tyr Arg Asn Glu Lys Asp Ser Val Asp Trp His Ser | | | |
| 180 | 185 | 190 | |
| gat gat gaa ccc tca cta ggg agg tgc ccc att att gct tca cta agt | | | 624 |
| Asp Asp Glu Pro Ser Leu Gly Arg Cys Pro Ile Ile Ala Ser Leu Ser | | | |
| 195 | 200 | 205 | |
| ttt ggt gcc aca cgc aca ttt gag atg aga aag aag cca cca cca gaa | | | 672 |
| Phe Gly Ala Thr Arg Thr Phe Glu Met Arg Lys Lys Pro Pro Pro Glu | | | |
| 210 | 215 | 220 | |
| gag aat gga gac tac aca tat gtg gaa aga gtg aag ata ccc ttg gat | | | 720 |
| Glu Asn Gly Asp Tyr Thr Tyr Val Glu Arg Val Lys Ile Pro Leu Asp | | | |
| 225 | 230 | 235 | 240 |
| cat ggt acc ttg tta atc atg gaa gga gcg aca caa gct gac tgg cag | | | 768 |
| His Gly Thr Leu Leu Ile Met Glu Gly Ala Thr Gln Ala Asp Trp Gln | | | |
| 245 | 250 | 255 | |
| cat cga gtg ccc aaa gaa tac cac tct aga gaa ccg aga gtg aac ctg | | | 816 |
| His Arg Val Pro Lys Glu Tyr His Ser Arg Glu Pro Arg Val Asn Leu | | | |
| 260 | 265 | 270 | |
| acc ttt cgg aca gtc tat cca gac cct cga ggg gca ccc tgg tga | | | 861 |
| Thr Phe Arg Thr Val Tyr Pro Asp Pro Arg Gly Ala Pro Trp * | | | |
| 275 | 280 | 285 | |

<210> 204

<211> 286

<212> PRT

<213> Homo sapiens

287

<400> 204

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Met Glu Glu Lys Arg Arg Arg Ala Arg Val Gln Gly Ala Trp Ala Ala
 1          5          10          15
Pro Val Lys Ser Gln Ala Ile Ala Gln Pro Ala Thr Thr Ala Lys Ser
      20          25          30
His Leu His Gln Lys Pro Gly Gln Thr Trp Lys Asn Lys Glu His His
      35          40          45
Leu Ser Asp Arg Glu Phe Val Phe Lys Glu Pro Gln Gln Val Val Arg
      50          55          60
Arg Ala Pro Glu Pro Arg Val Ile Asp Arg Glu Gly Val Tyr Glu Ile
      65          70          75          80
Ser Leu Ser Pro Thr Gly Val Ser Arg Val Cys Leu Tyr Pro Gly Phe
      85          90          95
Val Asp Val Lys Glu Ala Asp Trp Ile Leu Glu Gln Leu Cys Gln Asp
      100          105          110
Val Pro Trp Lys Gln Arg Thr Gly Ile Arg Glu Asp Ile Thr Tyr Gln
      115          120          125
Gln Pro Arg Leu Thr Ala Trp Tyr Gly Glu Leu Pro Tyr Thr Tyr Ser
      130          135          140
Arg Ile Thr Met Glu Pro Asn Pro His Trp His Pro Val Leu Arg Thr
      145          150          155          160
Leu Lys Asn Arg Ile Glu Glu Asn Thr Gly His Thr Phe Asn Ser Leu
      165          170          175
Leu Cys Asn Leu Tyr Arg Asn Glu Lys Asp Ser Val Asp Trp His Ser
      180          185          190
Asp Asp Glu Pro Ser Leu Gly Arg Cys Pro Ile Ile Ala Ser Leu Ser
      195          200          205
Phe Gly Ala Thr Arg Thr Phe Glu Met Arg Lys Lys Pro Pro Pro Glu
      210          215          220
Glu Asn Gly Asp Tyr Thr Tyr Val Glu Arg Val Lys Ile Pro Leu Asp
      225          230          235          240
His Gly Thr Leu Leu Ile Met Glu Gly Ala Thr Gln Ala Asp Trp Gln
      245          250          255
His Arg Val Pro Lys Glu Tyr His Ser Arg Glu Pro Arg Val Asn Leu
      260          265          270
Thr Phe Arg Thr Val Tyr Pro Asp Pro Arg Gly Ala Pro Trp
      275          280          285

```

<210> 205

<211> 561

<212> DNA

<213> Homo sapiens

<220>

288

<221> CDS

<222> (1)...(561)

<400> 205

atg att cac tgg cat tct gag aaa gca act ctt ctt tta aat gct cca 48
Met Ile His Trp His Ser Glu Lys Ala Thr Leu Leu Leu Asn Ala Pro
1 5 10 15

tca ttt tca gat caa ctt cct ggt aca atg gcc acc ctt tct ctg gtg 96
Ser Phe Ser Asp Gln Leu Pro Gly Thr Met Ala Thr Leu Ser Leu Val
20 25 30

aat gag gca cag tat ctg ctg atc aac aca tcc agt att ttg gaa ctt 144
Asn Glu Ala Gln Tyr Leu Leu Ile Asn Thr Ser Ser Ile Leu Glu Leu
35 40 45

cac cgg caa cta aac acc agt gat gag aat gga aag gag gaa tta ttc 192
 His Arg Gln Leu Asn Thr Ser Asp Glu Asn Gly Lys Glu Glu Leu Phe
 50 55 60

tca ctg aag gat ctc agc ttg cgt ttt cgt gcc aat att att atc aat 240
Ser Leu Lys Asp Leu Ser Leu Arg Phe Arg Ala Asn Ile Ile Ile Asn
65 70 75 80

gga aaa agg gct ttt gaa gaa gag aaa tgg gat gag att tca att ggc 288
Gly Lys Arg Ala Phe Glu Glu Glu Lys Trp Asp Glu Ile Ser Ile Gly
85 90 95

tct ttg cgt ttc cag gtt ttg ggg cct tgt cac aga tgc cag atg att 336
Ser Leu Arg Phe Gln Val Leu Gly Pro Cys His Arg Cys Gln Met Ile
100 105 110

tgc atc gac cag caa act ggg caa cga aac cag cat gtt ttc caa aaa 384
Cys Ile Asp Gln Gln Thr Gly Gln Arg Asn Gln His Val Phe Gln Lys
115 120 125

ctt tct gag agt cgt gaa aca aag gtg aac ttt ggc atg tac ctg atg 432
Leu Ser Glu Ser Arg Glu Thr Lys Val Asn Phe Gly Met Tyr Leu Met
130 135 140

cat gca tca ttg gat tta tcc tcc cca tgt ttc ctg tct gta gga tct 480
His Ala Ser Leu Asp Leu Ser Ser Pro Cys Phe Leu Ser Val Gly Ser
145 150 155 160

289

cag gtg ctc cct gtg ttg aaa gag aat gtg gaa ggt cat gat tta cct 528
 Gln Val Leu Pro Val Leu Lys Glu Asn Val Glu Gly His Asp Leu Pro
 165 170 175

gca tct gag aaa cac cag gat gtt acc tcc taa 561
 Ala Ser Glu Lys His Gln Asp Val Thr Ser *
 180 185

<210> 206
 <211> 186
 <212> PRT
 <213> Homo sapiens

<400> 206
 Met Ile His Trp His Ser Glu Lys Ala Thr Leu Leu Leu Asn Ala Pro
 1 5 10 15
 Ser Phe Ser Asp Gln Leu Pro Gly Thr Met Ala Thr Leu Ser Leu Val
 20 25 30
 Asn Glu Ala Gln Tyr Leu Leu Ile Asn Thr Ser Ser Ile Leu Glu Leu
 35 40 45
 His Arg Gln Leu Asn Thr Ser Asp Glu Asn Gly Lys Glu Glu Leu Phe
 50 55 60
 Ser Leu Lys Asp Leu Ser Leu Arg Phe Arg Ala Asn Ile Ile Ile Asn
 65 70 75 80
 Gly Lys Arg Ala Phe Glu Glu Glu Lys Trp Asp Glu Ile Ser Ile Gly
 85 90 95
 Ser Leu Arg Phe Gln Val Leu Gly Pro Cys His Arg Cys Gln Met Ile
 100 105 110
 Cys Ile Asp Gln Gln Thr Gly Gln Arg Asn Gln His Val Phe Gln Lys
 115 120 125
 Leu Ser Glu Ser Arg Glu Thr Lys Val Asn Phe Gly Met Tyr Leu Met
 130 135 140
 His Ala Ser Leu Asp Leu Ser Ser Pro Cys Phe Leu Ser Val Gly Ser
 145 150 155 160
 Gln Val Leu Pro Val Leu Lys Glu Asn Val Glu Gly His Asp Leu Pro
 165 170 175
 Ala Ser Glu Lys His Gln Asp Val Thr Ser
 180 185

<210> 207
 <211> 1272
 <212> DNA
 <213> Homo sapiens

| | |
|---|-----|
| atg cac aat tac tgc ttt gtg ttt gct ctg gga tac ctc aca gtg tgc | 48 |
| Met His Asn Tyr Cys Phe Val Phe Ala Leu Gly Tyr Leu Thr Val Cys | |
| 1 5 10 15 | |
| caa gtt act cga gtc tat atc ttt gac tat gga caa tat tct gct gat | 96 |
| Gln Val Thr Arg Val Tyr Ile Phe Asp Tyr Gly Gln Tyr Ser Ala Asp | |
| 20 25 30 | |
| ttt tca ggc cca atg atg atc att act cag aag atc act agt ttg gct | 144 |
| Phe Ser Gly Pro Met Met Ile Ile Thr Gln Lys Ile Thr Ser Leu Ala | |
| 35 40 45 | |
| tgc gaa att cat gat ggg atg ttt cgg aag gat gaa gaa ctg act tcc | 192 |
| Cys Glu Ile His Asp Gly Met Phe Arg Lys Asp Glu Glu Leu Thr Ser | |
| 50 55 60 | |
| tca cag agg gat tta gct gta agg cgc atg cca agc tta ctg gag tat | 240 |
| Ser Gln Arg Asp Leu Ala Val Arg Arg Met Pro Ser Leu Leu Glu Tyr | |
| 65 70 75 80 | |
| ttg agt tac aac tgt aac ttc atg ggg atc ctg gca ngc cca ntt tgc | 288 |
| Leu Ser Tyr Asn Cys Asn Phe Met Gly Ile Leu Ala Xaa Pro Xaa Cys | |
| 85 90 95 | |
| tct tac aaa gac tac att act ttc att gaa ggc aga tca tac cat atc | 336 |
| Ser Tyr Lys Asp Tyr Ile Thr Phe Ile Glu Gly Arg Ser Tyr His Ile | |
| 100 105 110 | |
| aca caa tct ggt gaa aat gga aaa gaa gag aca cag tat gaa aga aca | 384 |
| Thr Gln Ser Gly Glu Asn Gly Lys Glu Glu Thr Gln Tyr Glu Arg Thr | |
| 115 120 125 | |
| gag cca tct cca aat act gcg gtt gtt cag aag ctc tta gtt tgt ggg | 432 |
| Glu Pro Ser Pro Asn Thr Ala Val Val Gln Lys Leu Leu Val Cys Gly | |

291

| 130 | 135 | 140 | |
|---|-----|-----|-----|
| ctg tcc ttg tta ttt cac ttg acc atc tgt aca aca tta cct gtg gag | | | 480 |
| Leu Ser Leu Leu Phe His Leu Thr Ile Cys Thr Thr Leu Pro Val Glu | | | |
| 145 | 150 | 155 | 160 |
| tac aac att gat gag cat ttt caa gct aca gct tcg tgg cca aca aag | | | 528 |
| Tyr Asn Ile Asp Glu His Phe Gln Ala Thr Ala Ser Trp Pro Thr Lys | | | |
| | 165 | 170 | 175 |
| att atc tat ctg tat atc tct ctt ttg gct gcc aga ccc aaa tac tat | | | 576 |
| Ile Ile Tyr Leu Tyr Ile Ser Leu Leu Ala Ala Arg Pro Lys Tyr Tyr | | | |
| | 180 | 185 | 190 |
| ttt gca tgg acg cta gct gat gcc att aat aat gct gca ggc ttt ggt | | | 624 |
| Phe Ala Trp Thr Leu Ala Asp Ala Ile Asn Asn Ala Ala Gly Phe Gly | | | |
| | 195 | 200 | 205 |
| ttc aga ggg tat gac gaa aat gga gca gct cgc tgg gac tta att tcc | | | 672 |
| Phe Arg Gly Tyr Asp Glu Asn Gly Ala Ala Arg Trp Asp Leu Ile Ser | | | |
| | 210 | 215 | 220 |
| aat ttg aga att caa caa ata gag atg tca aca agt ttc aag atg ttt | | | 720 |
| Asn Leu Arg Ile Gln Gln Ile Glu Met Ser Thr Ser Phe Lys Met Phe | | | |
| | 225 | 230 | 235 |
| ctt gat aat tgg aat att cag aca gct ctt tgg ctc aaa agg gtg tgt | | | 768 |
| Leu Asp Asn Trp Asn Ile Gln Thr Ala Leu Trp Leu Lys Arg Val Cys | | | |
| | 245 | 250 | 255 |
| tat gaa cga acc tcc ttc agt cca act atc cag acg ttc att ctc tct | | | 816 |
| Tyr Glu Arg Thr Ser Phe Ser Pro Thr Ile Gln Thr Phe Ile Leu Ser | | | |
| | 260 | 265 | 270 |
| gcc att tgg cac ggg gta tac cca gga tat tat cta acg ttt cta aca | | | 864 |
| Ala Ile Trp His Gly Val Tyr Pro Gly Tyr Tyr Leu Thr Phe Leu Thr | | | |
| | 275 | 280 | 285 |
| ggg gtg tta atg aca tta gca gca aga gct atg aga aat aac ttt aga | | | 912 |
| Gly Val Leu Met Thr Leu Ala Ala Arg Ala Met Arg Asn Asn Phe Arg | | | |
| | 290 | 295 | 300 |
| cat tat ttc att gaa cct tcc caa ctg aaa tta ttt tat gat gtt ata | | | 960 |
| His Tyr Phe Ile Glu Pro Ser Gln Leu Lys Leu Phe Tyr Asp Val Ile | | | |

| | | | | | | | |
|---|-----|-----|--|-----|--|-----|------|
| 305 | | 310 | | 315 | | 320 | |
| aca tgg ata gta act caa gta gca ata agt tac aca gtt gtg cca ttt | | | | | | | 1008 |
| Thr Trp Ile Val Thr Gln Val Ala Ile Ser Tyr Thr Val Val Pro Phe | | | | | | | |
| | 325 | | | 330 | | 335 | |
| gtg ctt ctt tct ata aaa cca tca ctc acg ttt tac agc tcc tgg tat | | | | | | | 1056 |
| Val Leu Leu Ser Ile Lys Pro Ser Leu Thr Phe Tyr Ser Ser Trp Tyr | | | | | | | |
| | 340 | | | 345 | | 350 | |
| tat tgc ctg cac att ctt ggt atc tta gta tta ttg ttg ttg cca gtg | | | | | | | 1104 |
| Tyr Cys Leu His Ile Leu Gly Ile Leu Val Leu Leu Leu Leu Pro Val | | | | | | | |
| | 355 | | | 360 | | 365 | |
| aaa aaa act caa aga aga aag aat aca cat gaa aac att cag ctc tca | | | | | | | 1152 |
| Lys Lys Thr Gln Arg Arg Lys Asn Thr His Glu Asn Ile Gln Leu Ser | | | | | | | |
| | 370 | | | 375 | | 380 | |
| caa tcc aaa aag ttt gat gaa gga gaa aat tct ttg gga cag aac agt | | | | | | | 1200 |
| Gln Ser Lys Lys Phe Asp Glu Gly Glu Asn Ser Leu Gly Gln Asn Ser | | | | | | | |
| | 385 | | | 390 | | 395 | 400 |
| ttt tct aca aca aac aat gtt tgc aat cag aat caa gaa ata gcc tcg | | | | | | | 1248 |
| Phe Ser Thr Thr Asn Asn Val Cys Asn Gln Asn Gln Glu Ile Ala Ser | | | | | | | |
| | 405 | | | 410 | | 415 | |
| aga cat tca tca cta aag cag tga | | | | | | | 1272 |
| Arg His Ser Ser Leu Lys Gln * | | | | | | | |
| | 420 | | | | | | |

```
<210> 208
<211> 423
<212> PRT
<213> Homo sapiens
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```
<220>  
<221> VARIANT  
<222> (1)...(423)  
<223> Xaa = Any Amino Acid
```

<400> 208
Met His Asn Tyr Cys Phe Val Phe Ala Leu Gly Tyr Leu Thr Val Cys
1 5 10 15

293

Gln Val Thr Arg Val Tyr Ile Phe Asp Tyr Gly Gln Tyr Ser Ala Asp
 20 25 30
 Phe Ser Gly Pro Met Met Ile Ile Thr Gln Lys Ile Thr Ser Leu Ala
 35 40 45
 Cys Glu Ile His Asp Gly Met Phe Arg Lys Asp Glu Glu Leu Thr Ser
 50 55 60
 Ser Gln Arg Asp Leu Ala Val Arg Arg Met Pro Ser Leu Leu Glu Tyr
 65 70 75 80
 Leu Ser Tyr Asn Cys Asn Phe Met Gly Ile Leu Ala Xaa Pro Xaa Cys
 85 90 95
 Ser Tyr Lys Asp Tyr Ile Thr Phe Ile Glu Gly Arg Ser Tyr His Ile
 100 105 110
 Thr Gln Ser Gly Glu Asn Gly Lys Glu Glu Thr Gln Tyr Glu Arg Thr
 115 120 125
 Glu Pro Ser Pro Asn Thr Ala Val Val Gln Lys Leu Leu Val Cys Gly
 130 135 140
 Leu Ser Leu Leu Phe His Leu Thr Ile Cys Thr Thr Leu Pro Val Glu
 145 150 155 160
 Tyr Asn Ile Asp Glu His Phe Gln Ala Thr Ala Ser Trp Pro Thr Lys
 165 170 175
 Ile Ile Tyr Leu Tyr Ile Ser Leu Leu Ala Ala Arg Pro Lys Tyr Tyr
 180 185 190
 Phe Ala Trp Thr Leu Ala Asp Ala Ile Asn Asn Ala Ala Gly Phe Gly
 195 200 205
 Phe Arg Gly Tyr Asp Glu Asn Gly Ala Ala Arg Trp Asp Leu Ile Ser
 210 215 220
 Asn Leu Arg Ile Gln Gln Ile Glu Met Ser Thr Ser Phe Lys Met Phe
 225 230 235 240
 Leu Asp Asn Trp Asn Ile Gln Thr Ala Leu Trp Leu Lys Arg Val Cys
 245 250 255
 Tyr Glu Arg Thr Ser Phe Ser Pro Thr Ile Gln Thr Phe Ile Leu Ser
 260 265 270
 Ala Ile Trp His Gly Val Tyr Pro Gly Tyr Tyr Leu Thr Phe Leu Thr
 275 280 285
 Gly Val Leu Met Thr Leu Ala Ala Arg Ala Met Arg Asn Asn Phe Arg
 290 295 300
 His Tyr Phe Ile Glu Pro Ser Gln Leu Lys Leu Phe Tyr Asp Val Ile
 305 310 315 320
 Thr Trp Ile Val Thr Gln Val Ala Ile Ser Tyr Thr Val Val Pro Phe
 325 330 335
 Val Leu Leu Ser Ile Lys Pro Ser Leu Thr Phe Tyr Ser Ser Trp Tyr
 340 345 350
 Tyr Cys Leu His Ile Leu Gly Ile Leu Val Leu Leu Leu Leu Pro Val
 355 360 365

294

Lys Lys Thr Gln Arg Arg Lys Asn Thr His Glu Asn Ile Gln Leu Ser
 370 375 380
 Gln Ser Lys Lys Phe Asp Glu Gly Glu Asn Ser Leu Gly Gln Asn Ser
 385 390 395 400
 Phe Ser Thr Thr Asn Asn Val Cys Asn Gln Asn Gln Glu Ile Ala Ser
 405 410 415
 Arg His Ser Ser Leu Lys Gln
 420

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 <213> Homo sapiens

<220>
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 Met Ser Arg Leu Gly Ala Leu Gly Gly Ala Arg Ala Gly Leu Gly Leu
 1 5 10 15

 ttg ctg ggt acc gcc gcc ggc ctt gga ttc ctg tgc ctc ctt tac agc 96
 Leu Leu Gly Thr Ala Ala Gly Leu Gly Phe Leu Cys Leu Leu Tyr Ser
 20 25 30

 cag cga tgg aaa cgg acc cag cgt cat ggc cgc agc cag agc ctg ccc 144
 Gln Arg Trp Lys Arg Thr Gln Arg His Gly Arg Ser Gln Ser Leu Pro
 35 40 45

 aac tcc ctg gac tat acg cag act tca gat ccc gga cgc cac gtg atg 192
 Asn Ser Leu Asp Tyr Thr Gln Thr Ser Asp Pro Gly Arg His Val Met
 50 55 60

 ctc ctg cgg gct gtc cca ggt ggg gct gga gat gcc tca gtg ctg ccc 240
 Leu Leu Arg Ala Val Pro Gly Gly Ala Gly Asp Ala Ser Val Leu Pro
 65 70 75 80

 agc ctt cca cgg gaa gga cag gag aag gtg ctg gac cgc ctg gac ttt 288
 Ser Leu Pro Arg Glu Gly Gln Glu Lys Val Leu Asp Arg Leu Asp Phe
 85 90 95

 gtg ctg acc agc ctt gtg gcg ctg cgg cgg gag gtg gag gag ctg aga 336

295

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Thr | Ser | Leu | Val | Ala | Leu | Arg | Arg | Glu | Val | Glu | Glu | Leu | Arg | |
| | | | 100 | | | | | 105 | | | | | | 110 | | |
| agc | agc | ctg | cga | ggg | ctt | gcg | ggg | gag | att | gtt | ggg | gag | gtc | cga | tgc | 384 |
| Ser | Ser | Leu | Arg | Gly | Leu | Ala | Gly | Glu | Ile | Val | Gly | Glu | Val | Arg | Cys | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| cac | atg | gaa | gag | aac | cag | aga | gtg | gct | cgg | cgg | cga | agg | ttt | ccg | ttt | 432 |
| His | Met | Glu | Glu | Asn | Gln | Arg | Val | Ala | Arg | Arg | Arg | Arg | Phe | Pro | Phe | |
| | 130 | | | | | 135 | | | | | | 140 | | | | |
| gtc | cgg | gag | agg | agt | gac | tcc | act | ggc | tcc | agc | tct | gtc | tac | ttc | acg | 480 |
| Val | Arg | Glu | Arg | Ser | Asp | Ser | Thr | Gly | Ser | Ser | Ser | Val | Tyr | Phe | Thr | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| gcc | tcc | tcg | gga | gcc | acg | ttc | aca | gat | gct | gag | agt | gaa | ggg | ggg | tac | 528 |
| Ala | Ser | Ser | Gly | Ala | Thr | Phe | Thr | Asp | Ala | Glu | Ser | Glu | Gly | Gly | Tyr | |
| | | | 165 | | | | | 170 | | | | | 175 | | | |
| aca | aca | gcc | aat | gcg | gag | tct | gac | aat | gag | cgg | gac | tct | gac | aaa | gaa | 576 |
| Thr | Thr | Ala | Asn | Ala | Glu | Ser | Asp | Asn | Glu | Arg | Asp | Ser | Asp | Lys | Glu | |
| | | 180 | | | | | | 185 | | | | | 190 | | | |
| agt | gag | gac | ggg | gaa | gat | gaa | gtg | agc | tgt | gag | act | gtg | aag | atg | ggg | 624 |
| Ser | Glu | Asp | Gly | Glu | Asp | Glu | Val | Ser | Cys | Glu | Thr | Val | Lys | Met | Gly | |
| | 195 | | | | | 200 | | | | | | 205 | | | | |
| aga | aag | gat | tct | ctt | gac | ttg | gag | gaa | gag | gca | gct | tca | ggg | gcc | tcc | 672 |
| Arg | Lys | Asp | Ser | Leu | Asp | Leu | Glu | Glu | Glu | Ala | Ala | Ser | Gly | Ala | Ser | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| agt | gcc | ctg | gag | gct | gga | ggg | tcc | tca | ggc | ttg | gag | gat | gtg | ctg | ccc | 720 |
| Ser | Ala | Leu | Glu | Ala | Gly | Gly | Ser | Ser | Gly | Leu | Glu | Asp | Val | Leu | Pro | |
| 225 | | | | 230 | | | | | 235 | | | | | 240 | | |
| ctc | ctg | cag | cag | gcc | gac | gag | ctg | cac | agg | ggg | gat | gag | caa | ggc | aag | 768 |
| Leu | Leu | Gln | Gln | Ala | Asp | Glu | Leu | His | Arg | Gly | Asp | Glu | Gln | Gly | Lys | |
| | | | 245 | | | | | 250 | | | | | 255 | | | |
| cgg | gag | ggc | ttc | cag | ctg | ctg | ctc | aac | aac | aag | ctg | gtg | tat | gga | agc | 816 |
| Arg | Glu | Gly | Phe | Gln | Leu | Leu | Leu | Asn | Asn | Lys | Leu | Val | Tyr | Gly | Ser | |
| | | 260 | | | | | | 265 | | | | 270 | | | | |
| cgg | cag | gac | ttt | ctc | tgg | cgc | ctg | gcc | cga | gcc | tac | agt | gac | atg | tgt | 864 |

296

| | |
|---|------|
| Arg Gln Asp Phe Leu Trp Arg Leu Ala Arg Ala Tyr Ser Asp Met Cys | |
| 275 280 285 | |
| gag ctc act gag gag gtg agc gag aag aag tca tat gcc cta gat gga | 912 |
| Glu Leu Thr Glu Glu Val Ser Glu Lys Lys Ser Tyr Ala Leu Asp Gly | |
| 290 295 300 | |
| aaa gaa gaa gca gag gct gct ctg gag aag ggg gat gag agt gct gac | 960 |
| Lys Glu Glu Ala Glu Ala Ala Leu Glu Lys Gly Asp Glu Ser Ala Asp | |
| 305 310 315 320 | |
| tgt cac ctg tgg tat gcg gtg ctt tgt ggt cag ctg gct gag cat gag | 1008 |
| Cys His Leu Trp Tyr Ala Val Leu Cys Gly Gln Leu Ala Glu His Glu | |
| 325 330 335 | |
| agc atc cag agg cgc atc cag agt ggc ttt agc ttc aag gag cat gtg | 1056 |
| Ser Ile Gln Arg Arg Ile Gln Ser Gly Phe Ser Phe Lys Glu His Val | |
| 340 345 350 | |
| gac aaa gcc att gct ctc cag cca gaa aac ccc atg gct cac ttt ctt | 1104 |
| Asp Lys Ala Ile Ala Leu Gln Pro Glu Asn Pro Met Ala His Phe Leu | |
| 355 360 365 | |
| ctt ggc agg tgg tgc tat cag gtc tct cac ctg agc tgg cta gaa aaa | 1152 |
| Leu Gly Arg Trp Cys Tyr Gln Val Ser His Leu Ser Trp Leu Glu Lys | |
| 370 375 380 | |
| aaa act gct aca gcc ttg ctt gaa agc cct ctc agt gcc act gtg gaa | 1200 |
| Lys Thr Ala Thr Ala Leu Leu Glu Ser Pro Leu Ser Ala Thr Val Glu | |
| 385 390 395 400 | |
| gat gcc ctc cag agc ttc cta aag gct gaa gaa cta cag cca gga ttt | 1248 |
| Asp Ala Leu Gln Ser Phe Leu Lys Ala Glu Glu Leu Gln Pro Gly Phe | |
| 405 410 415 | |
| tcc aaa gca gga agg gta tat att tcc aag tgc tac aga gaa cta ggg | 1296 |
| Ser Lys Ala Gly Arg Val Tyr Ile Ser Lys Cys Tyr Arg Glu Leu Gly | |
| 420 425 430 | |
| aaa aac tct gaa gct aga tgg tgg atg aag ttg gcc ctg gag ctg cca | 1344 |
| Lys Asn Ser Glu Ala Arg Trp Trp Met Lys Leu Ala Leu Glu Leu Pro | |
| 435 440 445 | |
| gat gtc acg aag gag gat ttg gct atc cag aag gac ctg gaa gaa ctg | 1392 |

297

Asp Val Thr Lys Glu Asp Leu Ala Ile Gln Lys Asp Leu Glu Glu Leu
 450 455 460

gaa gtc att tta cga gac taa
 Glu Val Ile Leu Arg Asp *
 465 470

1413

<210> 210
 <211> 470
 <212> PRT
 <213> Homo sapiens

<400> 210

Met Ser Arg Leu Gly Ala Leu Gly Gly Ala Arg Ala Gly Leu Gly Leu
 1 5 10 15
 Leu Leu Gly Thr Ala Ala Gly Leu Gly Phe Leu Cys Leu Leu Tyr Ser
 20 25 30
 Gln Arg Trp Lys Arg Thr Gln Arg His Gly Arg Ser Gln Ser Leu Pro
 35 40 45
 Asn Ser Leu Asp Tyr Thr Gln Thr Ser Asp Pro Gly Arg His Val Met
 50 55 60
 Leu Leu Arg Ala Val Pro Gly Gly Ala Gly Asp Ala Ser Val Leu Pro
 65 70 75 80
 Ser Leu Pro Arg Glu Gly Gln Glu Lys Val Leu Asp Arg Leu Asp Phe
 85 90 95
 Val Leu Thr Ser Leu Val Ala Leu Arg Arg Glu Val Glu Glu Leu Arg
 100 105 110
 Ser Ser Leu Arg Gly Leu Ala Gly Glu Ile Val Gly Glu Val Arg Cys
 115 120 125
 His Met Glu Glu Asn Gln Arg Val Ala Arg Arg Arg Phe Pro Phe
 130 135 140
 Val Arg Glu Arg Ser Asp Ser Thr Gly Ser Ser Ser Val Tyr Phe Thr
 145 150 155 160
 Ala Ser Ser Gly Ala Thr Phe Thr Asp Ala Glu Ser Glu Gly Gly Tyr
 165 170 175
 Thr Thr Ala Asn Ala Glu Ser Asp Asn Glu Arg Asp Ser Asp Lys Glu
 180 185 190
 Ser Glu Asp Gly Glu Asp Glu Val Ser Cys Glu Thr Val Lys Met Gly
 195 200 205
 Arg Lys Asp Ser Leu Asp Leu Glu Glu Glu Ala Ala Ser Gly Ala Ser
 210 215 220
 Ser Ala Leu Glu Ala Gly Ser Ser Gly Leu Glu Asp Val Leu Pro
 225 230 235 240

298

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|-----|
| Leu | Leu | Gln | Gln | Ala | Asp | Glu | Leu | His | Arg | Gly | Asp | Glu | Gln | Gly | Lys | | | |
| | | | | | | 245 | | | | | | | 250 | | | | | 255 |
| Arg | Glu | Gly | Phe | Gln | Leu | Leu | Leu | Asn | Asn | Lys | Leu | Val | Tyr | Gly | Ser | | | |
| | | | | | | 260 | | | | | | | 265 | | | | | 270 |
| Arg | Gln | Asp | Phe | Leu | Trp | Arg | Leu | Ala | Arg | Ala | Tyr | Ser | Asp | Met | Cys | | | |
| | | | | | | 275 | | | | | | | 280 | | | | | 285 |
| Glu | Leu | Thr | Glu | Glu | Val | Ser | Glu | Lys | Lys | Ser | Tyr | Ala | Leu | Asp | Gly | | | |
| | | | | | | 290 | | | | | | | 295 | | | | | 300 |
| Lys | Glu | Glu | Ala | Glu | Ala | Ala | Leu | Glu | Lys | Gly | Asp | Glu | Ser | Ala | Asp | | | |
| | | | | | | 305 | | | | | | | 310 | | | | | 315 |
| Cys | His | Leu | Trp | Tyr | Ala | Val | Leu | Cys | Gly | Gln | Leu | Ala | Glu | His | Glu | | | |
| | | | | | | 325 | | | | | | | 330 | | | | | 335 |
| Ser | Ile | Gln | Arg | Arg | Ile | Gln | Ser | Gly | Phe | Ser | Phe | Lys | Glu | His | Val | | | |
| | | | | | | 340 | | | | | | | 345 | | | | | 350 |
| Asp | Lys | Ala | Ile | Ala | Leu | Gln | Pro | Glu | Asn | Pro | Met | Ala | His | Phe | Leu | | | |
| | | | | | | 355 | | | | | | | 360 | | | | | 365 |
| Leu | Gly | Arg | Trp | Cys | Tyr | Gln | Val | Ser | His | Leu | Ser | Trp | Leu | Glu | Lys | | | |
| | | | | | | 370 | | | | | | | 375 | | | | | 380 |
| Lys | Thr | Ala | Thr | Ala | Leu | Leu | Glu | Ser | Pro | Leu | Ser | Ala | Thr | Val | Glu | | | |
| | | | | | | 385 | | | | | | | 390 | | | | | 395 |
| Asp | Ala | Leu | Gln | Ser | Phe | Leu | Lys | Ala | Glu | Glu | Leu | Gln | Pro | Gly | Phe | | | |
| | | | | | | 405 | | | | | | | 410 | | | | | 415 |
| Ser | Lys | Ala | Gly | Arg | Val | Tyr | Ile | Ser | Lys | Cys | Tyr | Arg | Glu | Leu | Gly | | | |
| | | | | | | 420 | | | | | | | 425 | | | | | 430 |
| Lys | Asn | Ser | Glu | Ala | Arg | Trp | Trp | Met | Lys | Leu | Ala | Leu | Glu | Leu | Pro | | | |
| | | | | | | 435 | | | | | | | 440 | | | | | 445 |
| Asp | Val | Thr | Lys | Glu | Asp | Leu | Ala | Ile | Gln | Lys | Asp | Leu | Glu | Glu | Leu | | | |
| | | | | | | 450 | | | | | | | 455 | | | | | 460 |
| Glu | Val | Ile | Leu | Arg | Asp | | | | | | | | | | | | | |
| | | | | | | 465 | | | | | | | 470 | | | | | |

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<210> 211
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<213> Homo sapiens
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<220>
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<400> 211

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Met Asp Leu Ala Gly Leu Leu Lys Ser Gln Phe Leu Cys His Leu Val
1 5 10 15

299

| | |
|---|-----|
| ttc tgc tac gtc ttt att gcc tca ggg cta atc atc aac acc att cag Phe Cys Tyr Val Phe Ile Ala Ser Gly Leu Ile Ile Asn Thr Ile Gln 20 25 30 | 96 |
| ctc ttc act ctc ctc ctc tgg ccc att aac aag cag ctc ttc cgg aag Leu Phe Thr Leu Leu Leu Trp Pro Ile Asn Lys Gln Leu Phe Arg Lys 35 40 45 | 144 |
| atc aac tgc aga ctg tcc tat tgc atc tca agc cag ctg gtg atg ctg Ile Asn Cys Arg Leu Ser Tyr Cys Ile Ser Ser Gln Leu Val Met Leu 50 55 60 | 192 |
| ctg gag tgg tgg tgc ggc acg gaa tgc acc atc ttc acg gac ccg cgc Leu Glu Trp Trp Ser Gly Thr Glu Cys Thr Ile Phe Thr Asp Pro Arg 65 70 75 80 | 240 |
| gcc tac ctc aag tat ggg aag gaa aat gcc atc gtg gtt ctc aac cac Ala Tyr Leu Lys Tyr Gly Lys Glu Asn Ala Ile Val Val Leu Asn His 85 90 95 | 288 |
| aag ttt gaa att gac ttt ctg tgt ggc tgg agc ctg tcc gaa cgc ttt Lys Phe Glu Ile Asp Phe Leu Cys Gly Trp Ser Leu Ser Glu Arg Phe 100 105 110 | 336 |
| ggg ctg tta ggg ggc tcc aag gtc ctg gcc aag aaa gag ctg gcc tat Gly Leu Leu Gly Gly Ser Lys Val Leu Ala Lys Lys Glu Leu Ala Tyr 115 120 125 | 384 |
| gtc cca att atc ggc tgg atg tgg tac ttc acc gag atg gtc ttc tgt Val Pro Ile Ile Gly Trp Met Trp Tyr Phe Thr Glu Met Val Phe Cys 130 135 140 | 432 |
| tcg cgc aag tgg gag cag gat cgc aag acg gtt gcc acc agt ttg cag Ser Arg Lys Trp Glu Gln Asp Arg Lys Thr Val Ala Thr Ser Leu Gln 145 150 155 160 | 480 |
| cac ctc cgg gac tac ccc gag aag tat ttt ttc ctg att cac tgt gag His Leu Arg Asp Tyr Pro Glu Lys Tyr Phe Phe Leu Ile His Cys Glu 165 170 175 | 528 |
| ggc aca cgg ttc acg gag aag aag cat gag atc agc atg cag gtg gcc Gly Thr Arg Phe Thr Glu Lys Lys His Glu Ile Ser Met Gln Val Ala 180 185 190 | 576 |

300

| | |
|---|------|
| cgg gcc aag ggg ctg cct cgc ctc aag cat cac ctg ttg cca cga acc Arg Ala Lys Gly Leu Pro Arg Leu Lys His His Leu Leu Pro Arg Thr 195 200 205 | 624 |
| aag ggc ttc gcc atc acc gtg agg agc ttg aga aat gta gtt tca gct Lys Gly Phe Ala Ile Thr Val Arg Ser Leu Arg Asn Val Val Ser Ala 210 215 220 | 672 |
| gta tat gac tgt aca ctc aat ttc aga aat aat gaa aat cca aca ctg Val Tyr Asp Cys Thr Leu Asn Phe Arg Asn Asn Glu Asn Pro Thr Leu 225 230 235 240 | 720 |
| ctg gga gtc cta aac gga aag aaa tac cat gca gat ttg tat gtt agg Leu Gly Val Leu Asn Gly Lys Lys Tyr His Ala Asp Leu Tyr Val Arg 245 250 255 | 768 |
| agg atc cca ctg gaa gac atc cct gaa gac gat gac gag tgc tcg gcc Arg Ile Pro Leu Glu Asp Ile Pro Glu Asp Asp Asp Glu Cys Ser Ala 260 265 270 | 816 |
| tgg ctg cac aag ctc tac cag gag aag gat gcc ttt cag gag gag tac Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Phe Gln Glu Glu Tyr 275 280 285 | 864 |
| tac agg acg ggc acc ttc cca gag acg ccc atg gtg ccc ccc cgg cgg Tyr Arg Thr Gly Thr Phe Pro Glu Thr Pro Met Val Pro Pro Arg Arg 290 295 300 | 912 |
| ccc tgg acc ctc gtg aac tgg ctg ttt tgg gcc tcg ctg gtg ctc tac Pro Trp Thr Leu Val Asn Trp Leu Phe Trp Ala Ser Leu Val Leu Tyr 305 310 315 320 | 960 |
| cct ttc ttc cag ttc ctg gtc agc atg atc agg agc ggg tct tcc ctg Pro Phe Phe Gln Phe Leu Val Ser Met Ile Arg Ser Gly Ser Ser Leu 325 330 335 | 1008 |
| acg ctg gcc agc ttc atc ctc gtc ttc ttt gtg gcc tct gtg gga gtt Thr Leu Ala Ser Phe Ile Leu Val Phe Phe Val Ala Ser Val Gly Val 340 345 350 | 1056 |
| cga tgg atg att ggt gtg acg gaa att gac aag ggc tct gcc tac ggc Arg Trp Met Ile Gly Val Thr Glu Ile Asp Lys Gly Ser Ala Tyr Gly 355 360 365 | 1104 |

301

aac tct gac agc aag cag aaa ctg aat gac tga
 Asn Ser Asp Ser Lys Gln Lys Leu Asn Asp *
 370 375

1137

<210> 212
 <211> 378
 <212> PRT
 <213> Homo sapiens

<400> 212

Met Asp Leu Ala Gly Leu Leu Lys Ser Gln Phe Leu Cys His Leu Val
 1 5 10 15
 Phe Cys Tyr Val Phe Ile Ala Ser Gly Leu Ile Ile Asn Thr Ile Gln
 20 25 30
 Leu Phe Thr Leu Leu Leu Trp Pro Ile Asn Lys Gln Leu Phe Arg Lys
 35 40 45
 Ile Asn Cys Arg Leu Ser Tyr Cys Ile Ser Ser Gln Leu Val Met Leu
 50 55 60
 Leu Glu Trp Trp Ser Gly Thr Glu Cys Thr Ile Phe Thr Asp Pro Arg
 65 70 75 80
 Ala Tyr Leu Lys Tyr Gly Lys Glu Asn Ala Ile Val Val Leu Asn His
 85 90 95
 Lys Phe Glu Ile Asp Phe Leu Cys Gly Trp Ser Leu Ser Glu Arg Phe
 100 105 110
 Gly Leu Leu Gly Gly Ser Lys Val Leu Ala Lys Lys Glu Leu Ala Tyr
 115 120 125
 Val Pro Ile Ile Gly Trp Met Trp Tyr Phe Thr Glu Met Val Phe Cys
 130 135 140
 Ser Arg Lys Trp Glu Gln Asp Arg Lys Thr Val Ala Thr Ser Leu Gln
 145 150 155 160
 His Leu Arg Asp Tyr Pro Glu Lys Tyr Phe Phe Leu Ile His Cys Glu
 165 170 175
 Gly Thr Arg Phe Thr Glu Lys Lys His Glu Ile Ser Met Gln Val Ala
 180 185 190
 Arg Ala Lys Gly Leu Pro Arg Leu Lys His His Leu Leu Pro Arg Thr
 195 200 205
 Lys Gly Phe Ala Ile Thr Val Arg Ser Leu Arg Asn Val Val Ser Ala
 210 215 220
 Val Tyr Asp Cys Thr Leu Asn Phe Arg Asn Asn Glu Asn Pro Thr Leu
 225 230 235 240
 Leu Gly Val Leu Asn Gly Lys Lys Tyr His Ala Asp Leu Tyr Val Arg
 245 250 255

302

Arg Ile Pro Leu Glu Asp Ile Pro Glu Asp Asp Asp Glu Cys Ser Ala
 260 265 270
 Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Phe Gln Glu Glu Tyr
 275 280 285
 Tyr Arg Thr Gly Thr Phe Pro Glu Thr Pro Met Val Pro Pro Arg Arg
 290 295 300
 Pro Trp Thr Leu Val Asn Trp Leu Phe Trp Ala Ser Leu Val Leu Tyr
 305 310 315 320
 Pro Phe Phe Gln Phe Leu Val Ser Met Ile Arg Ser Gly Ser Ser Leu
 325 330 335
 Thr Leu Ala Ser Phe Ile Leu Val Phe Phe Val Ala Ser Val Gly Val
 340 345 350
 Arg Trp Met Ile Gly Val Thr Glu Ile Asp Lys Gly Ser Ala Tyr Gly
 355 360 365
 Asn Ser Asp Ser Lys Gln Lys Leu Asn Asp
 370 375

<210> 213

<211> 495

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(495)

<400> 213

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| atg tcg gtg aac atg gac gag ctg cgg cac cag gtc atg atc aac cag | 48 |
| Met Ser Val Asn Met Asp Glu Leu Arg His Gln Val Met Ile Asn Gln | |
| 1 5 10 15 | |
| ttc gtg ctg gcc gcg ggc tgc gcg gcc gac cag gcg aag cag ttg ctg | 96 |
| Phe Val Leu Ala Ala Gly Cys Ala Ala Asp Gln Ala Lys Gln Leu Leu | |
| 20 25 30 | |
| cag gcg gcc cac tgg cag ttc gag acc gcg ctg agc acg ttc ttc caa | 144 |
| Gln Ala Ala His Trp Gln Phe Glu Thr Ala Leu Ser Thr Phe Phe Gln | |
| 35 40 45 | |
| gaa acc aac att ccc aac agc cac cac cac cag atg atg tgc act | 192 |
| Glu Thr Asn Ile Pro Asn Ser His His His His Gln Met Met Cys Thr | |
| 50 55 60 | |
| ccc agc aac acc cct gcc acg ccg ccc aac ttc ccc gat gcg ctg gcc | 240 |

303

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|
| Pro | Ser | Asn | Thr | Pro | Ala | Thr | Pro | Pro | Asn | Phe | Pro | Asp | Ala | Leu | Ala | | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | | |
| atg | ttc | tcc | aag | ctc | cgc | gcc | tcc | gag | ggc | ctg | cag | agc | agc | aac | agc | | 288 |
| Met | Phe | Ser | Lys | Leu | Arg | Ala | Ser | Glu | Gly | Leu | Gln | Ser | Ser | Asn | Ser | | |
| | | | 85 | | | | | 90 | | | | | | 95 | | | |
| ccc | atg | aca | gcc | gca | gcc | tgc | tcc | cca | cct | gca | aac | ttc | agc | ccc | ttc | | 336 |
| Pro | Met | Thr | Ala | Ala | Ala | Cys | Ser | Pro | Pro | Ala | Asn | Phe | Ser | Pro | Phe | | |
| | | | 100 | | | | | 105 | | | | | | 110 | | | |
| tgg | gcc | tcg | tcc | ccg | ccc | agc | cac | cag | gcg | ccc | tgg | atc | ccg | ccc | tcc | | 384 |
| Trp | Ala | Ser | Ser | Pro | Pro | Ser | His | Gln | Ala | Pro | Trp | Ile | Pro | Pro | Ser | | |
| | | | 115 | | | | 120 | | | | | 125 | | | | | |
| tcc | ccc | acc | acc | ttc | cac | cac | ctc | cac | cgc | cca | cag | ccc | acg | tgg | ccc | | 432 |
| Ser | Pro | Thr | Thr | Phe | His | His | Leu | His | Arg | Pro | Gln | Pro | Thr | Trp | Pro | | |
| | | | 130 | | | | 135 | | | | 140 | | | | | | |
| cca | gga | gca | cag | cag | ggg | ggc | gcc | cag | cag | aaa | gcc | atg | gcg | gcc | atg | | 480 |
| Pro | Gly | Ala | Gln | Gln | Gly | Gly | Ala | Gln | Gln | Lys | Ala | Met | Ala | Ala | Met | | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | | |
| gac | ggc | cag | aga | tga | | | | | | | | | | | | | 495 |
| Asp | Gly | Gln | Arg | * | | | | | | | | | | | | | |

<210> 214

<211> 164

<212> PRT

<213> Homo sapiens

<400> 214

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Ser | Val | Asn | Met | Asp | Glu | Leu | Arg | His | Gln | Val | Met | Ile | Asn | Gln | | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | | |
| Phe | Val | Leu | Ala | Ala | Gly | Cys | Ala | Ala | Asp | Gln | Ala | Lys | Gln | Leu | Leu | | |
| | | | 20 | | | | | 25 | | | | | 30 | | | | |
| Gln | Ala | Ala | His | Trp | Gln | Phe | Glu | Thr | Ala | Leu | Ser | Thr | Phe | Phe | Gln | | |
| | | | 35 | | | | 40 | | | | | 45 | | | | | |
| Glu | Thr | Asn | Ile | Pro | Asn | Ser | His | His | His | His | Gln | Met | Met | Cys | Thr | | |
| | 50 | | | | | 55 | | | | | 60 | | | | | | |
| Pro | Ser | Asn | Thr | Pro | Ala | Thr | Pro | Pro | Asn | Phe | Pro | Asp | Ala | Leu | Ala | | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | | |

304

Met Phe Ser Lys Leu Arg Ala Ser Glu Gly Leu Gln Ser Ser Asn Ser
 85 90 95
 Pro Met Thr Ala Ala Ala Cys Ser Pro Pro Ala Asn Phe Ser Pro Phe
 100 105 110
 Trp Ala Ser Ser Pro Pro Ser His Gln Ala Pro Trp Ile Pro Pro Ser
 115 120 125
 Ser Pro Thr Thr Phe His His Leu His Arg Pro Gln Pro Thr Trp Pro
 130 135 140
 Pro Gly Ala Gln Gln Gly Gly Ala Gln Gln Lys Ala Met Ala Ala Met
 145 150 155 160
 Asp Gly Gln Arg

<210> 215
 <211> 3105
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(3105)

<400> 215
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 Met Ala Ala Ala Thr Gly Ala Val Ala Ala Ser Ala Ala Ser Gly Gln
 1 5 10 15
 gcg gaa ggt aaa aag atc acc gat ctg cgg gtc atc gat ctg aag tcc 96
 Ala Glu Gly Lys Lys Ile Thr Asp Leu Arg Val Ile Asp Leu Lys Ser
 20 25 30
 gag ctg aag cgg cgg aac tta gac atc acc gga gtc aag acc gtg ctc 144
 Glu Leu Lys Arg Arg Asn Leu Asp Ile Thr Gly Val Lys Thr Val Leu
 35 40 45
 atc tcc cga ctc aag cag gct att gaa gag gaa gga ggc gat cca gat 192
 Ile Ser Arg Leu Lys Gln Ala Ile Glu Glu Glu Gly Gly Asp Pro Asp
 50 55 60
 aat att gaa tta act gtt tca act gat act cca aac aag aaa cca act 240
 Asn Ile Glu Leu Thr Val Ser Thr Asp Thr Pro Asn Lys Lys Pro Thr
 65 70 75 80
 aaa ggc aaa ggt aaa aaa cat gaa gca gat gag ttg agt gga gat gct 288

305

| | |
|---|-----|
| Lys Gly Lys Gly Lys Lys His Glu Ala Asp Glu Leu Ser Gly Asp Ala | |
| 85 90 95 | |
| tct gtg gaa gat gat gct ttt atc aag gac tgt gaa ttg gag aat caa | 336 |
| Ser Val Glu Asp Asp Ala Phe Ile Lys Asp Cys Glu Leu Glu Asn Gln | |
| 100 105 110 | |
| gag gca cat gag caa gat gga aat gat gaa cta aag gac tct gaa gaa | 384 |
| Glu Ala His Glu Gln Asp Gly Asn Asp Glu Leu Lys Asp Ser Glu Glu | |
| 115 120 125 | |
| ttt ggt gaa aat gaa gaa gaa aat gtg cat tcc aag gag tta ctc tct | 432 |
| Phe Gly Glu Asn Glu Glu Glu Asn Val His Ser Lys Glu Leu Leu Ser | |
| 130 135 140 | |
| gca gaa gaa aac aag aga gct cat gaa tta ata gag gca gaa gga ata | 480 |
| Ala Glu Glu Asn Lys Arg Ala His Glu Leu Ile Glu Ala Glu Gly Ile | |
| 145 150 155 160 | |
| gaa gat ata gaa aaa gag gac atc gaa agt cag gaa att gaa gct caa | 528 |
| Glu Asp Ile Glu Lys Glu Asp Ile Glu Ser Gln Glu Ile Glu Ala Gln | |
| 165 170 175 | |
| gaa ggt gaa gat gat acc ttt cta aca gcc caa gat ggt gag gaa gaa | 576 |
| Glu Gly Glu Asp Asp Thr Phe Leu Thr Ala Gln Asp Gly Glu Glu Glu | |
| 180 185 190 | |
| gaa aat gag aaa gat ata gca ggt tct ggt gat ggt aca caa gaa gta | 624 |
| Glu Asn Glu Lys Asp Ile Ala Gly Ser Gly Asp Gly Thr Gln Glu Val | |
| 195 200 205 | |
| tct aaa cct ctt cct tca gaa ggg agc cta gct gag gct gat cac aca | 672 |
| Ser Lys Pro Leu Pro Ser Glu Gly Ser Leu Ala Glu Ala Asp His Thr | |
| 210 215 220 | |
| gct cat gaa gag atg gaa gct cat acg act gtg aaa gaa gct gag gat | 720 |
| Ala His Glu Glu Met Glu Ala His Thr Thr Val Lys Glu Ala Glu Asp | |
| 225 230 235 240 | |
| gac aac atc tcg gtc aca atc cag gct gaa gat gcc atc act ctg gat | 768 |
| Asp Asn Ile Ser Val Thr Ile Gln Ala Glu Asp Ala Ile Thr Leu Asp | |
| 245 250 255 | |
| ttt gat ggt gat gac ctc cta gaa aca ggt aaa aat gtg aaa att aca | 816 |

306

| | |
|---|------|
| Phe Asp Gly Asp Asp Leu Leu Glu Thr Gly Lys Asn Val Lys Ile Thr | |
| 260 265 270 | |
| gat tct gaa gca agt aag cca aaa gat ggg cag gac gcc att gca cag | 864 |
| Asp Ser Glu Ala Ser Lys Pro Lys Asp Gly Gln Asp Ala Ile Ala Gln | |
| 275 280 285 | |
| agc ccg gag aag gaa agc aag gat tat gag atg aat gcg aac cat aaa | 912 |
| Ser Pro Glu Lys Glu Ser Lys Asp Tyr Glu Met Asn Ala Asn His Lys | |
| 290 295 300 | |
| gat ggt aag aag gaa gac tgc gtg aag ggt gac cct gtc gag aag gaa | 960 |
| Asp Gly Lys Lys Glu Asp Cys Val Lys Gly Asp Pro Val Glu Lys Glu | |
| 305 310 315 320 | |
| gcc aga gaa agt tct aag aaa gca gaa tct gga gac aaa gaa aag gat | 1008 |
| Ala Arg Glu Ser Ser Lys Lys Ala Glu Ser Gly Asp Lys Glu Lys Asp | |
| 325 330 335 | |
| act ttg aag aaa ggg ccc tcg tct act ggg gcc tct ggt caa gca aag | 1056 |
| Thr Leu Lys Lys Gly Pro Ser Ser Thr Gly Ala Ser Gly Gln Ala Lys | |
| 340 345 350 | |
| agc tct tca aag gaa tct aaa gac agc aag aca tca tct aaa gat gac | 1104 |
| Ser Ser Ser Lys Glu Ser Lys Asp Ser Lys Thr Ser Ser Lys Asp Asp | |
| 355 360 365 | |
| aaa gga agt aca agt agt act agt ggt agc agt gga agc tca act aaa | 1152 |
| Lys Gly Ser Thr Ser Ser Thr Ser Gly Ser Ser Gly Ser Ser Thr Lys | |
| 370 375 380 | |
| aat atc tgg gtt agt gga ctt tca tct aat acc aaa gct gct gat ttg | 1200 |
| Asn Ile Trp Val Ser Gly Leu Ser Ser Asn Thr Lys Ala Ala Asp Leu | |
| 385 390 395 400 | |
| aag aac ctc ttt ggc aaa tat gga aag gtt ctg agt gca aaa gta gtt | 1248 |
| Lys Asn Leu Phe Gly Lys Tyr Gly Lys Val Leu Ser Ala Lys Val Val | |
| 405 410 415 | |
| aca aat gct cga agt cct ggg gca aaa tgc tat ggc att gta act atg | 1296 |
| Thr Asn Ala Arg Ser Pro Gly Ala Lys Cys Tyr Gly Ile Val Thr Met | |
| 420 425 430 | |
| tct tca agc aca gag gtg tcc agg tgt att gca cat ctt cat cgc act | 1344 |

307

| | |
|---|------|
| Ser Ser Ser Thr Glu Val Ser Arg Cys Ile Ala His Leu His Arg Thr | |
| 435 440 445 | |
| gag ctg cat gga cag ctg att tct gtt gaa aaa gta aaa ggt gat ccc | 1392 |
| Glu Leu His Gly Gln Leu Ile Ser Val Glu Lys Val Lys Gly Asp Pro | |
| 450 455 460 | |
| tct aag aaa gaa atg aag aaa gaa aat gat gaa aag agt agt tca aga | 1440 |
| Ser Lys Lys Glu Met Lys Lys Glu Asn Asp Glu Lys Ser Ser Ser Arg | |
| 465 470 475 480 | |
| agt tct gga gat aaa aaa aat acg agt gat aga agt agc aag aca caa | 1488 |
| Ser Ser Gly Asp Lys Lys Asn Thr Ser Asp Arg Ser Ser Lys Thr Gln | |
| 485 490 495 | |
| gcc tct gtc aaa aaa gaa gag aaa aga tcg tct gag aaa tct gaa aaa | 1536 |
| Ala Ser Val Lys Lys Glu Glu Lys Arg Ser Ser Glu Lys Ser Glu Lys | |
| 500 505 510 | |
| aaa gaa agc aag gat act aag aaa ata gaa ggt aaa gat gag aag aat | 1584 |
| Lys Glu Ser Lys Asp Thr Lys Lys Ile Glu Gly Lys Asp Glu Lys Asn | |
| 515 520 525 | |
| gat aat gga gca agt ggc caa aca tca gaa tcg att aaa aaa agt gaa | 1632 |
| Asp Asn Gly Ala Ser Gly Gln Thr Ser Glu Ser Ile Lys Lys Ser Glu | |
| 530 535 540 | |
| gaa aag aag cga ata agt tcc aag agt cca gga cat atg gta ata cta | 1680 |
| Glu Lys Lys Arg Ile Ser Ser Lys Ser Pro Gly His Met Val Ile Leu | |
| 545 550 555 560 | |
| gac caa act aaa gga gat cat tgt aga cca tca aga aga gga aga tat | 1728 |
| Asp Gln Thr Lys Gly Asp His Cys Arg Pro Ser Arg Arg Gly Arg Tyr | |
| 565 570 575 | |
| gag aaa att cat gga aga agt aag gaa aag gag aga gct agt cta gat | 1776 |
| Glu Lys Ile His Gly Arg Ser Lys Glu Lys Glu Arg Ala Ser Leu Asp | |
| 580 585 590 | |
| aaa aaa aga gat aaa gac tac aga agg aaa gag atc ttg cct ttt gaa | 1824 |
| Lys Lys Arg Asp Lys Asp Tyr Arg Arg Lys Glu Ile Leu Pro Phe Glu | |
| 595 600 605 | |
| aag atg aag gaa caa agg ttg aga gaa cat tta gtt cgt ttt gaa agg | 1872 |

308

| | |
|---|------|
| Lys Met Lys Glu Gln Arg Leu Arg Glu His Leu Val Arg Phe Glu Arg | |
| 610 615 620 | |
| ctg cga cga gca atg gaa ctt cga aga cga aga gag att gca gag aga | 1920 |
| Leu Arg Arg Ala Met Glu Leu Arg Arg Arg Arg Glu Ile Ala Glu Arg | |
| 625 630 635 640 | |
| gag cgt cga gag cga gaa cgc att aga ata att cgt gaa cgg gaa gaa | 1968 |
| Glu Arg Arg Glu Arg Glu Arg Ile Arg Ile Ile Arg Glu Arg Glu Glu | |
| 645 650 655 | |
| cgg gaa cgc tta cag aga gag aga gag cgc cta gaa att gaa agg caa | 2016 |
| Arg Glu Arg Leu Gln Arg Glu Arg Glu Arg Leu Glu Ile Glu Arg Gln | |
| 660 665 670 | |
| aaa cta gag aga gag aga atg gaa cgc gaa cgc ttg gaa agg gaa cgc | 2064 |
| Lys Leu Glu Arg Glu Arg Met Glu Arg Glu Arg Leu Glu Arg Glu Arg | |
| 675 680 685 | |
| att cgt att gaa cag gaa cgt cgt aag gaa gct gaa cgg att gct cga | 2112 |
| Ile Arg Ile Glu Gln Glu Arg Arg Lys Glu Ala Glu Arg Ile Ala Arg | |
| 690 695 700 | |
| gaa aga gag gaa ctc aga agg caa caa cag cag ctt cgt tat gaa caa | 2160 |
| Glu Arg Glu Glu Leu Arg Arg Gln Gln Gln Gln Leu Arg Tyr Glu Gln | |
| 705 710 715 720 | |
| gaa aaa agg aat tcc ttg aaa cgc cca cgt gat gta gat cat agg cga | 2208 |
| Glu Lys Arg Asn Ser Leu Lys Arg Pro Arg Asp Val Asp His Arg Arg | |
| 725 730 735 | |
| gat gat cct tac tgg agc gag aat aaa aag ttg tct cta gat aca gat | 2256 |
| Asp Asp Pro Tyr Trp Ser Glu Asn Lys Lys Leu Ser Leu Asp Thr Asp | |
| 740 745 750 | |
| gca cga ttt ggc cat gga tcc gac tac tct cgc caa cag aac aga ttt | 2304 |
| Ala Arg Phe Gly His Gly Ser Asp Tyr Ser Arg Gln Gln Asn Arg Phe | |
| 755 760 765 | |
| aat gac ttt gat cac cga gag agg ggc agg ttt cct gag agt tca gca | 2352 |
| Asn Asp Phe Asp His Arg Glu Arg Gly Arg Phe Pro Glu Ser Ser Ala | |
| 770 775 780 | |
| gta cag tct tca tct ttt gaa agg cgg gat cgc ttt gtt ggt caa agt | 2400 |

309

| | | | | | | | | | | | | | | | | | |
|---|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| Val | Gln | Ser | Ser | Ser | Phe | Glu | Arg | Arg | Asp | Arg | Phe | Val | Gly | Gln | Ser | | |
| 785 | | | | | 790 | | | | | 795 | | | | | 800 | | |
| gag ggg aaa aaa gca cga cct act gca cga agg gaa gat cca agc ttc | | | | | | | | | | | | | | | | 2448 | |
| Glu Gly Lys Lys Ala Arg Pro Thr Ala Arg Arg Glu Asp Pro Ser Phe | | | | | | | | | | | | | | | | | |
| | | | | 805 | | | | | 810 | | | | | 815 | | | |
| gaa aga tat ccc aaa aat ttc agt gac tcc aga aga aat gag cct cca | | | | | | | | | | | | | | | | 2496 | |
| Glu Arg Tyr Pro Lys Asn Phe Ser Asp Ser Arg Arg Asn Glu Pro Pro | | | | | | | | | | | | | | | | | |
| | | | 820 | | | | | 825 | | | | | 830 | | | | |
| cca cca aga aat gaa ctt aga gaa tca gac agg cga gaa gta cga ggg | | | | | | | | | | | | | | | | 2544 | |
| Pro Pro Arg Asn Glu Leu Arg Glu Ser Asp Arg Arg Glu Val Arg Gly | | | | | | | | | | | | | | | | | |
| | | | 835 | | | | 840 | | | | | 845 | | | | | |
| gag cga gac gaa agg aga acg gtg att att cat gac agg cct gat atc | | | | | | | | | | | | | | | | 2592 | |
| Glu Arg Asp Glu Arg Arg Thr Val Ile Ile His Asp Arg Pro Asp Ile | | | | | | | | | | | | | | | | | |
| | | | 850 | | | 855 | | | 860 | | | | | | | | |
| act cat cct aga cat cct cga gag gca ggg ccc aat cct tcc aga ccc | | | | | | | | | | | | | | | | 2640 | |
| Thr His Pro Arg His Pro Arg Glu Ala Gly Pro Asn Pro Ser Arg Pro | | | | | | | | | | | | | | | | | |
| | | | 865 | | | 870 | | | 875 | | | | | 880 | | | |
| acc agc tgg aaa agt gaa gga agc atg tcc act gac aaa cgg gaa aca | | | | | | | | | | | | | | | | 2688 | |
| Thr Ser Trp Lys Ser Glu Gly Ser Met Ser Thr Asp Lys Arg Glu Thr | | | | | | | | | | | | | | | | | |
| | | | 885 | | | | | 890 | | | | | 895 | | | | |
| aga gtt gaa agg cca gaa cga tct ggg aga gaa gta tca ggg cac agt | | | | | | | | | | | | | | | | 2736 | |
| Arg Val Glu Arg Pro Glu Arg Ser Gly Arg Glu Val Ser Gly His Ser | | | | | | | | | | | | | | | | | |
| | | | 900 | | | | 905 | | | | | 910 | | | | | |
| gtg aga ggc gct ccc cct ggg aat cgt agc agc gct tcg ggg tac ggg | | | | | | | | | | | | | | | | 2784 | |
| Val Arg Gly Ala Pro Pro Gly Asn Arg Ser Ser Ala Ser Gly Tyr Gly | | | | | | | | | | | | | | | | | |
| | | | 915 | | | | 920 | | | | | 925 | | | | | |
| agc aga gag gga gac aga gga gtc atc aca gac cga gga ggt gga tca | | | | | | | | | | | | | | | | 2832 | |
| Ser Arg Glu Gly Asp Arg Gly Val Ile Thr Asp Arg Gly Gly Gly Ser | | | | | | | | | | | | | | | | | |
| | | | 930 | | | 935 | | | | 940 | | | | | | | |
| cag cac tat cct gag gag cga cat gtg gtt gaa cgc cat gga cgg gac | | | | | | | | | | | | | | | | 2880 | |
| Gln His Tyr Pro Glu Glu Arg His Val Val Glu Arg His Gly Arg Asp | | | | | | | | | | | | | | | | | |
| | | | 945 | | | 950 | | | 955 | | | | 960 | | | | |
| aca agc gga cca agg aaa gag tgg cat ggt cca ccc tct caa ggg cct | | | | | | | | | | | | | | | | 2928 | |

310

Thr Ser Gly Pro Arg Lys Glu Trp His Gly Pro Pro Ser Gln Gly Pro
 965 970 975
 agc tat cat gat acg agg cga atg ggt gac ggc cgg gca gga gca ggc 2976
 Ser Tyr His Asp Thr Arg Arg Met Gly Asp Gly Arg Ala Gly Ala Gly
 980 985 990
 atg ata acc caa cat tca agt aac gca tcc cca att aat aga att gta 3024
 Met Ile Thr Gln His Ser Ser Asn Ala Ser Pro Ile Asn Arg Ile Val
 995 1000 1005
 caa atc agt ggc aat tcc atg cca aga gga agt ggc tcc gga ttt aag 3072
 Gln Ile Ser Gly Asn Ser Met Pro Arg Gly Ser Gly Ser Gly Phe Lys
 1010 1015 1020
 cca ttt aag ggt gga cct ccg cga cga ttc tga 3105
 Pro Phe Lys Gly Gly Pro Pro Arg Arg Phe *
 1025 1030

<210> 216
 <211> 1034
 <212> PRT
 <213> Homo sapiens

<400> 216
 Met Ala Ala Ala Thr Gly Ala Val Ala Ala Ser Ala Ala Ser Gly Gln
 1 5 10 15
 Ala Glu Gly Lys Lys Ile Thr Asp Leu Arg Val Ile Asp Leu Lys Ser
 20 25 30
 Glu Leu Lys Arg Arg Asn Leu Asp Ile Thr Gly Val Lys Thr Val Leu
 35 40 45
 Ile Ser Arg Leu Lys Gln Ala Ile Glu Glu Glu Gly Gly Asp Pro Asp
 50 55 60
 Asn Ile Glu Leu Thr Val Ser Thr Asp Thr Pro Asn Lys Lys Pro Thr
 65 70 75 80
 Lys Gly Lys Gly Lys Lys His Glu Ala Asp Glu Leu Ser Gly Asp Ala
 85 90 95
 Ser Val Glu Asp Asp Ala Phe Ile Lys Asp Cys Glu Leu Glu Asn Gln
 100 105 110
 Glu Ala His Glu Gln Asp Gly Asn Asp Glu Leu Lys Asp Ser Glu Glu
 115 120 125
 Phe Gly Glu Asn Glu Glu Glu Asn Val His Ser Lys Glu Leu Leu Ser
 130 135 140

311

Ala Glu Glu Asn Lys Arg Ala His Glu Leu Ile Glu Ala Glu Gly Ile
 145 150 155 160
 Glu Asp Ile Glu Lys Glu Asp Ile Glu Ser Gln Glu Ile Glu Ala Gln
 165 170 175
 Glu Gly Glu Asp Asp Thr Phe Leu Thr Ala Gln Asp Gly Glu Glu Glu
 180 185 190
 Glu Asn Glu Lys Asp Ile Ala Gly Ser Gly Asp Gly Thr Gln Glu Val
 195 200 205
 Ser Lys Pro Leu Pro Ser Glu Gly Ser Leu Ala Glu Ala Asp His Thr
 210 215 220
 Ala His Glu Glu Met Glu Ala His Thr Thr Val Lys Glu Ala Glu Asp
 225 230 235 240
 Asp Asn Ile Ser Val Thr Ile Gln Ala Glu Asp Ala Ile Thr Leu Asp
 245 250 255
 Phe Asp Gly Asp Asp Leu Leu Glu Thr Gly Lys Asn Val Lys Ile Thr
 260 265 270
 Asp Ser Glu Ala Ser Lys Pro Lys Asp Gly Gln Asp Ala Ile Ala Gln
 275 280 285
 Ser Pro Glu Lys Glu Ser Lys Asp Tyr Glu Met Asn Ala Asn His Lys
 290 295 300
 Asp Gly Lys Lys Glu Asp Cys Val Lys Gly Asp Pro Val Glu Lys Glu
 305 310 315 320
 Ala Arg Glu Ser Ser Lys Lys Ala Glu Ser Gly Asp Lys Glu Lys Asp
 325 330 335
 Thr Leu Lys Lys Gly Pro Ser Ser Thr Gly Ala Ser Gly Gln Ala Lys
 340 345 350
 Ser Ser Ser Lys Glu Ser Lys Asp Ser Lys Thr Ser Ser Lys Asp Asp
 355 360 365
 Lys Gly Ser Thr Ser Ser Thr Ser Gly Ser Ser Gly Ser Ser Thr Lys
 370 375 380
 Asn Ile Trp Val Ser Gly Leu Ser Ser Asn Thr Lys Ala Ala Asp Leu
 385 390 395 400
 Lys Asn Leu Phe Gly Lys Tyr Gly Lys Val Leu Ser Ala Lys Val Val
 405 410 415
 Thr Asn Ala Arg Ser Pro Gly Ala Lys Cys Tyr Gly Ile Val Thr Met
 420 425 430
 Ser Ser Ser Thr Glu Val Ser Arg Cys Ile Ala His Leu His Arg Thr
 435 440 445
 Glu Leu His Gly Gln Leu Ile Ser Val Glu Lys Val Lys Gly Asp Pro
 450 455 460
 Ser Lys Lys Glu Met Lys Lys Glu Asn Asp Glu Lys Ser Ser Ser Arg
 465 470 475 480
 Ser Ser Gly Asp Lys Lys Asn Thr Ser Asp Arg Ser Ser Lys Thr Gln
 485 490 495

312

Ala Ser Val Lys Lys Glu Glu Lys Arg Ser Ser Glu Lys Ser Glu Lys
 500 505 510
 Lys Glu Ser Lys Asp Thr Lys Lys Ile Glu Gly Lys Asp Glu Lys Asn
 515 520 525
 Asp Asn Gly Ala Ser Gly Gln Thr Ser Glu Ser Ile Lys Lys Ser Glu
 530 535 540
 Glu Lys Lys Arg Ile Ser Ser Lys Ser Pro Gly His Met Val Ile Leu
 545 550 555 560
 Asp Gln Thr Lys Gly Asp His Cys Arg Pro Ser Arg Arg Gly Arg Tyr
 565 570 575
 Glu Lys Ile His Gly Arg Ser Lys Glu Lys Glu Arg Ala Ser Leu Asp
 580 585 590
 Lys Lys Arg Asp Lys Asp Tyr Arg Arg Lys Glu Ile Leu Pro Phe Glu
 595 600 605
 Lys Met Lys Glu Gln Arg Leu Arg Glu His Leu Val Arg Phe Glu Arg
 610 615 620
 Leu Arg Arg Ala Met Glu Leu Arg Arg Arg Arg Glu Ile Ala Glu Arg
 625 630 635 640
 Glu Arg Arg Glu Arg Glu Arg Ile Arg Ile Ile Arg Glu Arg Glu Glu
 645 650 655
 Arg Glu Arg Leu Gln Arg Glu Arg Glu Arg Leu Glu Ile Glu Arg Gln
 660 665 670
 Lys Leu Glu Arg Glu Arg Met Glu Arg Glu Arg Leu Glu Arg Glu Arg
 675 680 685
 Ile Arg Ile Glu Gln Glu Arg Arg Lys Glu Ala Glu Arg Ile Ala Arg
 690 695 700
 Glu Arg Glu Glu Leu Arg Arg Gln Gln Gln Gln Leu Arg Tyr Glu Gln
 705 710 715 720
 Glu Lys Arg Asn Ser Leu Lys Arg Pro Arg Asp Val Asp His Arg Arg
 725 730 735
 Asp Asp Pro Tyr Trp Ser Glu Asn Lys Lys Leu Ser Leu Asp Thr Asp
 740 745 750
 Ala Arg Phe Gly His Gly Ser Asp Tyr Ser Arg Gln Gln Asn Arg Phe
 755 760 765
 Asn Asp Phe Asp His Arg Glu Arg Gly Arg Phe Pro Glu Ser Ser Ala
 770 775 780
 Val Gln Ser Ser Ser Phe Glu Arg Arg Asp Arg Phe Val Gly Gln Ser
 785 790 795 800
 Glu Gly Lys Lys Ala Arg Pro Thr Ala Arg Arg Glu Asp Pro Ser Phe
 805 810 815
 Glu Arg Tyr Pro Lys Asn Phe Ser Asp Ser Arg Arg Asn Glu Pro Pro
 820 825 830
 Pro Pro Arg Asn Glu Leu Arg Glu Ser Asp Arg Arg Glu Val Arg Gly
 835 840 845

313

Glu Arg Asp Glu Arg Arg Thr Val Ile Ile His Asp Arg Pro Asp Ile
 850 855 860
 Thr His Pro Arg His Pro Arg Glu Ala Gly Pro Asn Pro Ser Arg Pro
 865 870 875 880
 Thr Ser Trp Lys Ser Glu Gly Ser Met Ser Thr Asp Lys Arg Glu Thr
 885 890 895
 Arg Val Glu Arg Pro Glu Arg Ser Gly Arg Glu Val Ser Gly His Ser
 900 905 910
 Val Arg Gly Ala Pro Pro Gly Asn Arg Ser Ser Ala Ser Gly Tyr Gly
 915 920 925
 Ser Arg Glu Gly Asp Arg Gly Val Ile Thr Asp Arg Gly Gly Gly Ser
 930 935 940
 Gln His Tyr Pro Glu Glu Arg His Val Val Glu Arg His Gly Arg Asp
 945 950 955 960
 Thr Ser Gly Pro Arg Lys Glu Trp His Gly Pro Pro Ser Gln Gly Pro
 965 970 975
 Ser Tyr His Asp Thr Arg Arg Met Gly Asp Gly Arg Ala Gly Ala Gly
 980 985 990
 Met Ile Thr Gln His Ser Ser Asn Ala Ser Pro Ile Asn Arg Ile Val
 995 1000 1005
 Gln Ile Ser Gly Asn Ser Met Pro Arg Gly Ser Gly Ser Gly Phe Lys
 1010 1015 1020
 Pro Phe Lys Gly Gly Pro Pro Arg Arg Phe
 1025 1030

<210> 217
 <211> 1428
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1428)

<400> 217

| | |
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| atg cct cac agg aag aaa aag ccc ttt ata gag aag aag aaa gct gtg | 48 |
| Met Pro His Arg Lys Lys Lys Pro Phe Ile Glu Lys Lys Lys Ala Val | |
| 1 5 10 15 | |
| tct ttt cac ttg gtc cac cgg agc caa cga gat cct tta gca gca gat | 96 |
| Ser Phe His Leu Val His Arg Ser Gln Arg Asp Pro Leu Ala Ala Asp | |
| 20 25 30 | |
| gag agt gca ccc cag agg gtt cta ttg ccc aca caa aaa ata gac aat | 144 |

314

| | |
|---|-----|
| Glu Ser Ala Pro Gln Arg Val Leu Leu Pro Thr Gln Lys Ile Asp Asn | |
| 35 40 45 | |
| gaa gaa agg cga gca gaa cag agg aag tat gga gtg ttc ttt gat gac | 192 |
| Glu Glu Arg Arg Ala Glu Gln Arg Lys Tyr Gly Val Phe Phe Asp Asp | |
| 50 55 60 | |
| gac tat gac tac ctg cag cac ctg aag gaa cca tct ggg cct tca gag | 240 |
| Asp Tyr Asp Tyr Leu Gln His Leu Lys Glu Pro Ser Gly Pro Ser Glu | |
| 65 70 75 80 | |
| ctt att ccc tca agt acc ttc agt gca cac aac agg aga gag gag aaa | 288 |
| Leu Ile Pro Ser Ser Thr Phe Ser Ala His Asn Arg Arg Glu Glu Lys | |
| 85 90 95 | |
| gaa gaa acg cta gta att cca agc act gga att aag ttg cct tca tca | 336 |
| Glu Glu Thr Leu Val Ile Pro Ser Thr Gly Ile Lys Leu Pro Ser Ser | |
| 100 105 110 | |
| gtg ttt gct tca gag ttt gag gaa gat gtt gga ttg tta aat aaa gca | 384 |
| Val Phe Ala Ser Glu Phe Glu Glu Asp Val Gly Leu Leu Asn Lys Ala | |
| 115 120 125 | |
| gct cca gtt tca gga cct cga ctg gat ttt gat cct gac att gtt gca | 432 |
| Ala Pro Val Ser Gly Pro Arg Leu Asp Phe Asp Pro Asp Ile Val Ala | |
| 130 135 140 | |
| gct ctt gat gat gat ttt gac ttt gat gat cca gat aat ctg ctt gag | 480 |
| Ala Leu Asp Asp Asp Phe Asp Phe Asp Asp Pro Asp Asn Leu Leu Glu | |
| 145 150 155 160 | |
| gat gac ttt att ctt cag gcc aat aag gca aca gga gag gaa gag gga | 528 |
| Asp Asp Phe Ile Leu Gln Ala Asn Lys Ala Thr Gly Glu Glu Glu Gly | |
| 165 170 175 | |
| atg gat ata cag aaa tct gag aat gaa gat gac agc gag tgg gaa gat | 576 |
| Met Asp Ile Gln Lys Ser Glu Asn Glu Asp Asp Ser Glu Trp Glu Asp | |
| 180 185 190 | |
| gtg gat gat gag aag gga gat agc aat gat gac tat gac tct gca ggc | 624 |
| Val Asp Asp Glu Lys Gly Asp Ser Asn Asp Asp Tyr Asp Ser Ala Gly | |
| 195 200 205 | |
| cta ttg tca gat gaa gac tgt atg tct gtg ccc gga aaa act cac aga | 672 |

315

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| Leu | Leu | Ser | Asp | Glu | Asp | Cys | Met | Ser | Val | Pro | Gly | Lys | Thr | His | Arg | |
| 210 | | | | | | 215 | | | | | 220 | | | | | |
| gct | ata | gca | gat | cac | ttg | ttc | tgg | agt | gag | gaa | aca | aag | agt | cgc | ttc | 720 |
| Ala | Ile | Ala | Asp | His | Leu | Phe | Trp | Ser | Glu | Glu | Thr | Lys | Ser | Arg | Phe | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| acg | gag | tat | tcg | atg | act | tcc | tca | gtc | atg | agg | aga | aat | gaa | cag | ctg | 768 |
| Thr | Glu | Tyr | Ser | Met | Thr | Ser | Ser | Val | Met | Arg | Arg | Asn | Glu | Gln | Leu | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| acc | cta | cat | gat | gag | agg | ttt | gag | aag | ttt | tat | gag | caa | tat | gat | gat | 816 |
| Thr | Leu | His | Asp | Glu | Arg | Phe | Glu | Lys | Phe | Tyr | Glu | Gln | Tyr | Asp | Asp | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| gat | gaa | att | gga | gct | ctg | gat | aat | gca | gaa | ttg | gaa | ggc | tct | att | caa | 864 |
| Asp | Glu | Ile | Gly | Ala | Leu | Asp | Asn | Ala | Glu | Leu | Glu | Gly | Ser | Ile | Gln | |
| | 275 | | | | | | 280 | | | | | 285 | | | | |
| gtg | gac | agc | aat | cgc | tta | cag | gaa | ggt | ttg | aat | gac | tac | tat | aaa | gag | 912 |
| Val | Asp | Ser | Asn | Arg | Leu | Gln | Glu | Val | Leu | Asn | Asp | Tyr | Tyr | Lys | Glu | |
| | 290 | | | | | 295 | | | | | 300 | | | | | |
| aag | gca | gag | aat | tgt | gta | aaa | ttg | aat | acc | ctt | gaa | ccc | ttg | gag | gat | 960 |
| Lys | Ala | Glu | Asn | Cys | Val | Lys | Leu | Asn | Thr | Leu | Glu | Pro | Leu | Glu | Asp | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| caa | gac | ctg | cca | atg | aat | gag | ctt | gat | gag | tct | gag | gag | gaa | gaa | atg | 1008 |
| Gln | Asp | Leu | Pro | Met | Asn | Glu | Leu | Asp | Glu | Ser | Glu | Glu | Glu | Glu | Met | |
| | | | | 325 | | | | | 330 | | | | | 335 | | |
| att | act | gta | gtc | ctt | gaa | gaa | gcc | aaa | gag | aag | tgg | gat | tgt | gaa | tct | 1056 |
| Ile | Thr | Val | Val | Leu | Glu | Glu | Ala | Lys | Glu | Lys | Trp | Asp | Cys | Glu | Ser | |
| | | | 340 | | | | | 345 | | | | | 350 | | | |
| att | tgt | agt | aca | tac | tca | aat | tta | tat | aac | cat | cca | cag | ctt | atc | aag | 1104 |
| Ile | Cys | Ser | Thr | Tyr | Ser | Asn | Leu | Tyr | Asn | His | Pro | Gln | Leu | Ile | Lys | |
| | 355 | | | | | | 360 | | | | | 365 | | | | |
| tat | caa | cca | aag | ccc | aaa | caa | att | cga | ata | tct | tct | aaa | aca | gga | ata | 1152 |
| Tyr | Gln | Pro | Lys | Pro | Lys | Gln | Ile | Arg | Ile | Ser | Ser | Lys | Thr | Gly | Ile | |
| | 370 | | | | | 375 | | | | | 380 | | | | | |
| cct | ctc | aat | gtc | tta | cca | aag | aaa | gga | ctc | aca | gca | aag | caa | act | gaa | 1200 |

316

Pro Leu Asn Val Leu Pro Lys Lys Gly Leu Thr Ala Lys Gln Thr Glu
 385 390 395 400
 aga ata cag atg att aat ggc agt gat ctt cct aaa gta tca act cag 1248
 Arg Ile Gln Met Ile Asn Gly Ser Asp Leu Pro Lys Val Ser Thr Gln
 405 410 415
 cca cgt tct aaa aat gaa agc aaa gaa gat aaa aga gca aga aag caa 1296
 Pro Arg Ser Lys Asn Glu Ser Lys Glu Asp Lys Arg Ala Arg Lys Gln
 420 425 430
 gct ata aaa gaa gag cgc aag gaa cga aga gtg gag aag aaa gct aac 1344
 Ala Ile Lys Glu Glu Arg Lys Glu Arg Arg Val Glu Lys Lys Ala Asn
 435 440 445
 aaa tta gca ttt aaa ctg gag aaa aga agg caa gaa aaa gag ctg ctg 1392
 Lys Leu Ala Phe Lys Leu Glu Lys Arg Arg Gln Glu Lys Glu Leu Leu
 450 455 460
 aac ttg aag aag aat gtt gag ggt cta aag cta tag 1428
 Asn Leu Lys Lys Asn Val Glu Gly Leu Lys Leu *
 465 470 475

<210> 218
 <211> 475
 <212> PRT
 <213> Homo sapiens

<400> 218
 Met Pro His Arg Lys Lys Lys Pro Phe Ile Glu Lys Lys Lys Ala Val
 1 5 10 15
 Ser Phe His Leu Val His Arg Ser Gln Arg Asp Pro Leu Ala Ala Asp
 20 25 30
 Glu Ser Ala Pro Gln Arg Val Leu Leu Pro Thr Gln Lys Ile Asp Asn
 35 40 45
 Glu Glu Arg Arg Ala Glu Gln Arg Lys Tyr Gly Val Phe Phe Asp Asp
 50 55 60
 Asp Tyr Asp Tyr Leu Gln His Leu Lys Glu Pro Ser Gly Pro Ser Glu
 65 70 75 80
 Leu Ile Pro Ser Ser Thr Phe Ser Ala His Asn Arg Arg Glu Glu Lys
 85 90 95
 Glu Glu Thr Leu Val Ile Pro Ser Thr Gly Ile Lys Leu Pro Ser Ser
 100 105 110

317

Val Phe Ala Ser Glu Phe Glu Glu Asp Val Gly Leu Leu Asn Lys Ala
 115 120 125
 Ala Pro Val Ser Gly Pro Arg Leu Asp Phe Asp Pro Asp Ile Val Ala
 130 135 140
 Ala Leu Asp Asp Asp Phe Asp Phe Asp Asp Pro Asp Asn Leu Leu Glu
 145 150 155 160
 Asp Asp Phe Ile Leu Gln Ala Asn Lys Ala Thr Gly Glu Glu Glu Gly
 165 170 175
 Met Asp Ile Gln Lys Ser Glu Asn Glu Asp Asp Ser Glu Trp Glu Asp
 180 185 190
 Val Asp Asp Glu Lys Gly Asp Ser Asn Asp Asp Tyr Asp Ser Ala Gly
 195 200 205
 Leu Leu Ser Asp Glu Asp Cys Met Ser Val Pro Gly Lys Thr His Arg
 210 215 220
 Ala Ile Ala Asp His Leu Phe Trp Ser Glu Glu Thr Lys Ser Arg Phe
 225 230 235 240
 Thr Glu Tyr Ser Met Thr Ser Ser Val Met Arg Arg Asn Glu Gln Leu
 245 250 255
 Thr Leu His Asp Glu Arg Phe Glu Lys Phe Tyr Glu Gln Tyr Asp Asp
 260 265 270
 Asp Glu Ile Gly Ala Leu Asp Asn Ala Glu Leu Glu Gly Ser Ile Gln
 275 280 285
 Val Asp Ser Asn Arg Leu Gln Glu Val Leu Asn Asp Tyr Tyr Lys Glu
 290 295 300
 Lys Ala Glu Asn Cys Val Lys Leu Asn Thr Leu Glu Pro Leu Glu Asp
 305 310 315 320
 Gln Asp Leu Pro Met Asn Glu Leu Asp Glu Ser Glu Glu Glu Glu Met
 325 330 335
 Ile Thr Val Val Leu Glu Glu Ala Lys Glu Lys Trp Asp Cys Glu Ser
 340 345 350
 Ile Cys Ser Thr Tyr Ser Asn Leu Tyr Asn His Pro Gln Leu Ile Lys
 355 360 365
 Tyr Gln Pro Lys Pro Lys Gln Ile Arg Ile Ser Ser Lys Thr Gly Ile
 370 375 380
 Pro Leu Asn Val Leu Pro Lys Lys Gly Leu Thr Ala Lys Gln Thr Glu
 385 390 395 400
 Arg Ile Gln Met Ile Asn Gly Ser Asp Leu Pro Lys Val Ser Thr Gln
 405 410 415
 Pro Arg Ser Lys Asn Glu Ser Lys Glu Asp Lys Arg Ala Arg Lys Gln
 420 425 430
 Ala Ile Lys Glu Glu Arg Lys Glu Arg Arg Val Glu Lys Lys Ala Asn
 435 440 445
 Lys Leu Ala Phe Lys Leu Glu Lys Arg Arg Gln Glu Lys Glu Leu Leu
 450 455 460

318

Asn Leu Lys Lys Asn Val Glu Gly Leu Lys Leu
 465 470 475

<210> 219

<211> 300

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1)...(300)

<400> 219

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 Met Ala Phe Ser Ala Cys Phe Gly Gly Ile Ile Phe Asn Ile Leu Val
 1 5 10 15

ggt gtg ggg ctg ggc tgc ctg ctc cag atc tcc cga agc cac aca gaa 96
 Gly Val Gly Leu Gly Cys Leu Leu Gln Ile Ser Arg Ser His Thr Glu
 20 25 30

gtg aag ctg gag cca gac gga ctg ctg gtg tgg gtc ctg gca ggc gcc 144
 Val Lys Leu Glu Pro Asp Gly Leu Leu Val Trp Val Leu Ala Gly Ala
 35 40 45

ctg ggg ctc agc ctc gtc ttc tcc ctg gtc tca gtc cca ttg cag tgc 192
 Leu Gly Leu Ser Leu Val Phe Ser Leu Val Ser Val Pro Leu Gln Cys
 50 55 60

ttc cag ctc agc aga gtc tat ggc ttc tgc ctg ctc ctc ttc tac ctg 240
 Phe Gln Leu Ser Arg Val Tyr Gly Phe Cys Leu Leu Leu Phe Tyr Leu
 65 70 75 80

aac ttc ctt gtc gtg gcc ctc ctc act gaa ttt gga gtg att cac ctg 288
 Asn Phe Leu Val Val Ala Leu Leu Thr Glu Phe Gly Val Ile His Leu
 85 90 95

aaa agc atg tga 300
 Lys Ser Met *

<210> 220

<211> 99

319

<212> PRT

<213> Homo sapiens

<400> 220

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Met Ala Phe Ser Ala Cys Phe Gly Gly Ile Ile Phe Asn Ile Leu Val
 1           5           10           15
Gly Val Gly Leu Gly Cys Leu Leu Gln Ile Ser Arg Ser His Thr Glu
          20           25           30
Val Lys Leu Glu Pro Asp Gly Leu Leu Val Trp Val Leu Ala Gly Ala
        35           40           45
Leu Gly Leu Ser Leu Val Phe Ser Leu Val Ser Val Pro Leu Gln Cys
       50           55           60
Phe Gln Leu Ser Arg Val Tyr Gly Phe Cys Leu Leu Leu Phe Tyr Leu
      65           70           75           80
Asn Phe Leu Val Val Ala Leu Leu Thr Glu Phe Gly Val Ile His Leu
          85           90           95
Lys Ser Met

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<210> 221

<211> 1113

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1113)

<400> 221

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atg agt gcc tct gcg gcc acc ggg gtc ttc gtg ctg tcc ctc tcg gcc      48
Met Ser Ala Ser Ala Ala Thr Gly Val Phe Val Leu Ser Leu Ser Ala
 1           5           10           15

atc ccg gtc acc tat gtc ttc aac cac ctg gcg gcc cag cat gat tcc      96
Ile Pro Val Thr Tyr Val Phe Asn His Leu Ala Ala Gln His Asp Ser
          20           25           30

tgg act att gta ggg gtt gct gcc ctc atc ctg ttc ctg gta gca ctg     144
Trp Thr Ile Val Gly Val Ala Ala Leu Ile Leu Phe Leu Val Ala Leu
        35           40           45

ctg gct cgt gtc ctc gtc aaa aga aaa cca ccc cgg gac cca ctg ttc     192
Leu Ala Arg Val Leu Val Lys Arg Lys Pro Pro Arg Asp Pro Leu Phe
       50           55           60

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| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| tat | gtg | tat | gca | gtt | ttt | gga | ttt | acc | agc | gtg | gtg | aac | ctc | atc | ata | 240 |
| Tyr | Val | Tyr | Ala | Val | Phe | Gly | Phe | Thr | Ser | Val | Val | Asn | Leu | Ile | Ile | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| | | | | | | | | | | | | | | | | |
| gga | ctg | gag | caa | gat | gga | atc | att | gac | ggg | ttc | atg | aca | cac | tac | ttg | 288 |
| Gly | Leu | Glu | Gln | Asp | Gly | Ile | Ile | Asp | Gly | Phe | Met | Thr | His | Tyr | Leu | |
| | | | | 85 | | | | | 90 | | | | | | 95 | |
| | | | | | | | | | | | | | | | | |
| aga | gag | ggt | gaa | ccg | tat | ctg | aac | acc | gca | tat | ggg | cac | atg | atc | tgc | 336 |
| Arg | Glu | Gly | Glu | Pro | Tyr | Leu | Asn | Thr | Ala | Tyr | Gly | His | Met | Ile | Cys | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| | | | | | | | | | | | | | | | | |
| tac | tgg | gat | ggc | tct | gct | cat | tat | ctg | atg | tac | ctg | gtg | atg | gtg | gca | 384 |
| Tyr | Trp | Asp | Gly | Ser | Ala | His | Tyr | Leu | Met | Tyr | Leu | Val | Met | Val | Ala | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| | | | | | | | | | | | | | | | | |
| gcc | ata | gca | tgg | gag | gaa | act | tat | aga | acc | att | ggc | cta | tat | tgg | gtt | 432 |
| Ala | Ile | Ala | Trp | Glu | Glu | Thr | Tyr | Arg | Thr | Ile | Gly | Leu | Tyr | Trp | Val | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| | | | | | | | | | | | | | | | | |
| gga | tct | att | att | atg | agt | gtt | gtt | gtt | ttt | gtg | cca | gga | aac | att | gta | 480 |
| Gly | Ser | Ile | Ile | Met | Ser | Val | Val | Val | Phe | Val | Pro | Gly | Asn | Ile | Val | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| | | | | | | | | | | | | | | | | |
| ggg | aag | tat | gga | aca | cga | att | tgc | cct | gct | ttt | ttc | tta | agc | ata | cca | 528 |
| Gly | Lys | Tyr | Gly | Thr | Arg | Ile | Cys | Pro | Ala | Phe | Phe | Leu | Ser | Ile | Pro | |
| | | | | 165 | | | | 170 | | | | | | 175 | | |
| | | | | | | | | | | | | | | | | |
| tat | act | tgt | ctt | cct | gtc | tgg | gct | ggc | ttc | aga | atc | tat | aat | cag | cca | 576 |
| Tyr | Thr | Cys | Leu | Pro | Val | Trp | Ala | Gly | Phe | Arg | Ile | Tyr | Asn | Gln | Pro | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| | | | | | | | | | | | | | | | | |
| tca | gaa | aat | tat | aat | tac | ccc | tca | aag | gtt | att | caa | gaa | gcc | caa | gcg | 624 |
| Ser | Glu | Asn | Tyr | Asn | Tyr | Pro | Ser | Lys | Val | Ile | Gln | Glu | Ala | Gln | Ala | |
| | | 195 | | | | 200 | | | | | | 205 | | | | |
| | | | | | | | | | | | | | | | | |
| aaa | gac | ctg | ctg | aga | aga | cca | ttt | gat | tta | atg | ttg | gtt | gtg | tgt | ctc | 672 |
| Lys | Asp | Leu | Leu | Arg | Arg | Pro | Phe | Asp | Leu | Met | Leu | Val | Val | Cys | Leu | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| | | | | | | | | | | | | | | | | |
| ctc | ctg | gca | act | gga | ttt | tgc | ctg | ttc | aga | ggc | ttg | att | gct | ttg | gat | 720 |
| Leu | Leu | Ala | Thr | Gly | Phe | Cys | Leu | Phe | Arg | Gly | Leu | Ile | Ala | Leu | Asp | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |

321

| | |
|---|------|
| tgc cca tct gag ctc tgc cga tta tat acg caa ttt caa gag ccc tat Cys Pro Ser Glu Leu Cys Arg Leu Tyr Thr Gln Phe Gln Glu Pro Tyr 245 250 255 | 768 |
| cta aag gat cct gct gct tat cct aaa att cag atg ctg gca tat atg Leu Lys Asp Pro Ala Ala Tyr Pro Lys Ile Gln Met Leu Ala Tyr Met 260 265 270 | 816 |
| ttc tat tct gtt cct tac ttt gtg act gca ctg tat ggc tta gtg gtt Phe Tyr Ser Val Pro Tyr Phe Val Thr Ala Leu Tyr Gly Leu Val Val 275 280 285 | 864 |
| cct gga tgt tcc tgg atg cct gac atc aca ttg ata cat gct gga ggt Pro Gly Cys Ser Trp Met Pro Asp Ile Thr Leu Ile His Ala Gly Gly 290 295 300 | 912 |
| ctg gct cag gct cag ttt tct cac att ggt gca tct ctt cat gct aga Leu Ala Gln Ala Gln Phe Ser His Ile Gly Ala Ser Leu His Ala Arg 305 310 315 320 | 960 |
| act gct tat gtc tac aga gtc cct gaa gaa gca aaa atc ctt ttt tta Thr Ala Tyr Val Tyr Arg Val Pro Glu Glu Ala Lys Ile Leu Phe Leu 325 330 335 | 1008 |
| gca tta aac ata gca tat gga gtt ctt cct cag ctc ttg gcc tat cgt Ala Leu Asn Ile Ala Tyr Gly Val Leu Pro Gln Leu Leu Ala Tyr Arg 340 345 350 | 1056 |
| tgt atc tac aaa cca gag ttc ttc ata aaa aca aag gca gaa gaa aaa Cys Ile Tyr Lys Pro Glu Phe Phe Ile Lys Thr Lys Ala Glu Glu Lys 355 360 365 | 1104 |
| gtg gaa taa Val Glu * 370 | 1113 |

<210> 222

<211> 370

<212> PRT

<213> Homo sapiens

<400> 222

322

Met Ser Ala Ser Ala Ala Thr Gly Val Phe Val Leu Ser Leu Ser Ala
 1 5 10 15
 Ile Pro Val Thr Tyr Val Phe Asn His Leu Ala Ala Gln His Asp Ser
 20 25 30
 Trp Thr Ile Val Gly Val Ala Ala Leu Ile Leu Phe Leu Val Ala Leu
 35 40 45
 Leu Ala Arg Val Leu Val Lys Arg Lys Pro Pro Arg Asp Pro Leu Phe
 50 55 60
 Tyr Val Tyr Ala Val Phe Gly Phe Thr Ser Val Val Asn Leu Ile Ile
 65 70 75 80
 Gly Leu Glu Gln Asp Gly Ile Ile Asp Gly Phe Met Thr His Tyr Leu
 85 90 95
 Arg Glu Gly Glu Pro Tyr Leu Asn Thr Ala Tyr Gly His Met Ile Cys
 100 105 110
 Tyr Trp Asp Gly Ser Ala His Tyr Leu Met Tyr Leu Val Met Val Ala
 115 120 125
 Ala Ile Ala Trp Glu Glu Thr Tyr Arg Thr Ile Gly Leu Tyr Trp Val
 130 135 140
 Gly Ser Ile Ile Met Ser Val Val Val Phe Val Pro Gly Asn Ile Val
 145 150 155 160
 Gly Lys Tyr Gly Thr Arg Ile Cys Pro Ala Phe Phe Leu Ser Ile Pro
 165 170 175
 Tyr Thr Cys Leu Pro Val Trp Ala Gly Phe Arg Ile Tyr Asn Gln Pro
 180 185 190
 Ser Glu Asn Tyr Asn Tyr Pro Ser Lys Val Ile Gln Glu Ala Gln Ala
 195 200 205
 Lys Asp Leu Leu Arg Arg Pro Phe Asp Leu Met Leu Val Val Cys Leu
 210 215 220
 Leu Leu Ala Thr Gly Phe Cys Leu Phe Arg Gly Leu Ile Ala Leu Asp
 225 230 235 240
 Cys Pro Ser Glu Leu Cys Arg Leu Tyr Thr Gln Phe Gln Glu Pro Tyr
 245 250 255
 Leu Lys Asp Pro Ala Ala Tyr Pro Lys Ile Gln Met Leu Ala Tyr Met
 260 265 270
 Phe Tyr Ser Val Pro Tyr Phe Val Thr Ala Leu Tyr Gly Leu Val Val
 275 280 285
 Pro Gly Cys Ser Trp Met Pro Asp Ile Thr Leu Ile His Ala Gly Gly
 290 295 300
 Leu Ala Gln Ala Gln Phe Ser His Ile Gly Ala Ser Leu His Ala Arg
 305 310 315 320
 Thr Ala Tyr Val Tyr Arg Val Pro Glu Glu Ala Lys Ile Leu Phe Leu
 325 330 335
 Ala Leu Asn Ile Ala Tyr Gly Val Leu Pro Gln Leu Leu Ala Tyr Arg
 340 345 350

323

Cys Ile Tyr Lys Pro Glu Phe Phe Ile Lys Thr Lys Ala Glu Glu Lys
 355 360 365
 Val Glu
 370

<210> 223
 <211> 357
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)...(357)

<400> 223

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 Met Glu Arg Leu Gly Val Leu Trp Thr Leu Leu Val Ser Arg Trp Phe
 1 5 10 15

atc tgc ctg ttt gtg gac atc ttg ccc gtg gag aca gtg ctt cgg atc 96
 Ile Cys Leu Phe Val Asp Ile Leu Pro Val Glu Thr Val Leu Arg Ile
 20 25 30

tgg gac tgt ttg ttt aac gaa ggc tcg aag att atc ttc cgg gtg gcc 144
 Trp Asp Cys Leu Phe Asn Glu Gly Ser Lys Ile Ile Phe Arg Val Ala
 35 40 45

ctg acc tta att aag cag cac cag gag ttg att ttg gaa gcc acc agc 192
 Leu Thr Leu Ile Lys Gln His Gln Glu Leu Ile Leu Glu Ala Thr Ser
 50 55 60

gtt cca gac att tgc gat aag ttt aag cag ata acc aaa ggg agt ttc 240
 Val Pro Asp Ile Cys Asp Lys Phe Lys Gln Ile Thr Lys Gly Ser Phe
 65 70 75 80

gtg atg gag tgt cac acg ttt atg cag aaa ata ttt tca gaa cct gga 288
 Val Met Glu Cys His Thr Phe Met Gln Lys Ile Phe Ser Glu Pro Gly
 85 90 95

agc tta tcc atg gcc acc gtc gcc aag ctc cgc gag agc tgc agg gcc 336
 Ser Leu Ser Met Ala Thr Val Ala Lys Leu Arg Glu Ser Cys Arg Ala
 100 105 110

cgg ctg ctg gca cag ggg tga 357

324

Arg Leu Leu Ala Gln Gly *
115

<210> 224

<211> 118

<212> PRT

<213> Homo sapiens

<400> 224

Met Glu Arg Leu Gly Val Leu Trp Thr Leu Leu Val Ser Arg Trp Phe
1 5 10 15
Ile Cys Leu Phe Val Asp Ile Leu Pro Val Glu Thr Val Leu Arg Ile
20 25 30
Trp Asp Cys Leu Phe Asn Glu Gly Ser Lys Ile Ile Phe Arg Val Ala
35 40 45
Leu Thr Leu Ile Lys Gln His Gln Glu Leu Ile Leu Glu Ala Thr Ser
50 55 60
Val Pro Asp Ile Cys Asp Lys Phe Lys Gln Ile Thr Lys Gly Ser Phe
65 70 75 80
Val Met Glu Cys His Thr Phe Met Gln Lys Ile Phe Ser Glu Pro Gly
85 90 95
Ser Leu Ser Met Ala Thr Val Ala Lys Leu Arg Glu Ser Cys Arg Ala
100 105 110
Arg Leu Leu Ala Gln Gly
115

<210> 225

<211> 1764

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1764)

<400> 225

atg agg ccg cga ggt ctc ccg ccg ctc ctg gtg gtg ctc ctg ggc tgc 48
Met Arg Pro Arg Gly Leu Pro Pro Leu Leu Val Val Leu Leu Gly Cys
1 5 10 15
tgg gcc tcc gtg agc gcc cag acc gat gcc acc ccg gcg gtg acg aca 96
Trp Ala Ser Val Ser Ala Gln Thr Asp Ala Thr Pro Ala Val Thr Thr
20 25 30

325

| | |
|---|-----|
| gag ggc ctc aac tcc acc gag gca gcc ctg gcc acc ttc gga act ttc Glu Gly Leu Asn Ser Thr Glu Ala Ala Leu Ala Thr Phe Gly Thr Phe 35 40 45 | 144 |
| ccg tcg acc agg ccc ccc ggg act ccc agg gct cca ggg ccc tcc tcc Pro Ser Thr Arg Pro Pro Gly Thr Pro Arg Ala Pro Gly Pro Ser Ser 50 55 60 | 192 |
| ggc ccc agg cct acc cca gtc acg gac gtt gct gtt ctc tgt gtc tgt Gly Pro Arg Pro Thr Pro Val Thr Asp Val Ala Val Leu Cys Val Cys 65 70 75 80 | 240 |
| gac tta tcc cca gca cag tgt gac atc aac tgc tgc tgt gat ccc gac Asp Leu Ser Pro Ala Gln Cys Asp Ile Asn Cys Cys Cys Asp Pro Asp 85 90 95 | 288 |
| tgc agc tcc gtg gat ttc agt gtc ttt tct gcc tgc tca gtt cca gtt Cys Ser Ser Val Asp Phe Ser Val Phe Ser Ala Cys Ser Val Pro Val 100 105 110 | 336 |
| gtc acg ggc gac agc cag ttt tgt agt caa aaa gca gtc atc tat tca Val Thr Gly Asp Ser Gln Phe Cys Ser Gln Lys Ala Val Ile Tyr Ser 115 120 125 | 384 |
| ttg aat ttt aca gca aac cca cct caa aga gta ttt gaa ctt gtt gac Leu Asn Phe Thr Ala Asn Pro Pro Gln Arg Val Phe Glu Leu Val Asp 130 135 140 | 432 |
| cag att aat cca tct att ttc tgc att cat att aca aac tat aaa cct Gln Ile Asn Pro Ser Ile Phe Cys Ile His Ile Thr Asn Tyr Lys Pro 145 150 155 160 | 480 |
| gca tta tcc ttt att aat cca gaa gta cct gat gaa aac aat ttt gat Ala Leu Ser Phe Ile Asn Pro Glu Val Pro Asp Glu Asn Asn Phe Asp 165 170 175 | 528 |
| aca ttg atg aaa aca tct gat ggt ttt aca ttg aat gct gaa tca tat Thr Leu Met Lys Thr Ser Asp Gly Phe Thr Leu Asn Ala Glu Ser Tyr 180 185 190 | 576 |
| gtt tcc ttc aca acc aaa ctg gat att cct act gct gct aaa tat gag Val Ser Phe Thr Thr Lys Leu Asp Ile Pro Thr Ala Ala Lys Tyr Glu 195 200 205 | 624 |

326

| | |
|---|------|
| tat ggg gtt cct ctg cag act tca gat tcg ttt ctg aga ttt cct tcg Tyr Gly Val Pro Leu Gln Thr Ser Asp Ser Phe Leu Arg Phe Pro Ser 210 215 220 | 672 |
| tcc ctg aca tca tct ctg tgc act gat aat aac cct gca gcg ttt ctg Ser Leu Thr Ser Ser Leu Cys Thr Asp Asn Asn Pro Ala Ala Phe Leu 225 230 235 240 | 720 |
| gtg aac cag gct gtt aag tgc acc aga aaa ata aat tta gaa cag tgt Val Asn Gln Ala Val Lys Cys Thr Arg Lys Ile Asn Leu Glu Gln Cys 245 250 255 | 768 |
| gaa gaa att gaa gcc ctc agc atg gct ttt tac agc agc ccg gaa att Glu Glu Ile Glu Ala Leu Ser Met Ala Phe Tyr Ser Ser Pro Glu Ile 260 265 270 | 816 |
| ctg agg gta cct gat tca aga aaa aag gtc cct atc act gtt cag tcc Leu Arg Val Pro Asp Ser Arg Lys Lys Val Pro Ile Thr Val Gln Ser 275 280 285 | 864 |
| atc gtc att cag tct cta aat aaa acg ctc acc cga cgg gag gac act Ile Val Ile Gln Ser Leu Asn Lys Thr Leu Thr Arg Arg Glu Asp Thr 290 295 300 | 912 |
| gat gtg ctg cag ccg act ctc gtc aac gct gga cac ttt agc ctt tgc Asp Val Leu Gln Pro Thr Leu Val Asn Ala Gly His Phe Ser Leu Cys 305 310 315 320 | 960 |
| gtg aat gtt gtt ctt gag gta aag tac agc ctc aca tac aca gat gca Val Asn Val Val Leu Glu Val Lys Tyr Ser Leu Thr Tyr Thr Asp Ala 325 330 335 | 1008 |
| ggt gaa gtc acc aaa gct gat ctc tca ttc gtt ctg ggg aca gtt agc Gly Glu Val Thr Lys Ala Asp Leu Ser Phe Val Leu Gly Thr Val Ser 340 345 350 | 1056 |
| agc gta gtg gtc cca ctg cag caa aag ttt gaa att cat ttt ctt cag Ser Val Val Val Pro Leu Gln Gln Lys Phe Glu Ile His Phe Leu Gln 355 360 365 | 1104 |
| gaa aat acc cag cca gtc cct ctc agt gga aac cct ggt tat gtc gtg Glu Asn Thr Gln Pro Val Pro Leu Ser Gly Asn Pro Gly Tyr Val Val 370 375 380 | 1152 |

327

| | |
|---|------|
| ggg ctc cca tta gct gct gga ttc cag cct cat aag ggg tct ggg att Gly Leu Pro Leu Ala Ala Gly Phe Gln Pro His Lys Gly Ser Gly Ile 385 390 395 400 | 1200 |
| att cag acc aca aat aga tat gga cag ctt act att ctt cat agc aca Ile Gln Thr Thr Asn Arg Tyr Gly Gln Leu Thr Ile Leu His Ser Thr 405 410 415 | 1248 |
| act gag caa gac tgc tta gca ctg gag ggg gtc cgg acc cca gta tta Thr Glu Gln Asp Cys Leu Ala Leu Glu Gly Val Arg Thr Pro Val Leu 420 425 430 | 1296 |
| ttt ggt tac act atg caa tct ggc tgt aaa cta aga ctg act gga gct Phe Gly Tyr Thr Met Gln Ser Gly Cys Lys Leu Arg Leu Thr Gly Ala 435 440 445 | 1344 |
| ctc ccg tgt cag ctc gta gca cag aag gtg aag agc ctg ctg tgg ggc Leu Pro Cys Gln Leu Val Ala Gln Lys Val Lys Ser Leu Leu Trp Gly 450 455 460 | 1392 |
| cag ggc ttc cca gat tac gtg gcc cct ttt gga aat tcc cag gcc cag Gln Gly Phe Pro Asp Tyr Val Ala Pro Phe Gly Asn Ser Gln Ala Gln 465 470 475 480 | 1440 |
| gac atg ctg gac tgg gtg ccc atc cac ttc atc acc cag tca ttc aac Asp Met Leu Asp Trp Val Pro Ile His Phe Ile Thr Gln Ser Phe Asn 485 490 495 | 1488 |
| agg aag gat tcc tgc cag ctc cca ggg gct ttg gtt ata gaa gtg aag Arg Lys Asp Ser Cys Gln Leu Pro Gly Ala Leu Val Ile Glu Val Lys 500 505 510 | 1536 |
| tgg act aaa tac gga tcc ctg ctg aat cca cag gcc aaa ata gtc aat Trp Thr Lys Tyr Gly Ser Leu Leu Asn Pro Gln Ala Lys Ile Val Asn 515 520 525 | 1584 |
| gta act gca aat cta att tca tcc tcc ttt cct gag gcc aac tca gga Val Thr Ala Asn Leu Ile Ser Ser Ser Phe Pro Glu Ala Asn Ser Gly 530 535 540 | 1632 |
| aat gaa agg acg att ctt att tcc act gcg gtt act ttt gtg gat gtg Asn Glu Arg Thr Ile Leu Ile Ser Thr Ala Val Thr Phe Val Asp Val 545 550 555 560 | 1680 |

328

tct gca cct gca gag gca ggc ttc aga gct cca cca gcc atc aat gcc 1728
 Ser Ala Pro Ala Glu Ala Gly Phe Arg Ala Pro Pro Ala Ile Asn Ala
 565 570 575

agg ctg ccc ttt aac ttc ttc ttc ccg ttt gtt tga 1764
 Arg Leu Pro Phe Asn Phe Phe Phe Pro Phe Val *
 580 585

<210> 226

<211> 587

<212> PRT

<213> Homo sapiens

<400> 226

Met Arg Pro Arg Gly Leu Pro Pro Leu Leu Val Val Leu Leu Gly Cys
 1 5 10 15
 Trp Ala Ser Val Ser Ala Gln Thr Asp Ala Thr Pro Ala Val Thr Thr
 20 25 30
 Glu Gly Leu Asn Ser Thr Glu Ala Ala Leu Ala Thr Phe Gly Thr Phe
 35 40 45
 Pro Ser Thr Arg Pro Pro Gly Thr Pro Arg Ala Pro Gly Pro Ser Ser
 50 55 60
 Gly Pro Arg Pro Thr Pro Val Thr Asp Val Ala Val Leu Cys Val Cys
 65 70 75 80
 Asp Leu Ser Pro Ala Gln Cys Asp Ile Asn Cys Cys Cys Asp Pro Asp
 85 90 95
 Cys Ser Ser Val Asp Phe Ser Val Phe Ser Ala Cys Ser Val Pro Val
 100 105 110
 Val Thr Gly Asp Ser Gln Phe Cys Ser Gln Lys Ala Val Ile Tyr Ser
 115 120 125
 Leu Asn Phe Thr Ala Asn Pro Pro Gln Arg Val Phe Glu Leu Val Asp
 130 135 140
 Gln Ile Asn Pro Ser Ile Phe Cys Ile His Ile Thr Asn Tyr Lys Pro
 145 150 155 160
 Ala Leu Ser Phe Ile Asn Pro Glu Val Pro Asp Glu Asn Asn Phe Asp
 165 170 175
 Thr Leu Met Lys Thr Ser Asp Gly Phe Thr Leu Asn Ala Glu Ser Tyr
 180 185 190
 Val Ser Phe Thr Thr Lys Leu Asp Ile Pro Thr Ala Ala Lys Tyr Glu
 195 200 205
 Tyr Gly Val Pro Leu Gln Thr Ser Asp Ser Phe Leu Arg Phe Pro Ser
 210 215 220

329

Ser Leu Thr Ser Ser Leu Cys Thr Asp Asn Asn Pro Ala Ala Phe Leu
 225 230 235 240
 Val Asn Gln Ala Val Lys Cys Thr Arg Lys Ile Asn Leu Glu Gln Cys
 245 250 255
 Glu Glu Ile Glu Ala Leu Ser Met Ala Phe Tyr Ser Ser Pro Glu Ile
 260 265 270
 Leu Arg Val Pro Asp Ser Arg Lys Lys Val Pro Ile Thr Val Gln Ser
 275 280 285
 Ile Val Ile Gln Ser Leu Asn Lys Thr Leu Thr Arg Arg Glu Asp Thr
 290 295 300
 Asp Val Leu Gln Pro Thr Leu Val Asn Ala Gly His Phe Ser Leu Cys
 305 310 315 320
 Val Asn Val Val Leu Glu Val Lys Tyr Ser Leu Thr Tyr Thr Asp Ala
 325 330 335
 Gly Glu Val Thr Lys Ala Asp Leu Ser Phe Val Leu Gly Thr Val Ser
 340 345 350
 Ser Val Val Val Pro Leu Gln Gln Lys Phe Glu Ile His Phe Leu Gln
 355 360 365
 Glu Asn Thr Gln Pro Val Pro Leu Ser Gly Asn Pro Gly Tyr Val Val
 370 375 380
 Gly Leu Pro Leu Ala Ala Gly Phe Gln Pro His Lys Gly Ser Gly Ile
 385 390 395 400
 Ile Gln Thr Thr Asn Arg Tyr Gly Gln Leu Thr Ile Leu His Ser Thr
 405 410 415
 Thr Glu Gln Asp Cys Leu Ala Leu Glu Val Arg Thr Pro Val Leu
 420 425 430
 Phe Gly Tyr Thr Met Gln Ser Gly Cys Lys Leu Arg Leu Thr Gly Ala
 435 440 445
 Leu Pro Cys Gln Leu Val Ala Gln Lys Val Lys Ser Leu Leu Trp Gly
 450 455 460
 Gln Gly Phe Pro Asp Tyr Val Ala Pro Phe Gly Asn Ser Gln Ala Gln
 465 470 475 480
 Asp Met Leu Asp Trp Val Pro Ile His Phe Ile Thr Gln Ser Phe Asn
 485 490 495
 Arg Lys Asp Ser Cys Gln Leu Pro Gly Ala Leu Val Ile Glu Val Lys
 500 505 510
 Trp Thr Lys Tyr Gly Ser Leu Leu Asn Pro Gln Ala Lys Ile Val Asn
 515 520 525
 Val Thr Ala Asn Leu Ile Ser Ser Ser Phe Pro Glu Ala Asn Ser Gly
 530 535 540
 Asn Glu Arg Thr Ile Leu Ile Ser Thr Ala Val Thr Phe Val Asp Val
 545 550 555 560
 Ser Ala Pro Ala Glu Ala Gly Phe Arg Ala Pro Pro Ala Ile Asn Ala
 565 570 575

330

Arg Leu Pro Phe Asn Phe Phe Phe Pro Phe Val
 580 585

<210> 227
 <211> 963
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(963)

<400> 227

atg gcc ggc ctg gcg gcg cgg ttg gtc ctg cta gct ggg gca gcg gcg 48
 Met Ala Gly Leu Ala Ala Arg Leu Val Leu Leu Ala Gly Ala Ala Ala
 1 5 10 15

ctg gcg agc ggc tcc cag ggc gac cgt gag ccg gtg tac cgc gac tgc 96
 Leu Ala Ser Gly Ser Gln Gly Asp Arg Glu Pro Val Tyr Arg Asp Cys
 20 25 30

gta ctg cag tgc gaa gag cag aac tgc tct ggg ggc gct ctg aat cac 144
 Val Leu Gln Cys Glu Glu Gln Asn Cys Ser Gly Gly Ala Leu Asn His
 35 40 45

ttc cgc tcc cgc cag cca atc tac atg agt cta gca ggc tgg acc tgt 192
 Phe Arg Ser Arg Gln Pro Ile Tyr Met Ser Leu Ala Gly Trp Thr Cys
 50 55 60

cgg gac gac tgt aag tat gag tgt atg tgg gtc acc gtt ggg ctc tac 240
 Arg Asp Asp Cys Lys Tyr Glu Cys Met Trp Val Thr Val Gly Leu Tyr
 65 70 75 80

ctc cag gaa ggt cac aaa gtg cct cag ttc cat ggc aag tgg ccc ttc 288
 Leu Gln Glu Gly His Lys Val Pro Gln Phe His Gly Lys Trp Pro Phe
 85 90 95

tcc cgg ttc ctg ttc ttt caa gag ccg gca tcg gcc gtg gcc tcg ttt 336
 Ser Arg Phe Leu Phe Phe Gln Glu Pro Ala Ser Ala Val Ala Ser Phe
 100 105 110

ctc aat ggc ctg gcc agc ctg gtg atg ctc tgc cgc tac cgc acc ttc 384
 Leu Asn Gly Leu Ala Ser Leu Val Met Leu Cys Arg Tyr Arg Thr Phe
 115 120 125

331

| | |
|---|-----|
| gtg cca gcc tcc tcc ccc atg tac cac acc tgt gtg gcc ttc gcc tgg | 432 |
| Val Pro Ala Ser Ser Pro Met Tyr His Thr Cys Val Ala Phe Ala Trp | |
| 130 135 140 | |
| gtg tcc ctc aat gca tgg ttc tgg tcc aca gtc ttc cac acc agg gac | 480 |
| Val Ser Leu Asn Ala Trp Phe Trp Ser Thr Val Phe His Thr Arg Asp | |
| 145 150 155 160 | |
| act gac ctc aca gag aaa atg gac tac ttc tgt gcc tcc act gtc atc | 528 |
| Thr Asp Leu Thr Glu Lys Met Asp Tyr Phe Cys Ala Ser Thr Val Ile | |
| 165 170 175 | |
| cta cac tca atc tac ctg tgc tgc gtc agg acc gtg ggg ctg cag cac | 576 |
| Leu His Ser Ile Tyr Leu Cys Cys Val Arg Thr Val Gly Leu Gln His | |
| 180 185 190 | |
| cca gct gtg gtc agt gcc ttc cgg gct ctc ctg ctg ctc atg ctg acc | 624 |
| Pro Ala Val Val Ser Ala Phe Arg Ala Leu Leu Leu Leu Met Leu Thr | |
| 195 200 205 | |
| gtg cac gtc tcc tac ctg agc ctc atc cgc ttc gac tat ggc tac aac | 672 |
| Val His Val Ser Tyr Leu Ser Leu Ile Arg Phe Asp Tyr Gly Tyr Asn | |
| 210 215 220 | |
| ctg gtg gcc aac gtg gct att ggc ctg gtc aac gtg gtg tgg tgg ctg | 720 |
| Leu Val Ala Asn Val Ala Ile Gly Leu Val Asn Val Val Trp Trp Leu | |
| 225 230 235 240 | |
| gcc tgg tgc ctg tgg aac cag cgg cgg ctg cct cac gtg cgc aag tgc | 768 |
| Ala Trp Cys Leu Trp Asn Gln Arg Arg Leu Pro His Val Arg Lys Cys | |
| 245 250 255 | |
| gtg gtg gtg gtc ttg ctg ctg cag ggg ctg tcc ctg ctc gag ctg ctt | 816 |
| Val Val Val Val Leu Leu Leu Gln Gly Leu Ser Leu Leu Glu Leu Leu | |
| 260 265 270 | |
| gac ttc cca ccg ctc ttc tgg gtc ctg gat gcc cat gcc atc tgg cac | 864 |
| Asp Phe Pro Pro Leu Phe Trp Val Leu Asp Ala His Ala Ile Trp His | |
| 275 280 285 | |
| atc agc acc atc cct gtc cac gtc ctc ttt ttc agc ttt ctg gaa gat | 912 |
| Ile Ser Thr Ile Pro Val His Val Leu Phe Phe Ser Phe Leu Glu Asp | |
| 290 295 300 | |

332

gac agc ctg tac ctg ctg aag gaa tca gag gac aag ttc aag ctg gac 960
 Asp Ser Leu Tyr Leu Leu Lys Glu Ser Glu Asp Lys Phe Lys Leu Asp
 305 310 315 320

tga 963
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<210> 228

<211> 320

<212> PRT

<213> Homo sapiens

<400> 228

Met Ala Gly Leu Ala Ala Arg Leu Val Leu Leu Ala Gly Ala Ala Ala
 1 5 10 15
 Leu Ala Ser Gly Ser Gln Gly Asp Arg Glu Pro Val Tyr Arg Asp Cys
 20 25 30
 Val Leu Gln Cys Glu Glu Gln Asn Cys Ser Gly Gly Ala Leu Asn His
 35 40 45
 Phe Arg Ser Arg Gln Pro Ile Tyr Met Ser Leu Ala Gly Trp Thr Cys
 50 55 60
 Arg Asp Asp Cys Lys Tyr Glu Cys Met Trp Val Thr Val Gly Leu Tyr
 65 70 75 80
 Leu Gln Glu Gly His Lys Val Pro Gln Phe His Gly Lys Trp Pro Phe
 85 90 95
 Ser Arg Phe Leu Phe Phe Gln Glu Pro Ala Ser Ala Val Ala Ser Phe
 100 105 110
 Leu Asn Gly Leu Ala Ser Leu Val Met Leu Cys Arg Tyr Arg Thr Phe
 115 120 125
 Val Pro Ala Ser Ser Pro Met Tyr His Thr Cys Val Ala Phe Ala Trp
 130 135 140
 Val Ser Leu Asn Ala Trp Phe Trp Ser Thr Val Phe His Thr Arg Asp
 145 150 155 160
 Thr Asp Leu Thr Glu Lys Met Asp Tyr Phe Cys Ala Ser Thr Val Ile
 165 170 175
 Leu His Ser Ile Tyr Leu Cys Cys Val Arg Thr Val Gly Leu Gln His
 180 185 190
 Pro Ala Val Val Ser Ala Phe Arg Ala Leu Leu Leu Leu Met Leu Thr
 195 200 205
 Val His Val Ser Tyr Leu Ser Leu Ile Arg Phe Asp Tyr Gly Tyr Asn
 210 215 220

333

Leu Val Ala Asn Val Ala Ile Gly Leu Val Asn Val Val Trp Trp Leu
 225 230 235 240
 Ala Trp Cys Leu Trp Asn Gln Arg Arg Leu Pro His Val Arg Lys Cys
 245 250 255
 Val Val Val Val Leu Leu Leu Gln Gly Leu Ser Leu Leu Glu Leu Leu
 260 265 270
 Asp Phe Pro Pro Leu Phe Trp Val Leu Asp Ala His Ala Ile Trp His
 275 280 285
 Ile Ser Thr Ile Pro Val His Val Leu Phe Phe Ser Phe Leu Glu Asp
 290 295 300
 Asp Ser Leu Tyr Leu Leu Lys Glu Ser Glu Asp Lys Phe Lys Leu Asp
 305 310 315 320

<210> 229

<211> 657

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(657)

<221> misc_feature

<222> (1)...(657)

<223> n = A,T,C or G

<400> 229

atg gcg cgg aag aag gtg cgt ccg cgg ctg atc gcg gan ctg gcc cgc 48
 Met Ala Arg Lys Lys Val Arg Pro Arg Leu Ile Ala Xaa Leu Ala Arg
 1 5 10 15

cgc gtg cgc gcc ctg cgg gag caa ctg aac agg ccg cgc gac tcc cag 96
 Arg Val Arg Ala Leu Arg Glu Gln Leu Asn Arg Pro Arg Asp Ser Gln
 20 25 30

ctc tac gcg gtg gac tac gag acc ttg acg cgg ccg ttc tct gga cgc 144
 Leu Tyr Ala Val Asp Tyr Glu Thr Leu Thr Arg Pro Phe Ser Gly Arg
 35 40 45

cgg ctg ccg gtc cgg gcc tgg gcc gac gtg cgc cgc gag anc cgc ctc 192
 Arg Leu Pro Val Arg Ala Trp Ala Asp Val Arg Arg Glu Xaa Arg Leu
 50 55 60

ttg cag ctg ctc ggc cgc ctc ccg ctc ttc ggc ctg ggc cgc ctg gtc 240

334

Leu Gln Leu Leu Gly Arg Leu Pro Leu Phe Gly Leu Gly Arg Leu Val
 65 70 75 80
 acg cgc aag tcc tgg ctg tgg cag cac gac gag ccg tgc tac tgg cgc 288
 Thr Arg Lys Ser Trp Leu Trp Gln His Asp Glu Pro Cys Tyr Trp Arg
 85 90 95
 ctc acg cgg gtg cgg ccc gac tac acg gcg cag aac ttg gac cac ggg 336
 Leu Thr Arg Val Arg Pro Asp Tyr Thr Ala Gln Asn Leu Asp His Gly
 100 105 110
 aag gcc tgg ggc atc ctg acc ttc aaa ggg aag act gag agc gag gcg 384
 Lys Ala Trp Gly Ile Leu Thr Phe Lys Gly Lys Thr Glu Ser Glu Ala
 115 120 125
 cgg gag atc gaa cac gtc atg tac cat gac tgg cgg ctg gtg ccc aag 432
 Arg Glu Ile Glu His Val Met Tyr His Asp Trp Arg Leu Val Pro Lys
 130 135 140
 cac gag gag gag gcc ttc acc gcg ttc acg ccg gcg ccg gaa gac agc 480
 His Glu Glu Glu Ala Phe Thr Ala Phe Thr Pro Ala Pro Glu Asp Ser
 145 150 155 160
 ctg gcc tcc gtg ccg tac ccg cct ctc ctc cgg gcc atg att atc gca 528
 Leu Ala Ser Val Pro Tyr Pro Pro Leu Leu Arg Ala Met Ile Ile Ala
 165 170 175
 gaa cga cag aaa aat gga gac aca agc acc gag gag ccc atg ctg aat 576
 Glu Arg Gln Lys Asn Gly Asp Thr Ser Thr Glu Glu Pro Met Leu Asn
 180 185 190
 gtg cag agg ata cgc atg gaa ccc tgg gat tac cct gca aaa cag gaa 624
 Val Gln Arg Ile Arg Met Glu Pro Trp Asp Tyr Pro Ala Lys Gln Glu
 195 200 205
 gac aaa gga agg gcc aag ggc acc ccc gtc tag 657
 Asp Lys Gly Arg Ala Lys Gly Thr Pro Val *
 210 215

<210> 230

<211> 218

<212> PRT

<213> Homo sapiens

335

<220>

<221> VARIANT

<222> (1)...(218)

<223> Xaa = Any Amino Acid

<400> 230

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Met Ala Arg Lys Lys Val Arg Pro Arg Leu Ile Ala Xaa Leu Ala Arg
 1           5           10           15
Arg Val Arg Ala Leu Arg Glu Gln Leu Asn Arg Pro Arg Asp Ser Gln
          20           25           30
Leu Tyr Ala Val Asp Tyr Glu Thr Leu Thr Arg Pro Phe Ser Gly Arg
        35           40           45
Arg Leu Pro Val Arg Ala Trp Ala Asp Val Arg Arg Glu Xaa Arg Leu
        50           55           60
Leu Gln Leu Leu Gly Arg Leu Pro Leu Phe Gly Leu Gly Arg Leu Val
65           70           75           80
Thr Arg Lys Ser Trp Leu Trp Gln His Asp Glu Pro Cys Tyr Trp Arg
          85           90           95
Leu Thr Arg Val Arg Pro Asp Tyr Thr Ala Gln Asn Leu Asp His Gly
        100          105          110
Lys Ala Trp Gly Ile Leu Thr Phe Lys Gly Lys Thr Glu Ser Glu Ala
        115          120          125
Arg Glu Ile Glu His Val Met Tyr His Asp Trp Arg Leu Val Pro Lys
        130          135          140
His Glu Glu Glu Ala Phe Thr Ala Phe Thr Pro Ala Pro Glu Asp Ser
145          150          155          160
Leu Ala Ser Val Pro Tyr Pro Pro Leu Leu Arg Ala Met Ile Ile Ala
        165          170          175
Glu Arg Gln Lys Asn Gly Asp Thr Ser Thr Glu Glu Pro Met Leu Asn
        180          185          190
Val Gln Arg Ile Arg Met Glu Pro Trp Asp Tyr Pro Ala Lys Gln Glu
        195          200          205
Asp Lys Gly Arg Ala Lys Gly Thr Pro Val
        210          215

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<210> 231

<211> 1116

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1116)

336

<221> misc_feature
 <222> (1)...(1116)
 <223> n = A,T,C or G

<400> 231

| | |
|---|-----|
| atg tct gtg gcc cac tgt ttc tcc atc aaa ggc caa ggc act gtg atg | 48 |
| Met Ser Val Ala His Cys Phe Ser Ile Lys Gly Gln Gly Thr Val Met | |
| 1 5 10 15 | |
| aca ggg acc atc ctt tca ggc tcc atc agc ctc ggt gac agt gtg gag | 96 |
| Thr Gly Thr Ile Leu Ser Gly Ser Ile Ser Leu Gly Asp Ser Val Glu | |
| 20 25 30 | |
| atc cct gcc ctc aag gtg gtg aag aag gtg aag tcc atg cag atg ttc | 144 |
| Ile Pro Ala Leu Lys Val Val Lys Lys Val Lys Ser Met Gln Met Phe | |
| 35 40 45 | |
| cac atg ccc atc act tca gcc atg caa gga gac cgg ctg ggc atc tgc | 192 |
| His Met Pro Ile Thr Ser Ala Met Gln Gly Asp Arg Leu Gly Ile Cys | |
| 50 55 60 | |
| gtc acc cag ttt gac cct aag ctg ctg gag cgc ggg ttg gtg tgt gcc | 240 |
| Val Thr Gln Phe Asp Pro Lys Leu Leu Glu Arg Gly Leu Val Cys Ala | |
| 65 70 75 80 | |
| ccc gag tcc ctg cac act gtc cat gcg gcc ctc atc tct gtg gaa aag | 288 |
| Pro Glu Ser Leu His Thr Val His Ala Ala Leu Ile Ser Val Glu Lys | |
| 85 90 95 | |
| ata ccg tat ttc cgg ggg ccc ctg caa acc aag gcc aag ttc cac att | 336 |
| Ile Pro Tyr Phe Arg Gly Pro Leu Gln Thr Lys Ala Lys Phe His Ile | |
| 100 105 110 | |
| aca gtg ggc cat gaa aca gtc atg ggc cgg ttg atg ttc ttc agt cct | 384 |
| Thr Val Gly His Glu Thr Val Met Gly Arg Leu Met Phe Phe Ser Pro | |
| 115 120 125 | |
| gct cca gat aac ttt gac cag gag cct ata ctg gac tct ttc aac ttc | 432 |
| Ala Pro Asp Asn Phe Asp Gln Glu Pro Ile Leu Asp Ser Phe Asn Phe | |
| 130 135 140 | |
| tct caa gaa tac ctt ttc cag gag cag tac ctg tcc aag gat ttg aca | 480 |
| Ser Gln Glu Tyr Leu Phe Gln Glu Gln Tyr Leu Ser Lys Asp Leu Thr | |

337

| | | | | |
|---|-----|-----|-----|------|
| 145 | 150 | 155 | 160 | |
| cca gca gtg aca gac aat gat gag gcc gac aag aag gcc ggc cag gcc | | | | 528 |
| Pro Ala Val Thr Asp Asn Asp Glu Ala Asp Lys Lys Ala Gly Gln Ala | | | | |
| | 165 | 170 | 175 | |
| aca gag ggc cat tgt cct cgg cag cag tgg gcc ctg gtg gag ttt gag | | | | 576 |
| Thr Glu Gly His Cys Pro Arg Gln Gln Trp Ala Leu Val Glu Phe Glu | | | | |
| | 180 | 185 | 190 | |
| aag ccc gtc acc tgc cct cgg ctg tgc ctg gtg att ggc tcc agg cta | | | | 624 |
| Lys Pro Val Thr Cys Pro Arg Leu Cys Leu Val Ile Gly Ser Arg Leu | | | | |
| | 195 | 200 | 205 | |
| gat gcg gac att cac acc aac acg tgc cgg cta gcc ttc cat ggc atc | | | | 672 |
| Asp Ala Asp Ile His Thr Asn Thr Cys Arg Leu Ala Phe His Gly Ile | | | | |
| | 210 | 215 | 220 | |
| ctg ctc cac ggg cta gag gac agg aac tac gcc gac agc ttc ctg ccc | | | | 720 |
| Leu Leu His Gly Leu Glu Asp Arg Asn Tyr Ala Asp Ser Phe Leu Pro | | | | |
| | 225 | 230 | 235 | 240 |
| agg ctg aag gtg tac aag ctg aag cac aag cat ggc ctt gtg gag cgg | | | | 768 |
| Arg Leu Lys Val Tyr Lys Leu Lys His Lys His Gly Leu Val Glu Arg | | | | |
| | 245 | 250 | 255 | |
| gcg atg gat gac tac agt gtg atc ggc cgc tcc ctg ttc aaa aag gaa | | | | 816 |
| Ala Met Asp Asp Tyr Ser Val Ile Gly Arg Ser Leu Phe Lys Lys Glu | | | | |
| | 260 | 265 | 270 | |
| acc aac atc cag ctc ttc gtg ggg ctc aag gtg cac ttg tcc act ggg | | | | 864 |
| Thr Asn Ile Gln Leu Phe Val Gly Leu Lys Val His Leu Ser Thr Gly | | | | |
| | 275 | 280 | 285 | |
| gaa ctg ggc atc atc gac agt gcc ttc ggc cag agc ggc aag ttc aag | | | | 912 |
| Glu Leu Gly Ile Ile Asp Ser Ala Phe Gly Gln Ser Gly Lys Phe Lys | | | | |
| | 290 | 295 | 300 | |
| atc cac atc cca ggt ggc ctc agc ccc gag tcc aag aag atc ctg aca | | | | 960 |
| Ile His Ile Pro Gly Gly Leu Ser Pro Glu Ser Lys Lys Ile Leu Thr | | | | |
| | 305 | 310 | 315 | 320 |
| ccc gcc ctc aag aag cgg gcc cgg gct ggc cgt ggg gag gcc acc agg | | | | 1008 |
| Pro Ala Leu Lys Lys Arg Ala Arg Ala Gly Arg Gly Glu Ala Thr Arg | | | | |

338

325

330

335

cag gag gag agc gcc gag cgg agn agg ccc tca cag cat gtg gtg ctc 1056
 Gln Glu Glu Ser Ala Glu Arg Xaa Arg Pro Ser Gln His Val Val Leu
 340 345 350

agc ctg act ttc aag cgt tat gtc ttc gac acc cac aag cgc atg gtt 1104
 Ser Leu Thr Phe Lys Arg Tyr Val Phe Asp Thr His Lys Arg Met Val
 355 360 365

cag tct ccc tga 1116
 Gln Ser Pro *
 370

<210> 232

<211> 371

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(371)

<223> Xaa = Any Amino Acid

<400> 232

Met Ser Val Ala His Cys Phe Ser Ile Lys Gly Gln Gly Thr Val Met
 1 5 10 15
 Thr Gly Thr Ile Leu Ser Gly Ser Ile Ser Leu Gly Asp Ser Val Glu
 20 25 30
 Ile Pro Ala Leu Lys Val Val Lys Lys Val Lys Ser Met Gln Met Phe
 35 40 45
 His Met Pro Ile Thr Ser Ala Met Gln Gly Asp Arg Leu Gly Ile Cys
 50 55 60
 Val Thr Gln Phe Asp Pro Lys Leu Leu Glu Arg Gly Leu Val Cys Ala
 65 70 75 80
 Pro Glu Ser Leu His Thr Val His Ala Ala Leu Ile Ser Val Glu Lys
 85 90 95
 Ile Pro Tyr Phe Arg Gly Pro Leu Gln Thr Lys Ala Lys Phe His Ile
 100 105 110
 Thr Val Gly His Glu Thr Val Met Gly Arg Leu Met Phe Phe Ser Pro
 115 120 125
 Ala Pro Asp Asn Phe Asp Gln Glu Pro Ile Leu Asp Ser Phe Asn Phe
 130 135 140

339

Ser Gln Glu Tyr Leu Phe Gln Glu Gln Tyr Leu Ser Lys Asp Leu Thr
 145 150 155 160
 Pro Ala Val Thr Asp Asn Asp Glu Ala Asp Lys Lys Ala Gly Gln Ala
 165 170 175
 Thr Glu Gly His Cys Pro Arg Gln Gln Trp Ala Leu Val Glu Phe Glu
 180 185 190
 Lys Pro Val Thr Cys Pro Arg Leu Cys Leu Val Ile Gly Ser Arg Leu
 195 200 205
 Asp Ala Asp Ile His Thr Asn Thr Cys Arg Leu Ala Phe His Gly Ile
 210 215 220
 Leu Leu His Gly Leu Glu Asp Arg Asn Tyr Ala Asp Ser Phe Leu Pro
 225 230 235 240
 Arg Leu Lys Val Tyr Lys Leu Lys His Lys His Gly Leu Val Glu Arg
 245 250 255
 Ala Met Asp Asp Tyr Ser Val Ile Gly Arg Ser Leu Phe Lys Lys Glu
 260 265 270
 Thr Asn Ile Gln Leu Phe Val Gly Leu Lys Val His Leu Ser Thr Gly
 275 280 285
 Glu Leu Gly Ile Ile Asp Ser Ala Phe Gly Gln Ser Gly Lys Phe Lys
 290 295 300
 Ile His Ile Pro Gly Gly Leu Ser Pro Glu Ser Lys Lys Ile Leu Thr
 305 310 315 320
 Pro Ala Leu Lys Lys Arg Ala Arg Ala Gly Arg Gly Glu Ala Thr Arg
 325 330 335
 Gln Glu Glu Ser Ala Glu Arg Xaa Arg Pro Ser Gln His Val Val Leu
 340 345 350
 Ser Leu Thr Phe Lys Arg Tyr Val Phe Asp Thr His Lys Arg Met Val
 355 360 365
 Gln Ser Pro
 370

<210> 233

<211> 1275

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1275)

<221> misc_feature

<222> (1)...(1275)

<223> n = A,T,C or G

340

<400> 233

| | |
|---|-----|
| atg gcg gca gtg gca acc tgc ggt agt gtt gcc gcg agt act ggg tct | 48 |
| Met Ala Ala Val Ala Thr Cys Gly Ser Val Ala Ala Ser Thr Gly Ser | |
| 1 5 10 15 | |
| gca gtg gcg aca gca gnc aag agc aac gtc acc agt ttc cag agg agg | 96 |
| Ala Val Ala Thr Ala Xaa Lys Ser Asn Val Thr Ser Phe Gln Arg Arg | |
| 20 25 30 | |
| ggt cct aga gcc agc gtg acc aac gac agc ggc cct cga ctg gtg tcc | 144 |
| Gly Pro Arg Ala Ser Val Thr Asn Asp Ser Gly Pro Arg Leu Val Ser | |
| 35 40 45 | |
| att gcg ggc acg cga ccg tcg gtg cgg aat gga cag ctg ctg gta tca | 192 |
| Ile Ala Gly Thr Arg Pro Ser Val Arg Asn Gly Gln Leu Leu Val Ser | |
| 50 55 60 | |
| acc ggg ctc cca gcc cta gac cag ctc tta ggt gga ggt tta gcc gtt | 240 |
| Thr Gly Leu Pro Ala Leu Asp Gln Leu Leu Gly Gly Gly Leu Ala Val | |
| 65 70 75 80 | |
| gga aca gtt ctt cta att gag gag gat aaa tat aat att tac tca cct | 288 |
| Gly Thr Val Leu Leu Ile Glu Glu Asp Lys Tyr Asn Ile Tyr Ser Pro | |
| 85 90 95 | |
| ttg ctc ttc aag tat ttc ctg gca gaa gga att gtc aat ggg cat act | 336 |
| Leu Leu Phe Lys Tyr Phe Leu Ala Glu Gly Ile Val Asn Gly His Thr | |
| 100 105 110 | |
| ttg ttg gtt gca tct gct aaa gag gat cct gcc aac att tta cag gaa | 384 |
| Leu Leu Val Ala Ser Ala Lys Glu Asp Pro Ala Asn Ile Leu Gln Glu | |
| 115 120 125 | |
| ctt cca gca cca tta ctt gat gat aaa tgt aaa aag gaa ttt gat gaa | 432 |
| Leu Pro Ala Pro Leu Leu Asp Asp Lys Cys Lys Lys Glu Phe Asp Glu | |
| 130 135 140 | |
| gat gta tac aat cat aaa aca cca gaa tct aat att aag atg aaa ata | 480 |
| Asp Val Tyr Asn His Lys Thr Pro Glu Ser Asn Ile Lys Met Lys Ile | |
| 145 150 155 160 | |
| gct tgg cgt tac cag tta tta ccc aag atg gag att gga cca gta tca | 528 |
| Ala Trp Arg Tyr Gln Leu Leu Pro Lys Met Glu Ile Gly Pro Val Ser | |
| 165 170 175 | |

341

| | |
|---|------|
| tct tca aga ttt ggt cac tat tat gat gca tca aaa aga atg cca caa Ser Ser Arg Phe Gly His Tyr Tyr Asp Ala Ser Lys Arg Met Pro Gln 180 185 190 | 576 |
| gaa cta att gag gct tca aat tgg cat gga ttt ttt ctt cca gag aaa Glu Leu Ile Glu Ala Ser Asn Trp His Gly Phe Phe Leu Pro Glu Lys 195 200 205 | 624 |
| ata tct tca act ctc aaa gta gaa ccc tgt tct ttg acc cct ggc tac Ile Ser Ser Thr Leu Lys Val Glu Pro Cys Ser Leu Thr Pro Gly Tyr 210 215 220 | 672 |
| aca aag ctg ctt cag ttt atc cag aac atc att tat gag gaa gga ttt Thr Lys Leu Leu Gln Phe Ile Gln Asn Ile Ile Tyr Glu Glu Gly Phe 225 230 235 240 | 720 |
| gat gga tcc aat cct cag aaa aaa cag aga aac att tta aga ata gga Asp Gly Ser Asn Pro Gln Lys Lys Gln Arg Asn Ile Leu Arg Ile Gly 245 250 255 | 768 |
| att cag aat ctt ggc tca cct tta tgg gga gac gat att tgc tgt gca Ile Gln Asn Leu Gly Ser Pro Leu Trp Gly Asp Asp Ile Cys Cys Ala 260 265 270 | 816 |
| gaa aat ggt ggc aac agt cac agc ctt acc aag ttc ctc tat gtt ctc Glu Asn Gly Gly Asn Ser His Ser Leu Thr Lys Phe Leu Tyr Val Leu 275 280 285 | 864 |
| cgt ggt ctt ctg aga acc tct ctt tca gcc tgc atc atc aca atg cca Arg Gly Leu Leu Arg Thr Ser Leu Ser Ala Cys Ile Ile Thr Met Pro 290 295 300 | 912 |
| aca cat ctg atc cag aat aaa gcc att att gcc cgt gtc aca acc ttg Thr His Leu Ile Gln Asn Lys Ala Ile Ile Ala Arg Val Thr Thr Leu 305 310 315 320 | 960 |
| tca gat gta gta gtt ggt ctg gaa tca ttt att ggt tct gag aga gaa Ser Asp Val Val Val Gly Leu Glu Ser Phe Ile Gly Ser Glu Arg Glu 325 330 335 | 1008 |
| act aac cca ttg tat aag gat tat cat gga ttg att cat ata cgg cag Thr Asn Pro Leu Tyr Lys Asp Tyr His Gly Leu Ile His Ile Arg Gln 340 345 350 | 1056 |

342

att cct cgg ctt aat aac ttg atc tgt gat gaa tca gat gtc aaa gac 1104
 Ile Pro Arg Leu Asn Asn Leu Ile Cys Asp Glu Ser Asp Val Lys Asp
 355 360 365

tta gct ttt aaa tta aaa agg aag cta ttc acc att gag cga ctg cat 1152
 Leu Ala Phe Lys Leu Lys Arg Lys Leu Phe Thr Ile Glu Arg Leu His
 370 375 380

ttg cct cca gac ttg tca gac aca gtg agc cgc tca agc aaa atg gat 1200
 Leu Pro Pro Asp Leu Ser Asp Thr Val Ser Arg Ser Ser Lys Met Asp
 385 390 395 400

ctg gca gaa tcc gcc aag cgg ctg ggc cca ggc tgt ggc atg atg gcc 1248
 Leu Ala Glu Ser Ala Lys Arg Leu Gly Pro Gly Cys Gly Met Met Ala
 405 410 415

gga ggc aag aag cac ctg gac ttc tag 1275
 Gly Gly Lys Lys His Leu Asp Phe *
 420

<210> 234

<211> 424

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(424)

<223> Xaa = Any Amino Acid

<400> 234

Met Ala Ala Val Ala Thr Cys Gly Ser Val Ala Ala Ser Thr Gly Ser
 1 5 10 15
 Ala Val Ala Thr Ala Xaa Lys Ser Asn Val Thr Ser Phe Gln Arg Arg
 20 25 30
 Gly Pro Arg Ala Ser Val Thr Asn Asp Ser Gly Pro Arg Leu Val Ser
 35 40 45
 Ile Ala Gly Thr Arg Pro Ser Val Arg Asn Gly Gln Leu Leu Val Ser
 50 55 60
 Thr Gly Leu Pro Ala Leu Asp Gln Leu Leu Gly Gly Gly Leu Ala Val
 65 70 75 80
 Gly Thr Val Leu Leu Ile Glu Glu Asp Lys Tyr Asn Ile Tyr Ser Pro

343

85 90 95
 Leu Leu Phe Lys Tyr Phe Leu Ala Glu Gly Ile Val Asn Gly His Thr
 100 105 110
 Leu Leu Val Ala Ser Ala Lys Glu Asp Pro Ala Asn Ile Leu Gln Glu
 115 120 125
 Leu Pro Ala Pro Leu Leu Asp Asp Lys Cys Lys Lys Glu Phe Asp Glu
 130 135 140
 Asp Val Tyr Asn His Lys Thr Pro Glu Ser Asn Ile Lys Met Lys Ile
 145 150 155 160
 Ala Trp Arg Tyr Gln Leu Leu Pro Lys Met Glu Ile Gly Pro Val Ser
 165 170 175
 Ser Ser Arg Phe Gly His Tyr Tyr Asp Ala Ser Lys Arg Met Pro Gln
 180 185 190
 Glu Leu Ile Glu Ala Ser Asn Trp His Gly Phe Phe Leu Pro Glu Lys
 195 200 205
 Ile Ser Ser Thr Leu Lys Val Glu Pro Cys Ser Leu Thr Pro Gly Tyr
 210 215 220
 Thr Lys Leu Leu Gln Phe Ile Gln Asn Ile Ile Tyr Glu Glu Gly Phe
 225 230 235 240
 Asp Gly Ser Asn Pro Gln Lys Lys Gln Arg Asn Ile Leu Arg Ile Gly
 245 250 255
 Ile Gln Asn Leu Gly Ser Pro Leu Trp Gly Asp Asp Ile Cys Cys Ala
 260 265 270
 Glu Asn Gly Gly Asn Ser His Ser Leu Thr Lys Phe Leu Tyr Val Leu
 275 280 285
 Arg Gly Leu Leu Arg Thr Ser Leu Ser Ala Cys Ile Ile Thr Met Pro
 290 295 300
 Thr His Leu Ile Gln Asn Lys Ala Ile Ile Ala Arg Val Thr Thr Leu
 305 310 315 320
 Ser Asp Val Val Val Gly Leu Glu Ser Phe Ile Gly Ser Glu Arg Glu
 325 330 335
 Thr Asn Pro Leu Tyr Lys Asp Tyr His Gly Leu Ile His Ile Arg Gln
 340 345 350
 Ile Pro Arg Leu Asn Asn Leu Ile Cys Asp Glu Ser Asp Val Lys Asp
 355 360 365
 Leu Ala Phe Lys Leu Lys Arg Lys Leu Phe Thr Ile Glu Arg Leu His
 370 375 380
 Leu Pro Pro Asp Leu Ser Asp Thr Val Ser Arg Ser Ser Lys Met Asp
 385 390 395 400
 Leu Ala Glu Ser Ala Lys Arg Leu Gly Pro Gly Cys Gly Met Met Ala
 405 410 415
 Gly Gly Lys Lys His Leu Asp Phe
 420

344

<210> 235
 <211> 1188
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1188)

<400> 235
 atg gag gag ctc cca ggc tat gaa gag acc ctg acc cgc ctg gct gcc 48
 Met Glu Glu Leu Pro Gly Tyr Glu Glu Thr Leu Thr Arg Leu Ala Ala
 1 5 10 15
 att ctc gcc aaa cac ttt gcc gac gca cgc att gtg ggc act gac atc 96
 Ile Leu Ala Lys His Phe Ala Asp Ala Arg Ile Val Gly Thr Asp Ile
 20 25 30
 cga gac tca ctg atg cag gcc ctg gcc agc tac gtg tgc tac cca cac 144
 Arg Asp Ser Leu Met Gln Ala Leu Ala Ser Tyr Val Cys Tyr Pro His
 35 40 45
 tcc ctg cgg gct gtg gag cga atc ccc gag gag cag cgt atc gcc atg 192
 Ser Leu Arg Ala Val Glu Arg Ile Pro Glu Glu Gln Arg Ile Ala Met
 50 55 60
 gtg agg aac ctc ctg gcg ccc tat gag cag cgg ccc tgg gcc cag acc 240
 Val Arg Asn Leu Leu Ala Pro Tyr Glu Gln Arg Pro Trp Ala Gln Thr
 65 70 75 80
 aac tgg atc ctg gtg cgg ctc tgg agg ggc tgt ggc ttc ggg tac cgc 288
 Asn Trp Ile Leu Val Arg Leu Trp Arg Gly Cys Gly Phe Gly Tyr Arg
 85 90 95
 tat aca cgg ctg cca cat ctg ctg aaa acc aaa ctt gag gac gcc aat 336
 Tyr Thr Arg Leu Pro His Leu Leu Lys Thr Lys Leu Glu Asp Ala Asn
 100 105 110
 ttg ccc agc ctc cag aag ccc tgc cct tcc acc ctg ctg cag cag cac 384
 Leu Pro Ser Leu Gln Lys Pro Cys Pro Ser Thr Leu Leu Gln Gln His
 115 120 125
 atg gcg gac ctc cta cag cag ggt cct gat gtg gca ccc agc ttc ctc 432
 Met Ala Asp Leu Leu Gln Gln Gly Pro Asp Val Ala Pro Ser Phe Leu

345

| 130 | 135 | 140 | |
|---|-----|-----|-----|
| aac agc gtc ctc aat cag ctc aac tgg gcc ttc tct gaa ttc att ggc | | | 480 |
| Asn Ser Val Leu Asn Gln Leu Asn Trp Ala Phe Ser Glu Phe Ile Gly | | | |
| 145 | 150 | 155 | 160 |
| atg atc caa gag atc cag cag gct gct gag cgc ctg gag cgg aac ttt | | | 528 |
| Met Ile Gln Glu Ile Gln Gln Ala Ala Glu Arg Leu Glu Arg Asn Phe | | | |
| | 165 | 170 | 175 |
| gtg gac agc cgg cag ctc aag gta tgt gcc acc tgc ttt gac ctc tcg | | | 576 |
| Val Asp Ser Arg Gln Leu Lys Val Cys Ala Thr Cys Phe Asp Leu Ser | | | |
| | 180 | 185 | 190 |
| gtc agc ctg ctg cgt gtc ttg gag atg act atc aca ctg gtg cct gag | | | 624 |
| Val Ser Leu Leu Arg Val Leu Glu Met Thr Ile Thr Leu Val Pro Glu | | | |
| | 195 | 200 | 205 |
| ata ttc ctt gac tgg acc cgg cct acc tct gag atg ctg ctg cgg cgt | | | 672 |
| Ile Phe Leu Asp Trp Thr Arg Pro Thr Ser Glu Met Leu Leu Arg Arg | | | |
| | 210 | 215 | 220 |
| ctt gca cag ctg cta aac cag gtg ctg aac cgg gtg aca gct gag agg | | | 720 |
| Leu Ala Gln Leu Leu Asn Gln Val Leu Asn Arg Val Thr Ala Glu Arg | | | |
| | 225 | 230 | 235 |
| aac ctg ttt gat cgt gtg gtc acc cta cgg ctg cct ggc cta gag agc | | | 768 |
| Asn Leu Phe Asp Arg Val Val Thr Leu Arg Leu Pro Gly Leu Glu Ser | | | |
| | 245 | 250 | 255 |
| gtg gac cac tat ccc att ctg gtg gca gtg acg ggc atc ctg gtg cag | | | 816 |
| Val Asp His Tyr Pro Ile Leu Val Ala Val Thr Gly Ile Leu Val Gln | | | |
| | 260 | 265 | 270 |
| ctc ctg gtg cgt ggc cca gcc tca gag aga gag caa gcc aca tca gtg | | | 864 |
| Leu Leu Val Arg Gly Pro Ala Ser Glu Arg Glu Gln Ala Thr Ser Val | | | |
| | 275 | 280 | 285 |
| ctc ctg gca gat ccc tgc ttc cag cta cgc tca ata tgc tat ctc ctg | | | 912 |
| Leu Leu Ala Asp Pro Cys Phe Gln Leu Arg Ser Ile Cys Tyr Leu Leu | | | |
| | 290 | 295 | 300 |
| gga cag cca gag ccc cca gca cct ggc act gct ctg cca gcc cct gac | | | 960 |
| Gly Gln Pro Glu Pro Pro Ala Pro Gly Thr Ala Leu Pro Ala Pro Asp | | | |

346

| | | | | |
|---|------|-----|-----|--|
| 305 | 310 | 315 | 320 | |
| cgg aag cgc ttc tcc ctg cag agc tat gcg gat tat atc agt gcc gat | 1008 | | | |
| Arg Lys Arg Phe Ser Leu Gln Ser Tyr Ala Asp Tyr Ile Ser Ala Asp | | | | |
| 325 | 330 | 335 | | |
| | | | | |
| gag ctg gcc caa gtg gaa cag atg ctg gcg cac ctg acc tct gca tct | 1056 | | | |
| Glu Leu Ala Gln Val Glu Gln Met Leu Ala His Leu Thr Ser Ala Ser | | | | |
| 340 | 345 | 350 | | |
| | | | | |
| gcc cag gca gca gct gcc tcc ctg ccc acc agt gag gag gac tct gcc | 1104 | | | |
| Ala Gln Ala Ala Ala Ala Ser Leu Pro Thr Ser Glu Glu Asp Ser Ala | | | | |
| 355 | 360 | 365 | | |
| | | | | |
| cca tct gct atg ccc acc cca tct ctg ctg tgt tcc agc cct gtg gcc | 1152 | | | |
| Pro Ser Ala Met Pro Thr Pro Ser Leu Leu Cys Ser Ser Pro Val Ala | | | | |
| 370 | 375 | 380 | | |
| | | | | |
| aca agt cct gca aag cct gta tca acc agc acc tga | 1188 | | | |
| Thr Ser Pro Ala Lys Pro Val Ser Thr Ser Thr * | | | | |
| 385 | 390 | 395 | | |

<210> 236
 <211> 395
 <212> PRT
 <213> Homo sapiens

<400> 236

| | |
|---|--|
| Met Glu Glu Leu Pro Gly Tyr Glu Glu Thr Leu Thr Arg Leu Ala Ala | |
| 1 5 10 15 | |
| Ile Leu Ala Lys His Phe Ala Asp Ala Arg Ile Val Gly Thr Asp Ile | |
| 20 25 30 | |
| Arg Asp Ser Leu Met Gln Ala Leu Ala Ser Tyr Val Cys Tyr Pro His | |
| 35 40 45 | |
| Ser Leu Arg Ala Val Glu Arg Ile Pro Glu Glu Gln Arg Ile Ala Met | |
| 50 55 60 | |
| Val Arg Asn Leu Leu Ala Pro Tyr Glu Gln Arg Pro Trp Ala Gln Thr | |
| 65 70 75 80 | |
| Asn Trp Ile Leu Val Arg Leu Trp Arg Gly Cys Gly Phe Gly Tyr Arg | |
| 85 90 95 | |
| Tyr Thr Arg Leu Pro His Leu Leu Lys Thr Lys Leu Glu Asp Ala Asn | |
| 100 105 110 | |
| Leu Pro Ser Leu Gln Lys Pro Cys Pro Ser Thr Leu Leu Gln Gln His | |

347

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      115              120              125
Met Ala Asp Leu Leu Gln Gln Gly Pro Asp Val Ala Pro Ser Phe Leu
  130              135              140
Asn Ser Val Leu Asn Gln Leu Asn Trp Ala Phe Ser Glu Phe Ile Gly
 145              150              155              160
Met Ile Gln Glu Ile Gln Gln Ala Ala Glu Arg Leu Glu Arg Asn Phe
      165              170              175
Val Asp Ser Arg Gln Leu Lys Val Cys Ala Thr Cys Phe Asp Leu Ser
      180              185              190
Val Ser Leu Leu Arg Val Leu Glu Met Thr Ile Thr Leu Val Pro Glu
      195              200              205
Ile Phe Leu Asp Trp Thr Arg Pro Thr Ser Glu Met Leu Leu Arg Arg
      210              215              220
Leu Ala Gln Leu Leu Asn Gln Val Leu Asn Arg Val Thr Ala Glu Arg
 225              230              235              240
Asn Leu Phe Asp Arg Val Val Thr Leu Arg Leu Pro Gly Leu Glu Ser
      245              250              255
Val Asp His Tyr Pro Ile Leu Val Ala Val Thr Gly Ile Leu Val Gln
      260              265              270
Leu Leu Val Arg Gly Pro Ala Ser Glu Arg Glu Gln Ala Thr Ser Val
      275              280              285
Leu Leu Ala Asp Pro Cys Phe Gln Leu Arg Ser Ile Cys Tyr Leu Leu
 290              295              300
Gly Gln Pro Glu Pro Pro Ala Pro Gly Thr Ala Leu Pro Ala Pro Asp
 305              310              315              320
Arg Lys Arg Phe Ser Leu Gln Ser Tyr Ala Asp Tyr Ile Ser Ala Asp
      325              330              335
Glu Leu Ala Gln Val Glu Gln Met Leu Ala His Leu Thr Ser Ala Ser
      340              345              350
Ala Gln Ala Ala Ala Ala Ser Leu Pro Thr Ser Glu Glu Asp Ser Ala
      355              360              365
Pro Ser Ala Met Pro Thr Pro Ser Leu Leu Cys Ser Ser Pro Val Ala
      370              375              380
Thr Ser Pro Ala Lys Pro Val Ser Thr Ser Thr
 385              390              395

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<210> 237

<211> 1278

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1278)

348

<221> misc_feature

<222> (1)...(1278)

<223> n = A,T,C or G

<400> 237

| | |
|---|-----|
| atg gat gac ttg caa aag ttg gga gtc ata ttg cac agt gct att tca | 48 |
| Met Asp Asp Leu Gln Lys Leu Gly Val Ile Leu His Ser Ala Ile Ser | |
| 1 5 10 15 | |
| gtc cca ata agt tca gat gca tcc cct ttt att ctt cca tct tat acc | 96 |
| Val Pro Ile Ser Ser Asp Ala Ser Pro Phe Ile Leu Pro Ser Tyr Thr | |
| 20 25 30 | |
| gaa gca gtt ttg aca agt tta cag gaa gct gta ctt aca gct tta gat | 144 |
| Glu Ala Val Leu Thr Ser Leu Gln Glu Ala Val Leu Thr Ala Leu Asp | |
| 35 40 45 | |
| gtt ctc caa aag gcc att tgt gta gga cca gaa aac atg cag ata atg | 192 |
| Val Leu Gln Lys Ala Ile Cys Val Gly Pro Glu Asn Met Gln Ile Met | |
| 50 55 60 | |
| tat cca gct ata ttt gac cag ttg ttg gca ttt gta gaa ttt tcc tgt | 240 |
| Tyr Pro Ala Ile Phe Asp Gln Leu Leu Ala Phe Val Glu Phe Ser Cys | |
| 65 70 75 80 | |
| aaa cct cca cag tat gga cag ctn gaa aca aag cac att gca aat gca | 288 |
| Lys Pro Pro Gln Tyr Gly Gln Xaa Glu Thr Lys His Ile Ala Asn Ala | |
| 85 90 95 | |
| aaa tat aat cag atc caa cta ttt gca ccg gcg gaa tgg gta gcc ttg | 336 |
| Lys Tyr Asn Gln Ile Gln Leu Phe Ala Pro Ala Glu Trp Val Ala Leu | |
| 100 105 110 | |
| aat tat gtg ccg ttt gct gaa agg tct tta gaa gta gtt gtg gat tta | 384 |
| Asn Tyr Val Pro Phe Ala Glu Arg Ser Leu Glu Val Val Val Asp Leu | |
| 115 120 125 | |
| tac caa aaa aca gcg tgt cac aaa gca gtg gtg aat gag aaa gtg ctc | 432 |
| Tyr Gln Lys Thr Ala Cys His Lys Ala Val Val Asn Glu Lys Val Leu | |
| 130 135 140 | |
| cag aat att att aag act ctt agg gtt cct ctc agt ttg aag tat tcc | 480 |
| Gln Asn Ile Ile Lys Thr Leu Arg Val Pro Leu Ser Leu Lys Tyr Ser | |

349

| | | | | |
|---|-----|-----|-----|------|
| 145 | 150 | 155 | 160 | |
| tgc cct tct gaa agc aca tgg aaa cta gca gta tcc tct ctc ctc aga | | | | 528 |
| Cys Pro Ser Glu Ser Thr Trp Lys Leu Ala Val Ser Ser Leu Leu Arg | | | | |
| | 165 | 170 | 175 | |
| gtt ctt tct att ggg cta cct gtt gcc cgg cag cat gct tct tct gga | | | | 576 |
| Val Leu Ser Ile Gly Leu Pro Val Ala Arg Gln His Ala Ser Ser Gly | | | | |
| | 180 | 185 | 190 | |
| aaa ttt gac agt atg tgg cca gaa cta gcc aat act ttt gaa gat ttt | | | | 624 |
| Lys Phe Asp Ser Met Trp Pro Glu Leu Ala Asn Thr Phe Glu Asp Phe | | | | |
| | 195 | 200 | 205 | |
| ctc ttt act aaa agc ata cct cca gat aat ctc tct att caa gag ttt | | | | 672 |
| Leu Phe Thr Lys Ser Ile Pro Pro Asp Asn Leu Ser Ile Gln Glu Phe | | | | |
| | 210 | 215 | 220 | |
| caa aga aat gaa aat att gat gtc gag gta gtt caa ctt atc agc aat | | | | 720 |
| Gln Arg Asn Glu Asn Ile Asp Val Glu Val Val Gln Leu Ile Ser Asn | | | | |
| | 225 | 230 | 235 | 240 |
| gag ata cta cct tat gcc aat ttt att cct aag gaa ttt gtt ggt caa | | | | 768 |
| Glu Ile Leu Pro Tyr Ala Asn Phe Ile Pro Lys Glu Phe Val Gly Gln | | | | |
| | 245 | 250 | 255 | |
| ata atg aca atg ctt aac aag ggc tca ata cat tct cag tca tct tca | | | | 816 |
| Ile Met Thr Met Leu Asn Lys Gly Ser Ile His Ser Gln Ser Ser Ser | | | | |
| | 260 | 265 | 270 | |
| ttt aca gaa gca gag att gat att cgt ttg aga gag gaa ttt tct aaa | | | | 864 |
| Phe Thr Glu Ala Glu Ile Asp Ile Arg Leu Arg Glu Glu Phe Ser Lys | | | | |
| | 275 | 280 | 285 | |
| atg tgt ttt gaa aca tta ctc cag ttt tcc ttc agt aat aaa gtc aca | | | | 912 |
| Met Cys Phe Glu Thr Leu Leu Gln Phe Ser Phe Ser Asn Lys Val Thr | | | | |
| | 290 | 295 | 300 | |
| aca cct caa gaa ggc tac atc tca cga atg gca ctc tca gtg ctt tta | | | | 960 |
| Thr Pro Gln Glu Gly Tyr Ile Ser Arg Met Ala Leu Ser Val Leu Leu | | | | |
| | 305 | 310 | 315 | 320 |
| aag agg tcc caa gat gta cta cat cgc tat ata gag gat gaa aga tta | | | | 1008 |
| Lys Arg Ser Gln Asp Val Leu His Arg Tyr Ile Glu Asp Glu Arg Leu | | | | |

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<210> 238
<211> 425
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> VARIANT  
<222> (1)...(425)  
<223> Xaa = Any Amino Acid
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<400> 238
Met Asp Asp Leu Gln Lys Leu Gly Val Ile Leu His Ser Ala Ile Ser
.1 5 10 15
Val Pro Ile Ser Ser Asp Ala Ser Pro Phe Ile Leu Pro Ser Tyr Thr
20 25 30
Glu Ala Val Leu Thr Ser Leu Gln Glu Ala Val Leu Thr Ala Leu Asp
35 40 45

351

Val Leu Gln Lys Ala Ile Cys Val Gly Pro Glu Asn Met Gln Ile Met
 50 55 60
 Tyr Pro Ala Ile Phe Asp Gln Leu Leu Ala Phe Val Glu Phe Ser Cys
 65 70 75 80
 Lys Pro Pro Gln Tyr Gly Gln Xaa Glu Thr Lys His Ile Ala Asn Ala
 85 90 95
 Lys Tyr Asn Gln Ile Gln Leu Phe Ala Pro Ala Glu Trp Val Ala Leu
 100 105 110
 Asn Tyr Val Pro Phe Ala Glu Arg Ser Leu Glu Val Val Val Asp Leu
 115 120 125
 Tyr Gln Lys Thr Ala Cys His Lys Ala Val Val Asn Glu Lys Val Leu
 130 135 140
 Gln Asn Ile Ile Lys Thr Leu Arg Val Pro Leu Ser Leu Lys Tyr Ser
 145 150 155 160
 Cys Pro Ser Glu Ser Thr Trp Lys Leu Ala Val Ser Ser Leu Leu Arg
 165 170 175
 Val Leu Ser Ile Gly Leu Pro Val Ala Arg Gln His Ala Ser Ser Gly
 180 185 190
 Lys Phe Asp Ser Met Trp Pro Glu Leu Ala Asn Thr Phe Glu Asp Phe
 195 200 205
 Leu Phe Thr Lys Ser Ile Pro Pro Asp Asn Leu Ser Ile Gln Glu Phe
 210 215 220
 Gln Arg Asn Glu Asn Ile Asp Val Glu Val Val Gln Leu Ile Ser Asn
 225 230 235 240
 Glu Ile Leu Pro Tyr Ala Asn Phe Ile Pro Lys Glu Phe Val Gly Gln
 245 250 255
 Ile Met Thr Met Leu Asn Lys Gly Ser Ile His Ser Gln Ser Ser Ser
 260 265 270
 Phe Thr Glu Ala Glu Ile Asp Ile Arg Leu Arg Glu Glu Phe Ser Lys
 275 280 285
 Met Cys Phe Glu Thr Leu Leu Gln Phe Ser Phe Ser Asn Lys Val Thr
 290 295 300
 Thr Pro Gln Glu Gly Tyr Ile Ser Arg Met Ala Leu Ser Val Leu Leu
 305 310 315 320
 Lys Arg Ser Gln Asp Val Leu His Arg Tyr Ile Glu Asp Glu Arg Leu
 325 330 335
 Ser Gly Lys Cys Pro Leu Pro Arg Gln Gln Val Thr Glu Ile Ile Phe
 340 345 350
 Val Leu Lys Ala Val Ser Thr Leu Ile Asp Ser Leu Lys Lys Thr Gln
 355 360 365
 Pro Glu Asn Val Asp Gly Asn Thr Trp Ala Gln Val Ile Ala Leu Tyr
 370 375 380
 Pro Thr Leu Val Glu Cys Ile Thr Cys Ser Ser Ser Glu Val Cys Ser
 385 390 395 400

352

Ala Leu Lys Glu Ala Leu Val Pro Phe Lys Asp Phe Met Gln Pro Pro
 405 410 415
 Ala Ser Arg Val Gln Asn Gly Glu Ser
 420 425

<210> 239
 <211> 1053
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1053)

<400> 239
 atg gat ttg aag gct ctc ctt tct tcc ttg aat gac ttt gca tcc ctc 48
 Met Asp Leu Lys Ala Leu Leu Ser Ser Leu Asn Asp Phe Ala Ser Leu
 1 5 10 15
 tcg ttt gct gag agt tgg gac aat gtt gga tta ctg gtg gaa cca agc 96
 Ser Phe Ala Glu Ser Trp Asp Asn Val Gly Leu Leu Val Glu Pro Ser
 20 25 30
 cca cca cat act gta aat aca ctc ttc ctg acc aat gac ctg act gag 144
 Pro Pro His Thr Val Asn Thr Leu Phe Leu Thr Asn Asp Leu Thr Glu
 35 40 45
 gaa gtg atg gag gag gtg ctg caa aag aag gca gac ctc att ctc tcc 192
 Glu Val Met Glu Glu Val Leu Gln Lys Lys Ala Asp Leu Ile Leu Ser
 50 55 60
 tac cat ccg cct atc ttc cga ccc atg aag cgc ata acc tgg aac aca 240
 Tyr His Pro Pro Ile Phe Arg Pro Met Lys Arg Ile Thr Trp Asn Thr
 65 70 75 80
 tgg aag gag cgc ctg gtg atc cgg gct ctg gag aac aga gtc ggt atc 288
 Trp Lys Glu Arg Leu Val Ile Arg Ala Leu Glu Asn Arg Val Gly Ile
 85 90 95
 tac tct cct cat aca gcc tat gat gct gcg ccc cag ggc gtc aac aac 336
 Tyr Ser Pro His Thr Ala Tyr Asp Ala Ala Pro Gln Gly Val Asn Asn
 100 105 110
 tgg ttg gct aaa ggg ctt gga gct tgt acc tcc agg ccc ata cat cct 384

353

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|
| Trp | Leu | Ala | Lys | Gly | Leu | Gly | Ala | Cys | Thr | Ser | Arg | Pro | Ile | His | Pro | | |
| | | 115 | | | | | 120 | | | | | 125 | | | | | |
| tcc | aaa | gct | ccc | aac | tac | cct | aca | gag | gga | aac | cac | cga | gta | gaa | ttc | | 432 |
| Ser | Lys | Ala | Pro | Asn | Tyr | Pro | Thr | Glu | Gly | Asn | His | Arg | Val | Glu | Phe | | |
| | | 130 | | | | 135 | | | | | 140 | | | | | | |
| aac | gtt | aac | tac | acc | caa | gac | ctg | gac | aaa | gtc | atg | tct | gca | gtg | aaa | | 480 |
| Asn | Val | Asn | Tyr | Thr | Gln | Asp | Leu | Asp | Lys | Val | Met | Ser | Ala | Val | Lys | | |
| | | 145 | | | 150 | | | | | 155 | | | | | 160 | | |
| gga | att | gac | ggt | gtt | tct | gtc | act | tct | ttt | tct | gct | agg | act | ggt | aat | | 528 |
| Gly | Ile | Asp | Gly | Val | Ser | Val | Thr | Ser | Phe | Ser | Ala | Arg | Thr | Gly | Asn | | |
| | | | 165 | | | | | | 170 | | | | | 175 | | | |
| gag | gaa | caa | aca | cgg | att | aat | ctg | aat | tgt | act | cag | aag | gct | ttg | atg | | 576 |
| Glu | Glu | Gln | Thr | Arg | Ile | Asn | Leu | Asn | Cys | Thr | Gln | Lys | Ala | Leu | Met | | |
| | | | 180 | | | | | 185 | | | | | 190 | | | | |
| cag | gtg | gta | gat | ttt | ctt | tcc | cgg | aac | aaa | caa | ctt | tat | cag | aag | acg | | 624 |
| Gln | Val | Val | Asp | Phe | Leu | Ser | Arg | Asn | Lys | Gln | Leu | Tyr | Gln | Lys | Thr | | |
| | | 195 | | | | | 200 | | | | | 205 | | | | | |
| gaa | att | ctg | tca | ctg | gag | aag | cct | ttg | ctt | cta | cat | act | gga | atg | gga | | 672 |
| Glu | Ile | Leu | Ser | Leu | Glu | Lys | Pro | Leu | Leu | Leu | His | Thr | Gly | Met | Gly | | |
| | | 210 | | | | 215 | | | | | 220 | | | | | | |
| cgg | tta | tgc | aca | ctg | gat | gaa | tct | gtc | tcc | ctg | gca | acc | atg | att | gat | | 720 |
| Arg | Leu | Cys | Thr | Leu | Asp | Glu | Ser | Val | Ser | Leu | Ala | Thr | Met | Ile | Asp | | |
| | | 225 | | | 230 | | | | 235 | | | | | 240 | | | |
| cga | ata | aaa | aga | cac | cta | aaa | cta | tct | cat | att | cgc | tta | gcc | ctt | ggg | | 768 |
| Arg | Ile | Lys | Arg | His | Leu | Lys | Leu | Ser | His | Ile | Arg | Leu | Ala | Leu | Gly | | |
| | | | 245 | | | | | 250 | | | | | | 255 | | | |
| gtg | ggg | aga | acc | tta | gag | tct | caa | gtc | aaa | gtc | gtg | gcc | ctg | tgt | gct | | 816 |
| Val | Gly | Arg | Thr | Leu | Glu | Ser | Gln | Val | Lys | Val | Val | Ala | Leu | Cys | Ala | | |
| | | | 260 | | | | 265 | | | | | | 270 | | | | |
| ggt | tct | ggg | agc | agc | gtt | ctg | cag | ggt | gtt | gag | gct | gac | ctt | tac | ctc | | 864 |
| Gly | Ser | Gly | Ser | Ser | Val | Leu | Gln | Gly | Val | Glu | Ala | Asp | Leu | Tyr | Leu | | |
| | | 275 | | | | 280 | | | | | 285 | | | | | | |
| aca | ggt | gag | atg | tcc | cat | cat | gat | act | ttg | gat | gct | gct | tcc | caa | gga | | 912 |

354

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| Thr | Gly | Glu | Met | Ser | His | His | Asp | Thr | Leu | Asp | Ala | Ala | Ser | Gln | Gly | |
| 290 | | | | | | 295 | | | | | 300 | | | | | |
| ata | aat | gtc | atc | ctc | tgt | gaa | cac | agc | aac | act | gaa | cga | ggc | ttt | ctt | 960 |
| Ile | Asn | Val | Ile | Leu | Cys | Glu | His | Ser | Asn | Thr | Glu | Arg | Gly | Phe | Leu | |
| 305 | | | | 310 | | | | | 315 | | | | | 320 | | |
| tct | gac | ctt | cga | gat | atg | ctg | gat | tct | cac | ttg | gag | aat | aag | ata | aat | 1008 |
| Ser | Asp | Leu | Arg | Asp | Met | Leu | Asp | Ser | His | Leu | Glu | Asn | Lys | Ile | Asn | |
| | | | | 325 | | | | | 330 | | | | | 335 | | |
| att | atc | cta | tca | gag | act | gac | agg | gac | cct | ctt | cag | gtg | gta | taa | | 1053 |
| Ile | Ile | Leu | Ser | Glu | Thr | Asp | Arg | Asp | Pro | Leu | Gln | Val | Val | * | | |
| | | | 340 | | | | | 345 | | | | | 350 | | | |

<210> 240

<211> 350

<212> PRT

<213> Homo sapiens

<400> 240

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Asp | Leu | Lys | Ala | Leu | Leu | Ser | Ser | Leu | Asn | Asp | Phe | Ala | Ser | Leu | |
| 1 | | | 5 | | | | | | 10 | | | | | 15 | | |
| Ser | Phe | Ala | Glu | Ser | Trp | Asp | Asn | Val | Gly | Leu | Leu | Val | Glu | Pro | Ser | |
| | | 20 | | | | | 25 | | | | | | 30 | | | |
| Pro | Pro | His | Thr | Val | Asn | Thr | Leu | Phe | Leu | Thr | Asn | Asp | Leu | Thr | Glu | |
| | | 35 | | | | 40 | | | | | | 45 | | | | |
| Glu | Val | Met | Glu | Glu | Val | Leu | Gln | Lys | Lys | Ala | Asp | Leu | Ile | Leu | Ser | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| Tyr | His | Pro | Pro | Ile | Phe | Arg | Pro | Met | Lys | Arg | Ile | Thr | Trp | Asn | Thr | |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | | |
| Trp | Lys | Glu | Arg | Leu | Val | Ile | Arg | Ala | Leu | Glu | Asn | Arg | Val | Gly | Ile | |
| | | | 85 | | | | | | 90 | | | | | 95 | | |
| Tyr | Ser | Pro | His | Thr | Ala | Tyr | Asp | Ala | Ala | Pro | Gln | Gly | Val | Asn | Asn | |
| | | 100 | | | | | | 105 | | | | | 110 | | | |
| Trp | Leu | Ala | Lys | Gly | Leu | Gly | Ala | Cys | Thr | Ser | Arg | Pro | Ile | His | Pro | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| Ser | Lys | Ala | Pro | Asn | Tyr | Pro | Thr | Glu | Gly | Asn | His | Arg | Val | Glu | Phe | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| Asn | Val | Asn | Tyr | Thr | Gln | Asp | Leu | Asp | Lys | Val | Met | Ser | Ala | Val | Lys | |
| | 145 | | | | 150 | | | | | 155 | | | | | 160 | |
| Gly | Ile | Asp | Gly | Val | Ser | Val | Thr | Ser | Phe | Ser | Ala | Arg | Thr | Gly | Asn | |
| | | | | 165 | | | | | 170 | | | | | | 175 | |

355

Glu Glu Gln Thr Arg Ile Asn Leu Asn Cys Thr Gln Lys Ala Leu Met
 180 185 190
 Gln Val Val Asp Phe Leu Ser Arg Asn Lys Gln Leu Tyr Gln Lys Thr
 195 200 205
 Glu Ile Leu Ser Leu Glu Lys Pro Leu Leu Leu His Thr Gly Met Gly
 210 215 220
 Arg Leu Cys Thr Leu Asp Glu Ser Val Ser Leu Ala Thr Met Ile Asp
 225 230 235 240
 Arg Ile Lys Arg His Leu Lys Leu Ser His Ile Arg Leu Ala Leu Gly
 245 250 255
 Val Gly Arg Thr Leu Glu Ser Gln Val Lys Val Val Ala Leu Cys Ala
 260 265 270
 Gly Ser Gly Ser Ser Val Leu Gln Gly Val Glu Ala Asp Leu Tyr Leu
 275 280 285
 Thr Gly Glu Met Ser His His Asp Thr Leu Asp Ala Ala Ser Gln Gly
 290 295 300
 Ile Asn Val Ile Leu Cys Glu His Ser Asn Thr Glu Arg Gly Phe Leu
 305 310 315 320
 Ser Asp Leu Arg Asp Met Leu Asp Ser His Leu Glu Asn Lys Ile Asn
 325 330 335
 Ile Ile Leu Ser Glu Thr Asp Arg Asp Pro Leu Gln Val Val
 340 345 350

<210> 241

<211> 933

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(933)

<400> 241

| | |
|---|-----|
| atg ggc gga gaa ttt tgt gtg gct gct atc ttc gga aca tcc agg tca | 48 |
| Met Gly Gly Glu Phe Cys Val Ala Ala Ile Phe Gly Thr Ser Arg Ser | |
| 1 5 10 15 | |
| | |
| tgg ttt gca aat aat gca ggt ctg aaa aga gaa aaa gat cag tcc aaa | 96 |
| Trp Phe Ala Asn Asn Ala Gly Leu Lys Arg Glu Lys Asp Gln Ser Lys | |
| 20 25 30 | |
| | |
| caa gtt gta gtt gag tcc ctg tac att atc agt tgc tat ggc acc tta | 144 |
| Gln Val Val Val Glu Ser Leu Tyr Ile Ile Ser Cys Tyr Gly Thr Leu | |
| 35 40 45 | |

356

| | |
|---|-----|
| gtg gaa cac atg atg gag ccg cga ccc ctc agc act gca ccc aag att Val Glu His Met Met Glu Pro Arg Pro Leu Ser Thr Ala Pro Lys Ile 50 55 60 | 192 |
| agt gac gac aca cca ctg gaa atg atg aca tcg cct cga gcc agc tgg Ser Asp Asp Thr Pro Leu Glu Met Met Thr Ser Pro Arg Ala Ser Trp 65 70 75 80 | 240 |
| act ctg gtt aga acc cct caa tgg aat gaa ttg cag cca ccg ttt aat Thr Leu Val Arg Thr Pro Gln Trp Asn Glu Leu Gln Pro Pro Phe Asn 85 90 95 | 288 |
| gca aac cac cct ctg ctc ctc gct gca gat gca gta cag tat tat cag Ala Asn His Pro Leu Leu Leu Ala Ala Asp Ala Val Gln Tyr Tyr Gln 100 105 110 | 336 |
| ttc ctg ctt gct ggc ctg gtt ccc cct gga agt cct ggg ccc att act Phe Leu Leu Ala Gly Leu Val Pro Pro Gly Ser Pro Gly Pro Ile Thr 115 120 125 | 384 |
| cga cat ggg tct tac gac agt tta gct tct gac cat agt gga cag gaa Arg His Gly Ser Tyr Asp Ser Leu Ala Ser Asp His Ser Gly Gln Glu 130 135 140 | 432 |
| gat gaa gaa tgg ctt tcc cag gtt gaa att gta aca cac act gga ccc Asp Glu Glu Trp Leu Ser Gln Val Glu Ile Val Thr His Thr Gly Pro 145 150 155 160 | 480 |
| cat aga cgt ctg tgg atg ggt cca cag ttc cag ttc aaa acc atc cat His Arg Arg Leu Trp Met Gly Pro Gln Phe Gln Phe Lys Thr Ile His 165 170 175 | 528 |
| ccc tca ggc caa acc aca gtt atc tca tcc agt tca tct gtg ttg cag Pro Ser Gly Gln Thr Thr Val Ile Ser Ser Ser Ser Ser Val Leu Gln 180 185 190 | 576 |
| tct cat ggt ccg agt gac acg cca cag cct ctt ttg gat ttt gat aca Ser His Gly Pro Ser Asp Thr Pro Gln Pro Leu Leu Asp Phe Asp Thr 195 200 205 | 624 |
| gat gat ctt gat ctc aac agt ctc agg atc cag cca gtc cgc tct gac Asp Asp Leu Asp Leu Asn Ser Leu Arg Ile Gln Pro Val Arg Ser Asp 210 215 220 | 672 |

357

```

ccc gtc agc atg cca ggg tca tcc cgt cca gtc tct gat cga agg gga      720
Pro Val Ser Met Pro Gly Ser Ser Arg Pro Val Ser Asp Arg Arg Gly
225                230                235                240

gtt tcc aca gtg att gat gct gcc tca ggt acc ttt gac agg agc gtg      768
Val Ser Thr Val Ile Asp Ala Ala Ser Gly Thr Phe Asp Arg Ser Val
                245                250                255

acc ctg ctg gag gtg tgc ggg agc tgg cct gag ggc ttc ggg ctg cgg      816
Thr Leu Leu Glu Val Cys Gly Ser Trp Pro Glu Gly Phe Gly Leu Arg
                260                265                270

cac atg tcc tcc atg gag cac acg gag gag ggc tcc ggg agc gac ttg      864
His Met Ser Ser Met Glu His Thr Glu Glu Gly Ser Gly Ser Asp Leu
                275                280                285

ccg acg cca tgg ccg agt cac cta gcc ggg acg tcg tgg gat ccg gaa      912
Pro Thr Pro Trp Pro Ser His Leu Ala Gly Thr Ser Trp Asp Pro Glu
                290                295                300

cag aca cag ccc ttg acg tag                                          933
Gln Thr Gln Pro Leu Thr *
305                310

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<210> 242
<211> 310
<212> PRT
<213> Homo sapiens

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<400> 242
Met Gly Gly Glu Phe Cys Val Ala Ala Ile Phe Gly Thr Ser Arg Ser
 1                5                10                15
Trp Phe Ala Asn Asn Ala Gly Leu Lys Arg Glu Lys Asp Gln Ser Lys
                20                25                30
Gln Val Val Val Glu Ser Leu Tyr Ile Ile Ser Cys Tyr Gly Thr Leu
                35                40                45
Val Glu His Met Met Glu Pro Arg Pro Leu Ser Thr Ala Pro Lys Ile
                50                55                60
Ser Asp Asp Thr Pro Leu Glu Met Met Thr Ser Pro Arg Ala Ser Trp
65                70                75                80
Thr Leu Val Arg Thr Pro Gln Trp Asn Glu Leu Gln Pro Pro Phe Asn
                85                90                95

```

358

Ala Asn His Pro Leu Leu Leu Ala Ala Asp Ala Val Gln Tyr Tyr Gln
 100 105 110
 Phe Leu Leu Ala Gly Leu Val Pro Pro Gly Ser Pro Gly Pro Ile Thr
 115 120 125
 Arg His Gly Ser Tyr Asp Ser Leu Ala Ser Asp His Ser Gly Gln Glu
 130 135 140
 Asp Glu Glu Trp Leu Ser Gln Val Glu Ile Val Thr His Thr Gly Pro
 145 150 155 160
 His Arg Arg Leu Trp Met Gly Pro Gln Phe Gln Phe Lys Thr Ile His
 165 170 175
 Pro Ser Gly Gln Thr Thr Val Ile Ser Ser Ser Ser Ser Val Leu Gln
 180 185 190
 Ser His Gly Pro Ser Asp Thr Pro Gln Pro Leu Leu Asp Phe Asp Thr
 195 200 205
 Asp Asp Leu Asp Leu Asn Ser Leu Arg Ile Gln Pro Val Arg Ser Asp
 210 215 220
 Pro Val Ser Met Pro Gly Ser Ser Arg Pro Val Ser Asp Arg Arg Gly
 225 230 235 240
 Val Ser Thr Val Ile Asp Ala Ala Ser Gly Thr Phe Asp Arg Ser Val
 245 250 255
 Thr Leu Leu Glu Val Cys Gly Ser Trp Pro Glu Gly Phe Gly Leu Arg
 260 265 270
 His Met Ser Ser Met Glu His Thr Glu Glu Gly Ser Gly Ser Asp Leu
 275 280 285
 Pro Thr Pro Trp Pro Ser His Leu Ala Gly Thr Ser Trp Asp Pro Glu
 290 295 300
 Gln Thr Gln Pro Leu Thr
 305 310

<210> 243

<211> 465

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(465)

<221> misc_feature

<222> (1)...(465)

<223> n = A,T,C or G

<400> 243

atg tnc tct ggg gcg agg aca cgg ctt ntg gct nct ggc nct gct gtc

359

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Xaa | Ser | Gly | Ala | Arg | Thr | Arg | Leu | Xaa | Ala | Xaa | Gly | Xaa | Ala | Val | |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | | |
| tca | ctg | gcc | nct | ttg | ttg | aat | aag | gcg | gct | gat | aaa | gga | agc | agg | aag | 96 |
| Ser | Leu | Ala | Xaa | Leu | Leu | Asn | Lys | Ala | Ala | Asp | Lys | Gly | Ser | Arg | Lys | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| cgc | tat | gaa | cca | tca | gac | aag | gac | agg | cag | agc | cct | cct | cca | gcc | aag | 144 |
| Arg | Tyr | Glu | Pro | Ser | Asp | Lys | Asp | Arg | Gln | Ser | Pro | Pro | Pro | Ala | Lys | |
| | | | 35 | | | | 40 | | | | | 45 | | | | |
| cgg | ccc | aac | aca | tcc | cca | gac | cga | ggg | tct | cgg | gac | cgg | aag | tca | ggg | 192 |
| Arg | Pro | Asn | Thr | Ser | Pro | Asp | Arg | Gly | Ser | Arg | Asp | Arg | Lys | Ser | Gly | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| ggg | aga | ctg | ggc | tcc | ccg | aag | cca | gag | cgg | cag | aga | ggc | cag | aac | tcc | 240 |
| Gly | Arg | Leu | Gly | Ser | Pro | Lys | Pro | Glu | Arg | Gln | Arg | Gly | Gln | Asn | Ser | |
| 65 | | | | 70 | | | | 75 | | | | | | 80 | | |
| aaa | gcc | cct | gca | gcc | ccg | gct | gac | agg | aag | cgc | can | ntg | tca | ccc | cag | 288 |
| Lys | Ala | Pro | Ala | Ala | Pro | Ala | Asp | Arg | Lys | Arg | Xaa | Xaa | Ser | Pro | Gln | |
| | | | 85 | | | | | 90 | | | | | | 95 | | |
| tcc | aag | agc | tcc | agc | aag | gtc | acg | agc | gtg | ccc | ggc | aaa | gcc | tcg | gat | 336 |
| Ser | Lys | Ser | Ser | Ser | Lys | Val | Thr | Ser | Val | Pro | Gly | Lys | Ala | Ser | Asp | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| ccc | ggc | gcc | gcc | agc | acc | aaa | tca | ggg | aag | gcc | agc | acg | ctg | tct | cgg | 384 |
| Pro | Gly | Ala | Ala | Ser | Thr | Lys | Ser | Gly | Lys | Ala | Ser | Thr | Leu | Ser | Arg | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| cgg | gag | gag | ctg | ctg | aaa | cag | ctg | aag | gcc | gtg | gag | gat | gct | att | gca | 432 |
| Arg | Glu | Glu | Leu | Leu | Lys | Gln | Leu | Lys | Ala | Val | Glu | Asp | Ala | Ile | Ala | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| cgc | aag | cgg | gcc | aag | atc | ccc | ggg | aaa | gca | tag | | | | | | 465 |
| Arg | Lys | Arg | Ala | Lys | Ile | Pro | Gly | Lys | Ala | * | | | | | | |
| 145 | | | | | 150 | | | | | | | | | | | |

<210> 244

<211> 154

<212> PRT

<213> Homo sapiens

360

<220>

<221> VARIANT

<222> (1)...(154)

<223> Xaa = Any Amino Acid

<400> 244

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Met Xaa Ser Gly Ala Arg Thr Arg Leu Xaa Ala Xaa Gly Xaa Ala Val
 1              5              10              15
Ser Leu Ala Xaa Leu Leu Asn Lys Ala Ala Asp Lys Gly Ser Arg Lys
      20              25              30
Arg Tyr Glu Pro Ser Asp Lys Asp Arg Gln Ser Pro Pro Pro Ala Lys
      35              40              45
Arg Pro Asn Thr Ser Pro Asp Arg Gly Ser Arg Asp Arg Lys Ser Gly
      50              55              60
Gly Arg Leu Gly Ser Pro Lys Pro Glu Arg Gln Arg Gly Gln Asn Ser
65              70              75              80
Lys Ala Pro Ala Ala Pro Ala Asp Arg Lys Arg Xaa Xaa Ser Pro Gln
      85              90              95
Ser Lys Ser Ser Ser Lys Val Thr Ser Val Pro Gly Lys Ala Ser Asp
      100             105             110
Pro Gly Ala Ala Ser Thr Lys Ser Gly Lys Ala Ser Thr Leu Ser Arg
      115             120             125
Arg Glu Glu Leu Leu Lys Gln Leu Lys Ala Val Glu Asp Ala Ile Ala
      130             135             140
Arg Lys Arg Ala Lys Ile Pro Gly Lys Ala
145              150

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<210> 245

<211> 1839

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1839)

<400> 245

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atg gcg gcg gcg ggc cgg ctc ccg agc tcc tgg gcc ctc ttc tcg ccg      48
Met Ala Ala Ala Gly Arg Leu Pro Ser Ser Trp Ala Leu Phe Ser Pro
 1              5              10              15

ctc ctc gca ggg ctt gca cta ctg gga gtc ggg ccg gtc cca gcg ccg      96
Leu Leu Ala Gly Leu Ala Leu Leu Gly Val Gly Pro Val Pro Ala Arg

```

361

| 20 | 25 | 30 | |
|---|----|----|-----|
| gcg ctg cac aac gtc acg gcc gag ctc ttt ggg gcc gag gcc tgg ggc Ala Leu His Asn Val Thr Ala Glu Leu Phe Gly Ala Glu Ala Trp Gly 35 40 45 | | | 144 |
| acc ctt gcg gct ttc ggg gac ctc aac tcc gac aag cag acg gat ctc Thr Leu Ala Ala Phe Gly Asp Leu Asn Ser Asp Lys Gln Thr Asp Leu 50 55 60 | | | 192 |
| ttc gtg ctg cgg gaa aga aat gac tta atc gtc ttt ttg gca gac cag Phe Val Leu Arg Glu Arg Asn Asp Leu Ile Val Phe Leu Ala Asp Gln 65 70 75 80 | | | 240 |
| aat gca ccc tat ttt aaa ccc aaa gta aag gta tct ttc aag aat cac Asn Ala Pro Tyr Phe Lys Pro Lys Val Lys Val Ser Phe Lys Asn His 85 90 95 | | | 288 |
| agt gca ttg ata aca agt gta gtc cct ggg gat tat gat gga gat tct Ser Ala Leu Ile Thr Ser Val Val Pro Gly Asp Tyr Asp Gly Asp Ser 100 105 110 | | | 336 |
| caa atg gat gtc ctt ctg aca tat ctt ccc aaa aat tat gcc aag agt Gln Met Asp Val Leu Leu Thr Tyr Leu Pro Lys Asn Tyr Ala Lys Ser 115 120 125 | | | 384 |
| gaa tta gga gct gtt atc ttc tgg gga caa aat caa aca tta gat cct Glu Leu Gly Ala Val Ile Phe Trp Gly Gln Asn Gln Thr Leu Asp Pro 130 135 140 | | | 432 |
| aac aat atg acc ata ctc aat agg act ttt caa gat gag cca cta att Asn Asn Met Thr Ile Leu Asn Arg Thr Phe Gln Asp Glu Pro Leu Ile 145 150 155 160 | | | 480 |
| atg gat ttc aat ggt gat cta att cct gat att ttt ggt atc aca aat Met Asp Phe Asn Gly Asp Leu Ile Pro Asp Ile Phe Gly Ile Thr Asn 165 170 175 | | | 528 |
| gaa tcc aac cag cca cag ata cta tta gga ggg aat tta tca tgg cat Glu Ser Asn Gln Pro Gln Ile Leu Leu Gly Gly Asn Leu Ser Trp His 180 185 190 | | | 576 |
| cca gca ttg acc act aca agt aaa atg cga att cca cat tct cat gca Pro Ala Leu Thr Thr Thr Ser Lys Met Arg Ile Pro His Ser His Ala | | | 624 |

362

| | | | |
|---|------|-----|-----|
| 195 | 200 | 205 | |
| ttt att gat ctg act gaa gat ttt aca gca gat tta ttc ctg acg aca | 672 | | |
| Phe Ile Asp Leu Thr Glu Asp Phe Thr Ala Asp Leu Phe Leu Thr Thr | | | |
| 210 | 215 | 220 | |
| ttg aat gcc acc act agt acc ttc cag ttt gaa ata tgg gaa aat ttg | 720 | | |
| Leu Asn Ala Thr Thr Ser Thr Phe Gln Phe Glu Ile Trp Glu Asn Leu | | | |
| 225 | 230 | 235 | 240 |
| gat gga aac ttc tct gtc agt act ata ttg gaa aaa cct caa aat atg | 768 | | |
| Asp Gly Asn Phe Ser Val Ser Thr Ile Leu Glu Lys Pro Gln Asn Met | | | |
| | 245 | 250 | 255 |
| atg gtg gtt gga cag tca gca ttt gca gac ttt gat gga gat gga cac | 816 | | |
| Met Val Val Gly Gln Ser Ala Phe Ala Asp Phe Asp Gly Asp Gly His | | | |
| | 260 | 265 | 270 |
| atg gat cat tta ctg cca ggc tgt gaa gat aaa aat tgc caa aag agt | 864 | | |
| Met Asp His Leu Leu Pro Gly Cys Glu Asp Lys Asn Cys Gln Lys Ser | | | |
| | 275 | 280 | 285 |
| acc atc tac tta gtg aga tct ggg atg aag cag tgg gtt cca gtc cta | 912 | | |
| Thr Ile Tyr Leu Val Arg Ser Gly Met Lys Gln Trp Val Pro Val Leu | | | |
| | 290 | 295 | 300 |
| caa gat ttc agc aat aag ggc aca ctc tgg ggc ttt gtg cca ttt gtg | 960 | | |
| Gln Asp Phe Ser Asn Lys Gly Thr Leu Trp Gly Phe Val Pro Phe Val | | | |
| 305 | 310 | 315 | 320 |
| gat gaa cag caa cca act gaa ata cca att cca att acc ctt cat att | 1008 | | |
| Asp Glu Gln Gln Pro Thr Glu Ile Pro Ile Pro Ile Thr Leu His Ile | | | |
| | 325 | 330 | 335 |
| gga gac tac aat atg gat ggc tat cca gac gct ctg gtc ata cta aag | 1056 | | |
| Gly Asp Tyr Asn Met Asp Gly Tyr Pro Asp Ala Leu Val Ile Leu Lys | | | |
| | 340 | 345 | 350 |
| aac aca tct gga agc aac cag cag gcc ttt tta ctg gag aac gtc cct | 1104 | | |
| Asn Thr Ser Gly Ser Asn Gln Gln Ala Phe Leu Leu Glu Asn Val Pro | | | |
| | 355 | 360 | 365 |
| tgt aat aat gca agc tgt gaa gag gcg cgt cga atg ttt aaa gtc tac | 1152 | | |
| Cys Asn Asn Ala Ser Cys Glu Glu Ala Arg Arg Met Phe Lys Val Tyr | | | |

363

| 370 | 375 | 380 | |
|---|-----|-----|------|
| tgg gag ctg aca gac cta aat caa att aag gat gcc atg gtt gcc acc | | | 1200 |
| Trp Glu Leu Thr Asp Leu Asn Gln Ile Lys Asp Ala Met Val Ala Thr | | | |
| 385 | 390 | 395 | 400 |
| ttc ttt gac att tac gaa gat gga atc ttg gac att gta gtg cta agt | | | 1248 |
| Phe Phe Asp Ile Tyr Glu Asp Gly Ile Leu Asp Ile Val Val Leu Ser | | | |
| | 405 | 410 | 415 |
| aaa gga tat aca aag aat gat ttt gcc att cat aca cta aaa aat aac | | | 1296 |
| Lys Gly Tyr Thr Lys Asn Asp Phe Ala Ile His Thr Leu Lys Asn Asn | | | |
| | 420 | 425 | 430 |
| ttt gaa gca gat gct tat ttt gtt aaa gtt att gtt ctt agt ggt ctg | | | 1344 |
| Phe Glu Ala Asp Ala Tyr Phe Val Lys Val Ile Val Leu Ser Gly Leu | | | |
| | 435 | 440 | 445 |
| tgt tct aat gac tgt cct cgt aag ata aca ccc ttt gga gtg aat caa | | | 1392 |
| Cys Ser Asn Asp Cys Pro Arg Lys Ile Thr Pro Phe Gly Val Asn Gln | | | |
| | 450 | 455 | 460 |
| cct gga cct tat atc atg tat aca act gta gat gca aat ggg tat ctg | | | 1440 |
| Pro Gly Pro Tyr Ile Met Tyr Thr Thr Val Asp Ala Asn Gly Tyr Leu | | | |
| 465 | 470 | 475 | 480 |
| aaa aat gga tca gct ggc caa ctc agc caa tcc gca cat tta gct ctc | | | 1488 |
| Lys Asn Gly Ser Ala Gly Gln Leu Ser Gln Ser Ala His Leu Ala Leu | | | |
| | 485 | 490 | 495 |
| caa cta cca tac aac gtg ctt ggt tta ggt cgg agc gca aat ttt ctt | | | 1536 |
| Gln Leu Pro Tyr Asn Val Leu Gly Leu Gly Arg Ser Ala Asn Phe Leu | | | |
| | 500 | 505 | 510 |
| gac cat ctc tac gtt ggt att ccc cgt cca tct gga gaa aaa tct ata | | | 1584 |
| Asp His Leu Tyr Val Gly Ile Pro Arg Pro Ser Gly Glu Lys Ser Ile | | | |
| | 515 | 520 | 525 |
| cga aaa caa gag tgg act gca atc att cca aat tcc cag cta att gtc | | | 1632 |
| Arg Lys Gln Glu Trp Thr Ala Ile Ile Pro Asn Ser Gln Leu Ile Val | | | |
| | 530 | 535 | 540 |
| att cca tac cct cac aat gtc cct cga agt tgg agt gcc aaa ctg tat | | | 1680 |
| Ile Pro Tyr Pro His Asn Val Pro Arg Ser Trp Ser Ala Lys Leu Tyr | | | |

364

| | | | | |
|---|------|-----|-----|--|
| 545 | 550 | 555 | 560 | |
| ctt aca cca agt aat att gtt ctg ctt act gct ata gct ctc atc ggt | 1728 | | | |
| Leu Thr Pro Ser Asn Ile Val Leu Leu Thr Ala Ile Ala Leu Ile Gly | | | | |
| 565 | 570 | 575 | | |
| gtc tgt gtt ttc atc ttg gca ata att ggc att tta cat tgg cag gaa | 1776 | | | |
| Val Cys Val Phe Ile Leu Ala Ile Ile Gly Ile Leu His Trp Gln Glu | | | | |
| 580 | 585 | 590 | | |
| aag aaa gca gat gat aga gaa aaa cga caa gaa gcc cac cgg ttt cat | 1824 | | | |
| Lys Lys Ala Asp Asp Arg Glu Lys Arg Gln Glu Ala His Arg Phe His | | | | |
| 595 | 600 | 605 | | |
| ttt gat gct atg tga | 1839 | | | |
| Phe Asp Ala Met * | | | | |
| 610 | | | | |

<210> 246
 <211> 612
 <212> PRT
 <213> Homo sapiens

<400> 246

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Ala | Gly | Arg | Leu | Pro | Ser | Ser | Trp | Ala | Leu | Phe | Ser | Pro |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Leu | Leu | Ala | Gly | Leu | Ala | Leu | Leu | Gly | Val | Gly | Pro | Val | Pro | Ala | Arg |
| | | 20 | | | | | | 25 | | | | | 30 | | |
| Ala | Leu | His | Asn | Val | Thr | Ala | Glu | Leu | Phe | Gly | Ala | Glu | Ala | Trp | Gly |
| | | 35 | | | | 40 | | | | | | 45 | | | |
| Thr | Leu | Ala | Ala | Phe | Gly | Asp | Leu | Asn | Ser | Asp | Lys | Gln | Thr | Asp | Leu |
| | | 50 | | | | 55 | | | | | 60 | | | | |
| Phe | Val | Leu | Arg | Glu | Arg | Asn | Asp | Leu | Ile | Val | Phe | Leu | Ala | Asp | Gln |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| Asn | Ala | Pro | Tyr | Phe | Lys | Pro | Lys | Val | Lys | Val | Ser | Phe | Lys | Asn | His |
| | | | 85 | | | | | 90 | | | | | | 95 | |
| Ser | Ala | Leu | Ile | Thr | Ser | Val | Val | Pro | Gly | Asp | Tyr | Asp | Gly | Asp | Ser |
| | | 100 | | | | | | 105 | | | | | 110 | | |
| Gln | Met | Asp | Val | Leu | Leu | Thr | Tyr | Leu | Pro | Lys | Asn | Tyr | Ala | Lys | Ser |
| | | 115 | | | | 120 | | | | | | 125 | | | |
| Glu | Leu | Gly | Ala | Val | Ile | Phe | Trp | Gly | Gln | Asn | Gln | Thr | Leu | Asp | Pro |
| | | 130 | | | | 135 | | | | | 140 | | | | |
| Asn | Asn | Met | Thr | Ile | Leu | Asn | Arg | Thr | Phe | Gln | Asp | Glu | Pro | Leu | Ile |

365

145 150 155 160
 Met Asp Phe Asn Gly Asp Leu Ile Pro Asp Ile Phe Gly Ile Thr Asn
 165 170 175
 Glu Ser Asn Gln Pro Gln Ile Leu Leu Gly Gly Asn Leu Ser Trp His
 180 185 190
 Pro Ala Leu Thr Thr Thr Ser Lys Met Arg Ile Pro His Ser His Ala
 195 200 205
 Phe Ile Asp Leu Thr Glu Asp Phe Thr Ala Asp Leu Phe Leu Thr Thr
 210 215 220
 Leu Asn Ala Thr Thr Ser Thr Phe Gln Phe Glu Ile Trp Glu Asn Leu
 225 230 235 240
 Asp Gly Asn Phe Ser Val Ser Thr Ile Leu Glu Lys Pro Gln Asn Met
 245 250 255
 Met Val Val Gly Gln Ser Ala Phe Ala Asp Phe Asp Gly Asp Gly His
 260 265 270
 Met Asp His Leu Leu Pro Gly Cys Glu Asp Lys Asn Cys Gln Lys Ser
 275 280 285
 Thr Ile Tyr Leu Val Arg Ser Gly Met Lys Gln Trp Val Pro Val Leu
 290 295 300
 Gln Asp Phe Ser Asn Lys Gly Thr Leu Trp Gly Phe Val Pro Phe Val
 305 310 315 320
 Asp Glu Gln Gln Pro Thr Glu Ile Pro Ile Pro Ile Thr Leu His Ile
 325 330 335
 Gly Asp Tyr Asn Met Asp Gly Tyr Pro Asp Ala Leu Val Ile Leu Lys
 340 345 350
 Asn Thr Ser Gly Ser Asn Gln Gln Ala Phe Leu Leu Glu Asn Val Pro
 355 360 365
 Cys Asn Asn Ala Ser Cys Glu Glu Ala Arg Arg Met Phe Lys Val Tyr
 370 375 380
 Trp Glu Leu Thr Asp Leu Asn Gln Ile Lys Asp Ala Met Val Ala Thr
 385 390 395 400
 Phe Phe Asp Ile Tyr Glu Asp Gly Ile Leu Asp Ile Val Val Leu Ser
 405 410 415
 Lys Gly Tyr Thr Lys Asn Asp Phe Ala Ile His Thr Leu Lys Asn Asn
 420 425 430
 Phe Glu Ala Asp Ala Tyr Phe Val Lys Val Ile Val Leu Ser Gly Leu
 435 440 445
 Cys Ser Asn Asp Cys Pro Arg Lys Ile Thr Pro Phe Gly Val Asn Gln
 450 455 460
 Pro Gly Pro Tyr Ile Met Tyr Thr Thr Val Asp Ala Asn Gly Tyr Leu
 465 470 475 480
 Lys Asn Gly Ser Ala Gly Gln Leu Ser Gln Ser Ala His Leu Ala Leu
 485 490 495
 Gln Leu Pro Tyr Asn Val Leu Gly Leu Gly Arg Ser Ala Asn Phe Leu

366

500 505 510
 Asp His Leu Tyr Val Gly Ile Pro Arg Pro Ser Gly Glu Lys Ser Ile
 515 520 525
 Arg Lys Gln Glu Trp Thr Ala Ile Ile Pro Asn Ser Gln Leu Ile Val
 530 535 540
 Ile Pro Tyr Pro His Asn Val Pro Arg Ser Trp Ser Ala Lys Leu Tyr
 545 550 555 560
 Leu Thr Pro Ser Asn Ile Val Leu Leu Thr Ala Ile Ala Leu Ile Gly
 565 570 575
 Val Cys Val Phe Ile Leu Ala Ile Ile Gly Ile Leu His Trp Gln Glu
 580 585 590
 Lys Lys Ala Asp Asp Arg Glu Lys Arg Gln Glu Ala His Arg Phe His
 595 600 605
 Phe Asp Ala Met
 610

<210> 247
 <211> 462
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(462)

<400> 247
 atg ggc cgg ctc cca ttg ctc cgg cgc gtt ctc aag ggc ttg cag ctg 48
 Met Gly Arg Leu Pro Leu Leu Arg Arg Val Leu Lys Gly Leu Gln Leu
 1 5 10 15
 ttg ctg tct ctg ctg gcc ttc atc tgt gaa gaa gtt gta tca caa tgt 96
 Leu Leu Ser Leu Leu Ala Phe Ile Cys Glu Glu Val Val Ser Gln Cys
 20 25 30
 act tta tgt gga gga ctt tat ttt ttt gag ttt gta agc tgc agt gcc 144
 Thr Leu Cys Gly Gly Leu Tyr Phe Phe Glu Phe Val Ser Cys Ser Ala
 35 40 45
 ttt ctt ctg agt ctc ctt ata ctg att gtg tat tgc act cca ttt tat 192
 Phe Leu Leu Ser Leu Leu Ile Leu Ile Val Tyr Cys Thr Pro Phe Tyr
 50 55 60
 gag aga gtt gat acc aca aaa gta aaa tca tcg gat ttt tat att act 240
 Glu Arg Val Asp Thr Thr Lys Val Lys Ser Ser Asp Phe Tyr Ile Thr

367

| | | | | |
|---|-----|-----|-----|--|
| 65 | 70 | 75 | 80 | |
| ttg gga aca gga tgt gtg ttt ttg ttg gca tcc atc att ttt gtt tcc | 288 | | | |
| Leu Gly Thr Gly Cys Val Phe Leu Leu Ala Ser Ile Ile Phe Val Ser | | | | |
| | 85 | 90 | 95 | |
| aca cat gac agg act tca gct gag att gct gca att gtg ttt gga ttt | 336 | | | |
| Thr His Asp Arg Thr Ser Ala Glu Ile Ala Ala Ile Val Phe Gly Phe | | | | |
| | 100 | 105 | 110 | |
| ata gca agt ttt atg ttc cta ctt gac ttt atc act atg ctg tat gaa | 384 | | | |
| Ile Ala Ser Phe Met Phe Leu Leu Asp Phe Ile Thr Met Leu Tyr Glu | | | | |
| | 115 | 120 | 125 | |
| aaa cga cag gag tcc cag ctg aga aaa cct gaa aat acc act agg gct | 432 | | | |
| Lys Arg Gln Glu Ser Gln Leu Arg Lys Pro Glu Asn Thr Thr Arg Ala | | | | |
| | 130 | 135 | 140 | |
| gaa gcc ctc act gag cca ctt aat gcc taa | 462 | | | |
| Glu Ala Leu Thr Glu Pro Leu Asn Ala * | | | | |
| 145 | 150 | | | |

<210> 248
 <211> 153
 <212> PRT
 <213> Homo sapiens

<400> 248

| | |
|---|--|
| Met Gly Arg Leu Pro Leu Leu Arg Arg Val Leu Lys Gly Leu Gln Leu | |
| 1 5 10 15 | |
| Leu Leu Ser Leu Leu Ala Phe Ile Cys Glu Glu Val Val Ser Gln Cys | |
| 20 25 30 | |
| Thr Leu Cys Gly Gly Leu Tyr Phe Phe Glu Phe Val Ser Cys Ser Ala | |
| 35 40 45 | |
| Phe Leu Leu Ser Leu Leu Ile Leu Ile Val Tyr Cys Thr Pro Phe Tyr | |
| 50 55 60 | |
| Glu Arg Val Asp Thr Thr Lys Val Lys Ser Ser Asp Phe Tyr Ile Thr | |
| 65 70 75 80 | |
| Leu Gly Thr Gly Cys Val Phe Leu Leu Ala Ser Ile Ile Phe Val Ser | |
| 85 90 95 | |
| Thr His Asp Arg Thr Ser Ala Glu Ile Ala Ala Ile Val Phe Gly Phe | |
| 100 105 110 | |
| Ile Ala Ser Phe Met Phe Leu Leu Asp Phe Ile Thr Met Leu Tyr Glu | |

368

115 120 125
 Lys Arg Gln Glu Ser Gln Leu Arg Lys Pro Glu Asn Thr Thr Arg Ala
 130 135 140
 Glu Ala Leu Thr Glu Pro Leu Asn Ala
 145 150

<210> 249
 <211> 1071
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1071)

<221> misc_feature
 <222> (1)...(1071)
 <223> n = A,T,C or G

<400> 249
 atg aca ggg acc atc ctt tca ggc tcc atc agc ctc ggt gac agt gtg 48
 Met Thr Gly Thr Ile Leu Ser Gly Ser Ile Ser Leu Gly Asp Ser Val
 1 5 10 15
 gag atc cct gcc ctc aag gtg gtg aag aag gtg aag tcc atg cag atg 96
 Glu Ile Pro Ala Leu Lys Val Val Lys Lys Val Lys Ser Met Gln Met
 20 25 30
 ttc cac atg ccc atc act tca gcc atg caa gga gac cgg ctg ggc atc 144
 Phe His Met Pro Ile Thr Ser Ala Met Gln Gly Asp Arg Leu Gly Ile
 35 40 45
 tgc gtc acc cag ttt gac cct aag ctg ctg gag cgc ggg ttg gtg tgt 192
 Cys Val Thr Gln Phe Asp Pro Lys Leu Leu Glu Arg Gly Leu Val Cys
 50 55 60
 gcc ccc gag tcc ctg cac act gtc cat gcg gcc ctc atc tct gtg gaa 240
 Ala Pro Glu Ser Leu His Thr Val His Ala Ala Leu Ile Ser Val Glu
 65 70 75 80
 aag ata ccg tat ttc cgg ggg ccc ctg caa acc aag gcc aag ttc cac 288
 Lys Ile Pro Tyr Phe Arg Gly Pro Leu Gln Thr Lys Ala Lys Phe His
 85 90 95

369

| | |
|---|-----|
| att aca gtg ggc cat gaa aca gtc atg ggc cgg ttg atg ttc ttc agt | 336 |
| Ile Thr Val Gly His Glu Thr Val Met Gly Arg Leu Met Phe Phe Ser | |
| 100 105 110 | |
| cct gct cca gat aac ttt gac cag gag cct ata ctg gac tct ttc aac | 384 |
| Pro Ala Pro Asp Asn Phe Asp Gln Glu Pro Ile Leu Asp Ser Phe Asn | |
| 115 120 125 | |
| ttc tct caa gaa tac ctt ttc cag gag cag tac ctg tcc aag gat ttg | 432 |
| Phe Ser Gln Glu Tyr Leu Phe Gln Glu Gln Tyr Leu Ser Lys Asp Leu | |
| 130 135 140 | |
| aca cca gca gtg aca gac aat gat gag gcc gac aag aag gcc ggc cag | 480 |
| Thr Pro Ala Val Thr Asp Asn Asp Glu Ala Asp Lys Lys Ala Gly Gln | |
| 145 150 155 160 | |
| gcc aca gag ggc cat tgt cct cgg cag cag tgg gcc ctg gtg gag ttt | 528 |
| Ala Thr Glu Gly His Cys Pro Arg Gln Gln Trp Ala Leu Val Glu Phe | |
| 165 170 175 | |
| gag aag ccc gtc acc tgc cct cgg ctg tgc ctg gtg att ggc tcc agg | 576 |
| Glu Lys Pro Val Thr Cys Pro Arg Leu Cys Leu Val Ile Gly Ser Arg | |
| 180 185 190 | |
| cta gat gcg gac att cac acc aac acg tgc cgg cta gcc ttc cat ggc | 624 |
| Leu Asp Ala Asp Ile His Thr Asn Thr Cys Arg Leu Ala Phe His Gly | |
| 195 200 205 | |
| atc ctg ctc cac ggg cta gag gac agg aac tac gcc gac agc ttc ctg | 672 |
| Ile Leu Leu His Gly Leu Glu Asp Arg Asn Tyr Ala Asp Ser Phe Leu | |
| 210 215 220 | |
| ccc agg ctg aag gtg tac aag ctg aag cac aag cat ggc ctt gtg gag | 720 |
| Pro Arg Leu Lys Val Tyr Lys Leu Lys His Lys His Gly Leu Val Glu | |
| 225 230 235 240 | |
| cgg gcg atg gat gac tac agt gtg atc ggc cgc tcc ctg ttc aaa aag | 768 |
| Arg Ala Met Asp Asp Tyr Ser Val Ile Gly Arg Ser Leu Phe Lys Lys | |
| 245 250 255 | |
| gaa acc aac atc cag ctc ttc gtg ggg ctc aag gtg cac ttg tcc act | 816 |
| Glu Thr Asn Ile Gln Leu Phe Val Gly Leu Lys Val His Leu Ser Thr | |
| 260 265 270 | |

| | |
|---|------|
| ggg gaa ctg ggc atc atc gac agt gcc ttc ggc cag agc ggc aag ttc | 864 |
| Gly Glu Leu Gly Ile Ile Asp Ser Ala Phe Gly Gln Ser Gly Lys Phe | |
| 275 280 285 | |
| aag atc cac atc cca ggt ggc ctc agc ccc gag tcc aag aag atc ctg | 912 |
| Lys Ile His Ile Pro Gly Gly Leu Ser Pro Glu Ser Lys Lys Ile Leu | |
| 290 295 300 | |
| aca ccc gcc ctc aag aag cgg gcc cgg gct ggc cgt ggg gag gcc acc | 960 |
| Thr Pro Ala Leu Lys Lys Arg Ala Arg Ala Gly Arg Gly Glu Ala Thr | |
| 305 310 315 320 | |
| agg cag gag gag agc gcc gag cgg agn ngg ccc tca cag cat gtg gtg | 1008 |
| Arg Gln Glu Glu Ser Ala Glu Arg Xaa Xaa Pro Ser Gln His Val Val | |
| 325 330 335 | |
| ctc agc ctg act ttc aag cgt tat gtc ttc gac acc cac aag cgc atg | 1056 |
| Leu Ser Leu Thr Phe Lys Arg Tyr Val Phe Asp Thr His Lys Arg Met | |
| 340 345 350 | |
| gtt cag tct ccc tga | 1071 |
| Val Gln Ser Pro * | |
| 355 | |

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<210> 250
<211> 356
<212> PRT
<213> Homo sapiens
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<220>  
<221> VARIANT  
<222> (1)...(356)  
<223> Xaa = Any Amino Acid
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<400> 250
Met Thr Gly Thr Ile Leu Ser Gly Ser Ile Ser Leu Gly Asp Ser Val
1 5 10 15
Glu Ile Pro Ala Leu Lys Val Val Lys Lys Val Lys Ser Met Gln Met
20 25 30
Phe His Met Pro Ile Thr Ser Ala Met Gln Gly Asp Arg Leu Gly Ile
35 40 45
Cys Val Thr Gln Phe Asp Pro Lys Leu Leu Glu Arg Gly Leu Val Cys
50 55 60

371

Ala Pro Glu Ser Leu His Thr Val His Ala Ala Leu Ile Ser Val Glu
 65 70 75 80
 Lys Ile Pro Tyr Phe Arg Gly Pro Leu Gln Thr Lys Ala Lys Phe His
 85 90 95
 Ile Thr Val Gly His Glu Thr Val Met Gly Arg Leu Met Phe Phe Ser
 100 105 110
 Pro Ala Pro Asp Asn Phe Asp Gln Glu Pro Ile Leu Asp Ser Phe Asn
 115 120 125
 Phe Ser Gln Glu Tyr Leu Phe Gln Glu Gln Tyr Leu Ser Lys Asp Leu
 130 135 140
 Thr Pro Ala Val Thr Asp Asn Asp Glu Ala Asp Lys Lys Ala Gly Gln
 145 150 155 160
 Ala Thr Glu Gly His Cys Pro Arg Gln Gln Trp Ala Leu Val Glu Phe
 165 170 175
 Glu Lys Pro Val Thr Cys Pro Arg Leu Cys Leu Val Ile Gly Ser Arg
 180 185 190
 Leu Asp Ala Asp Ile His Thr Asn Thr Cys Arg Leu Ala Phe His Gly
 195 200 205
 Ile Leu Leu His Gly Leu Glu Asp Arg Asn Tyr Ala Asp Ser Phe Leu
 210 215 220
 Pro Arg Leu Lys Val Tyr Lys Leu Lys His Lys His Gly Leu Val Glu
 225 230 235 240
 Arg Ala Met Asp Asp Tyr Ser Val Ile Gly Arg Ser Leu Phe Lys Lys
 245 250 255
 Glu Thr Asn Ile Gln Leu Phe Val Gly Leu Lys Val His Leu Ser Thr
 260 265 270
 Gly Glu Leu Gly Ile Ile Asp Ser Ala Phe Gly Gln Ser Gly Lys Phe
 275 280 285
 Lys Ile His Ile Pro Gly Gly Leu Ser Pro Glu Ser Lys Lys Ile Leu
 290 295 300
 Thr Pro Ala Leu Lys Lys Arg Ala Arg Ala Gly Arg Gly Glu Ala Thr
 305 310 315 320
 Arg Gln Glu Glu Ser Ala Glu Arg Xaa Xaa Pro Ser Gln His Val Val
 325 330 335
 Leu Ser Leu Thr Phe Lys Arg Tyr Val Phe Asp Thr His Lys Arg Met
 340 345 350
 Val Gln Ser Pro
 355

<210> 251

<211> 567

<212> DNA

<213> Homo sapiens

372

<220>

<221> CDS

<222> (1)...(567)

<400> 251

| | |
|--|----|
| atg gct gcc tct gcc ttt gct ggt gca gtg aga gca gct tca gga atc | 48 |
| Met Ala Ala Ser Ala Phe Ala Gly Ala Val Arg Ala Ala Ser Gly Ile | |
| 1 5 10 15 | |

| | |
|---|----|
| cta cgg tcc ctg aat att ttg gca tct tca acc tac cgc aac tgt gtc | 96 |
| Leu Arg Ser Leu Asn Ile Leu Ala Ser Ser Thr Tyr Arg Asn Cys Val | |
| 20 25 30 | |

| | |
|---|-----|
| aag aat gcc tct ctt att tct gca ttg tcc act gga cgt ttt agt cat | 144 |
| Lys Asn Ala Ser Leu Ile Ser Ala Leu Ser Thr Gly Arg Phe Ser His | |
| 35 40 45 | |

| | |
|---|-----|
| att cag aca cca gtt gtt tcc tcc act ccc aga ctt acc aca tct gag | 192 |
| Ile Gln Thr Pro Val Val Ser Ser Thr Pro Arg Leu Thr Thr Ser Glu | |
| 50 55 60 | |

| | |
|--|-----|
| aga aac ctg aca tgt ggg cat acc tca gtg atc ctt aat aga atg gcc | 240 |
| Arg Asn Leu Thr Cys Gly His Thr Ser Val Ile Leu Asn Arg Met Ala | |
| 65 70 75 80 | |

| | |
|---|-----|
| ccc gtg ctt cca agt gtc ctg aag ctg cca gtc aga tct cta aca tac | 288 |
| Pro Val Leu Pro Ser Val Leu Lys Leu Pro Val Arg Ser Leu Thr Tyr | |
| 85 90 95 | |

| | |
|---|-----|
| ttc agt gca aga aaa ggc aag aga aag acc gtg aaa gct gtc atc gat | 336 |
| Phe Ser Ala Arg Lys Gly Lys Arg Lys Thr Val Lys Ala Val Ile Asp | |
| 100 105 110 | |

| | |
|---|-----|
| agg ttt ctt cga ctt cat tgt ggc ctt tgg gtg agg aga aag gct ggc | 384 |
| Arg Phe Leu Arg Leu His Cys Gly Leu Trp Val Arg Arg Lys Ala Gly | |
| 115 120 125 | |

| | |
|---|-----|
| tat aag aaa aaa tta tgg aaa aag aca cct gca agg aag aag cga ttg | 432 |
| Tyr Lys Lys Lys Leu Trp Lys Lys Thr Pro Ala Arg Lys Lys Arg Leu | |
| 130 135 140 | |

| | |
|--|-----|
| agg gaa ttt gta ttc tgc aat aaa acc cag agt aaa ctc tta gat aaa | 480 |
| Arg Glu Phe Val Phe Cys Asn Lys Thr Gln Ser Lys Leu Leu Asp Lys | |
| 145 150 155 160 | |

373

atg acg acg tcc ttc tgg aag agg cga aac tgg tac gtt gat gat cct 528
 Met Thr Thr Ser Phe Trp Lys Arg Arg Asn Trp Tyr Val Asp Asp Pro
 165 170 175

tat cag aag tat cat gat cga aca aac ctg aaa gta tag 567
 Tyr Gln Lys Tyr His Asp Arg Thr Asn Leu Lys Val *
 180 185

<210> 252

<211> 188

<212> PRT

<213> Homo sapiens

<400> 252

Met Ala Ala Ser Ala Phe Ala Gly Ala Val Arg Ala Ala Ser Gly Ile
 1 5 10 15
 Leu Arg Ser Leu Asn Ile Leu Ala Ser Ser Thr Tyr Arg Asn Cys Val
 20 25 30
 Lys Asn Ala Ser Leu Ile Ser Ala Leu Ser Thr Gly Arg Phe Ser His
 35 40 45
 Ile Gln Thr Pro Val Val Ser Ser Thr Pro Arg Leu Thr Thr Ser Glu
 50 55 60
 Arg Asn Leu Thr Cys Gly His Thr Ser Val Ile Leu Asn Arg Met Ala
 65 70 75 80
 Pro Val Leu Pro Ser Val Leu Lys Leu Pro Val Arg Ser Leu Thr Tyr
 85 90 95
 Phe Ser Ala Arg Lys Gly Lys Arg Lys Thr Val Lys Ala Val Ile Asp
 100 105 110
 Arg Phe Leu Arg Leu His Cys Gly Leu Trp Val Arg Arg Lys Ala Gly
 115 120 125
 Tyr Lys Lys Lys Leu Trp Lys Lys Thr Pro Ala Arg Lys Lys Arg Leu
 130 135 140
 Arg Glu Phe Val Phe Cys Asn Lys Thr Gln Ser Lys Leu Leu Asp Lys
 145 150 155 160
 Met Thr Thr Ser Phe Trp Lys Arg Arg Asn Trp Tyr Val Asp Asp Pro
 165 170 175
 Tyr Gln Lys Tyr His Asp Arg Thr Asn Leu Lys Val
 180 185

<210> 253

<211> 453

<212> DNA

374

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(453)

<400> 253

| | |
|---|-----|
| atg gac ttc cac ata ctg atc gtc atc ggt tgt gtg gtc agc gcc tcg | 48 |
| Met Asp Phe His Ile Leu Ile Val Ile Gly Cys Val Val Ser Ala Ser | |
| 1 5 10 15 | |
| ctg ctc tcg ttc ctg ttc atc aac aag atc ttc cgg cgc aag act ttt | 96 |
| Leu Leu Ser Phe Leu Phe Ile Asn Lys Ile Phe Arg Arg Lys Thr Phe | |
| 20 25 30 | |
| gag gag gtg gta gcc gag aag cgt gcc ctg agc gcc aat ctc tac aag | 144 |
| Glu Glu Val Val Ala Glu Lys Arg Ala Leu Ser Ala Asn Leu Tyr Lys | |
| 35 40 45 | |
| gcg gcc ggt ggt gcc gct acc aag aag ccc aag aag aag gaa ctt aag | 192 |
| Ala Ala Gly Gly Ala Ala Thr Lys Lys Pro Lys Lys Lys Glu Leu Lys | |
| 50 55 60 | |
| cgc gaa aag aag caa cgt cag cgg gaa cag cag agg gat gtg aac aac | 240 |
| Arg Glu Lys Lys Gln Arg Gln Arg Glu Gln Gln Arg Asp Val Asn Asn | |
| 65 70 75 80 | |
| gag ccg gaa cca gag gaa gcc gaa gac tac tcc gat ggt cag tcg gag | 288 |
| Glu Pro Glu Pro Glu Glu Ala Glu Asp Tyr Ser Asp Gly Gln Ser Glu | |
| 85 90 95 | |
| ggt cag ggc tcc gtg gct ggc gag gaa ccc ggt ctc tcc aag cag cat | 336 |
| Gly Gln Gly Ser Val Ala Gly Glu Glu Pro Gly Leu Ser Lys Gln His | |
| 100 105 110 | |
| gtt gaa ttt gaa ccc gat gca gag gtc ctc act gat cag cga cga ccc | 384 |
| Val Glu Phe Glu Pro Asp Ala Glu Val Leu Thr Asp Gln Arg Arg Pro | |
| 115 120 125 | |
| agt agc gtg gct gag aag gag aac caa cct tct ggg gct ggc aaa aag | 432 |
| Ser Ser Val Ala Glu Lys Glu Asn Gln Pro Ser Gly Ala Gly Lys Lys | |
| 130 135 140 | |
| gga aag aag gat aaa cgt taa | 453 |

375

Gly Lys Lys Asp Lys Arg *
 145 150

<210> 254
 <211> 150
 <212> PRT
 <213> Homo sapiens

<400> 254
 Met Asp Phe His Ile Leu Ile Val Ile Gly Cys Val Val Ser Ala Ser
 1 5 10 15
 Leu Leu Ser Phe Leu Phe Ile Asn Lys Ile Phe Arg Arg Lys Thr Phe
 20 25 30
 Glu Glu Val Val Ala Glu Lys Arg Ala Leu Ser Ala Asn Leu Tyr Lys
 35 40 45
 Ala Ala Gly Gly Ala Ala Thr Lys Lys Pro Lys Lys Lys Glu Leu Lys
 50 55 60
 Arg Glu Lys Lys Gln Arg Gln Arg Glu Gln Gln Arg Asp Val Asn Asn
 65 70 75 80
 Glu Pro Glu Pro Glu Glu Ala Glu Asp Tyr Ser Asp Gly Gln Ser Glu
 85 90 95
 Gly Gln Gly Ser Val Ala Gly Glu Glu Pro Gly Leu Ser Lys Gln His
 100 105 110
 Val Glu Phe Glu Pro Asp Ala Glu Val Leu Thr Asp Gln Arg Arg Pro
 115 120 125
 Ser Ser Val Ala Glu Lys Glu Asn Gln Pro Ser Gly Ala Gly Lys Lys
 130 135 140
 Gly Lys Lys Asp Lys Arg
 145 150

<210> 255
 <211> 489
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(489)

<400> 255
 atg gca ttt ctc tca ccc ttg gtt ctc att tgc cat cca acc cat ttt
 Met Ala Phe Leu Ser Pro Leu Val Leu Ile Cys His Pro Thr His Phe
 1 5 10 15

48

376

| | |
|---|-----|
| ctt gac cca aag ctt atg aaa gaa gaa caa atg tca cag gcc cag ctc | 96 |
| Leu Asp Pro Lys Leu Met Lys Glu Glu Gln Met Ser Gln Ala Gln Leu | |
| 20 25 30 | |
| ttc acc aga agc ttt gat gat ggc ctg ggc ttt gaa tac gtg atg ttc | 144 |
| Phe Thr Arg Ser Phe Asp Asp Gly Leu Gly Phe Glu Tyr Val Met Phe | |
| 35 40 45 | |
| tac aat gac att gag aaa agg atg gtt tgc tta ttt caa gga ggc cct | 192 |
| Tyr Asn Asp Ile Glu Lys Arg Met Val Cys Leu Phe Gln Gly Gly Pro | |
| 50 55 60 | |
| tac ctg gaa gga cca cct gga ttc att cat gga ggt gcc att gca acc | 240 |
| Tyr Leu Glu Gly Pro Pro Gly Phe Ile His Gly Gly Ala Ile Ala Thr | |
| 65 70 75 80 | |
| atg att gat gct act gtt ggt atg tgt gca atg atg gct ggg gga atc | 288 |
| Met Ile Asp Ala Thr Val Gly Met Cys Ala Met Met Ala Gly Gly Ile | |
| 85 90 95 | |
| gtc atg act gcc aat ctc aac atc aat tat aaa aga cct atc cct ctt | 336 |
| Val Met Thr Ala Asn Leu Asn Ile Asn Tyr Lys Arg Pro Ile Pro Leu | |
| 100 105 110 | |
| tgt tct gtt gtt atg ata aat agc caa ctt gat aaa gtt gaa gga agg | 384 |
| Cys Ser Val Val Met Ile Asn Ser Gln Leu Asp Lys Val Glu Gly Arg | |
| 115 120 125 | |
| aaa ttt ttt gtt tcc tgt aat gtt cag agt gtt gat gag aag acc cta | 432 |
| Lys Phe Phe Val Ser Cys Asn Val Gln Ser Val Asp Glu Lys Thr Leu | |
| 130 135 140 | |
| tac tca gag gcg aca agc tta ttt ata aag ctg aat cct gct aaa agt | 480 |
| Tyr Ser Glu Ala Thr Ser Leu Phe Ile Lys Leu Asn Pro Ala Lys Ser | |
| 145 150 155 160 | |
| ctg aca taa | 489 |
| Leu Thr * | |

<210> 256

<211> 162

377

<212> PRT

<213> Homo sapiens

<400> 256

```

Met Ala Phe Leu Ser Pro Leu Val Leu Ile Cys His Pro Thr His Phe
 1           5           10           15
Leu Asp Pro Lys Leu Met Lys Glu Glu Gln Met Ser Gln Ala Gln Leu
          20           25           30
Phe Thr Arg Ser Phe Asp Asp Gly Leu Gly Phe Glu Tyr Val Met Phe
          35           40           45
Tyr Asn Asp Ile Glu Lys Arg Met Val Cys Leu Phe Gln Gly Gly Pro
 50           55           60
Tyr Leu Glu Gly Pro Pro Gly Phe Ile His Gly Gly Ala Ile Ala Thr
 65           70           75           80
Met Ile Asp Ala Thr Val Gly Met Cys Ala Met Met Ala Gly Gly Ile
          85           90           95
Val Met Thr Ala Asn Leu Asn Ile Asn Tyr Lys Arg Pro Ile Pro Leu
          100          105          110
Cys Ser Val Val Met Ile Asn Ser Gln Leu Asp Lys Val Glu Gly Arg
          115          120          125
Lys Phe Phe Val Ser Cys Asn Val Gln Ser Val Asp Glu Lys Thr Leu
          130          135          140
Tyr Ser Glu Ala Thr Ser Leu Phe Ile Lys Leu Asn Pro Ala Lys Ser
 145          150          155          160
Leu Thr

```

<210> 257

<211> 480

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(480)

<400> 257

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atg tgt ctt ttg gca gtc agt cca gat ggg aat tgg cta gct gca tca      48
Met Cys Leu Leu Ala Val Ser Pro Asp Gly Asn Trp Leu Ala Ala Ser
 1           5           10           15

ggg acc agt gct gga gtc cat gtc tac aac gta aaa cag cta aag ctt      96
Gly Thr Ser Ala Gly Val His Val Tyr Asn Val Lys Gln Leu Lys Leu
          20           25           30

```

378

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| cac | tgc | acg | gtg | cct | gct | tac | aat | ttc | cca | gtg | act | gct | atg | gct | att | 144 |
| His | Cys | Thr | Val | Pro | Ala | Tyr | Asn | Phe | Pro | Val | Thr | Ala | Met | Ala | Ile | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| gcc | ccc | aat | acc | aac | aac | ctt | gtc | atc | gct | cat | tgc | gac | cag | cag | gta | 192 |
| Ala | Pro | Asn | Thr | Asn | Asn | Leu | Val | Ile | Ala | His | Ser | Asp | Gln | Gln | Val | |
| | | 50 | | | | 55 | | | | | 60 | | | | | |
| ttt | gag | tac | agc | atc | cca | gac | aaa | cag | tat | aca | gat | tgg | agc | cgg | act | 240 |
| Phe | Glu | Tyr | Ser | Ile | Pro | Asp | Lys | Gln | Tyr | Thr | Asp | Trp | Ser | Arg | Thr | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| gtc | cag | aag | cag | ggc | ttt | cac | cac | ctt | tgg | ctc | caa | agg | gat | act | cct | 288 |
| Val | Gln | Lys | Gln | Gly | Phe | His | His | Leu | Trp | Leu | Gln | Arg | Asp | Thr | Pro | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| atc | aca | cac | atc | agt | ttt | cat | ccc | aag | aga | ccg | atg | cac | atc | ctt | ctc | 336 |
| Ile | Thr | His | Ile | Ser | Phe | His | Pro | Lys | Arg | Pro | Met | His | Ile | Leu | Leu | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| cat | gat | gcc | tac | atg | ttc | tgc | atc | att | gac | aag | tca | ttg | ccc | ctt | cca | 384 |
| His | Asp | Ala | Tyr | Met | Phe | Cys | Ile | Ile | Asp | Lys | Ser | Leu | Pro | Leu | Pro | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| aat | gac | aaa | acc | tta | ctc | tac | aat | cca | ttt | cct | ccc | acg | aat | gac | atc | 432 |
| Asn | Asp | Lys | Thr | Leu | Leu | Tyr | Asn | Pro | Phe | Pro | Pro | Thr | Asn | Asp | Ile | |
| | | 130 | | | | 135 | | | | | 140 | | | | | |
| att | gct | cag | ctc | cca | cca | ccc | att | aaa | aag | aag | aaa | ttt | gga | acc | taa | 480 |
| Ile | Ala | Gln | Leu | Pro | Pro | Pro | Ile | Lys | Lys | Lys | Lys | Phe | Gly | Thr | * | |
| 145 | | | | | 150 | | | | | 155 | | | | | | |

<210> 258

<211> 159

<212> PRT

<213> Homo sapiens

<400> 258

Met Cys Leu Leu Ala Val Ser Pro Asp Gly Asn Trp Leu Ala Ala Ser
1 5 10 15
Gly Thr Ser Ala Gly Val His Val Tyr Asn Val Lys Gln Leu Lys Leu
20 25 30

379

His Cys Thr Val Pro Ala Tyr Asn Phe Pro Val Thr Ala Met Ala Ile
 35 40 45
 Ala Pro Asn Thr Asn Asn Leu Val Ile Ala His Ser Asp Gln Gln Val
 50 55 60
 Phe Glu Tyr Ser Ile Pro Asp Lys Gln Tyr Thr Asp Trp Ser Arg Thr
 65 70 75 80
 Val Gln Lys Gln Gly Phe His His Leu Trp Leu Gln Arg Asp Thr Pro
 85 90 95
 Ile Thr His Ile Ser Phe His Pro Lys Arg Pro Met His Ile Leu Leu
 100 105 110
 His Asp Ala Tyr Met Phe Cys Ile Ile Asp Lys Ser Leu Pro Leu Pro
 115 120 125
 Asn Asp Lys Thr Leu Leu Tyr Asn Pro Phe Pro Pro Thr Asn Asp Ile
 130 135 140
 Ile Ala Gln Leu Pro Pro Pro Ile Lys Lys Lys Lys Phe Gly Thr
 145 150 155

<210> 259
 <211> 627
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(627)

<400> 259
 atg gcg tcc tct ttg ctt gcg ggc gag cga ttg gtg cgt gct ttg ggc 48
 Met Ala Ser Ser Leu Leu Ala Gly Glu Arg Leu Val Arg Ala Leu Gly
 1 5 10 15

 ccc ggc ggg gag ctg gag cca gag cgg cta ccc cga aag ctg cgg gcc 96
 Pro Gly Gly Glu Leu Glu Pro Glu Arg Leu Pro Arg Lys Leu Arg Ala
 20 25 30

 gag ctt gag gcc gcg ctg ggg aag aag cac aag ggc ggt gat agc tcc 144
 Glu Leu Glu Ala Ala Leu Gly Lys Lys His Lys Gly Gly Asp Ser Ser
 35 40 45

 agt ggc ccc caa cgc ttg gtt tct ttc cgt ctc atc cgg gat ctg cac 192
 Ser Gly Pro Gln Arg Leu Val Ser Phe Arg Leu Ile Arg Asp Leu His
 50 55 60

 cag cat ctg aga gaa agg gat tcc aaa cta tac ctc cat gag ctc cta 240

380

[illegible]

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<210> 260
<211> 208
<212> PRT
<213> Homo sapiens
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381

<400> 260

Met Ala Ser Ser Leu Leu Ala Gly Glu Arg Leu Val Arg Ala Leu Gly
 1 5 10 15
 Pro Gly Gly Glu Leu Glu Pro Glu Arg Leu Pro Arg Lys Leu Arg Ala
 20 25 30
 Glu Leu Glu Ala Ala Leu Gly Lys Lys His Lys Gly Gly Asp Ser Ser
 35 40 45
 Ser Gly Pro Gln Arg Leu Val Ser Phe Arg Leu Ile Arg Asp Leu His
 50 55 60
 Gln His Leu Arg Glu Arg Asp Ser Lys Leu Tyr Leu His Glu Leu Leu
 65 70 75 80
 Glu Gly Ser Glu Ile Tyr Leu Pro Glu Val Val Lys Pro Pro Arg Asn
 85 90 95
 Pro Glu Leu Val Ala Arg Leu Glu Lys Ile Lys Ile Gln Leu Ala Asn
 100 105 110
 Glu Glu Tyr Lys Arg Ile Thr Arg Asn Val Thr Cys Gln Asp Thr Arg
 115 120 125
 His Gly Gly Thr Leu Ser Asp Leu Gly Lys Gln Val Arg Ser Leu Lys
 130 135 140
 Ala Leu Val Ile Thr Ile Phe Asn Phe Ile Val Thr Val Val Ala Ala
 145 150 155 160
 Phe Val Cys Thr Tyr Leu Gly Ser Gln Tyr Ile Phe Thr Glu Met Ala
 165 170 175
 Ser Arg Val Leu Ala Ala Leu Ile Val Ala Ser Val Val Gly Leu Ala
 180 185 190
 Glu Leu Tyr Val Met Val Arg Ala Met Glu Gly Glu Leu Gly Glu Leu
 195 200 205

<210> 261

<211> 1092

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1092)

<400> 261

atg gcc gca gcg gcg atg gcg gca gcg gca ggt gga ggg gct ggc gcg
 Met Ala Ala Ala Met Ala Ala Ala Ala Gly Gly Gly Ala Gly Ala
 1 5 10 15

48

gcc cgc tcc ctc tcg cgc ttc cga ggc tgc ctg gct ggc gcg ctg ctc

96

382

| | |
|---|-----|
| Ala Arg Ser Leu Ser Arg Phe Arg Gly Cys Leu Ala Gly Ala Leu Leu | |
| 20 25 30 | |
| ggg gac tgc gtg ggc tcc ttc tac gag gcc cac gac acc gtc gac ctg | 144 |
| Gly Asp Cys Val Gly Ser Phe Tyr Glu Ala His Asp Thr Val Asp Leu | |
| 35 40 45 | |
| acg tca gtc ctg cgt cat gtc cag agt ctg gag ccg gac ccc ggc acg | 192 |
| Thr Ser Val Leu Arg His Val Gln Ser Leu Glu Pro Asp Pro Gly Thr | |
| 50 55 60 | |
| ccc ggg agt gag cgg aca gaa gcc ttg tac tac aca gat gac aca gcc | 240 |
| Pro Gly Ser Glu Arg Thr Glu Ala Leu Tyr Tyr Thr Asp Asp Thr Ala | |
| 65 70 75 80 | |
| atg gcc agg gcc ctg gtg cag tcc ctg cta gcc aag gag gcc ttt gac | 288 |
| Met Ala Arg Ala Leu Val Gln Ser Leu Leu Ala Lys Glu Ala Phe Asp | |
| 85 90 95 | |
| gag gtg gac atg gct cac aga ttt gct cag gag tac aag aaa gac cct | 336 |
| Glu Val Asp Met Ala His Arg Phe Ala Gln Glu Tyr Lys Lys Asp Pro | |
| 100 105 110 | |
| gac agg ggc tat ggt gct gga gta gtc act gtc ttc aag aag ctc ctg | 384 |
| Asp Arg Gly Tyr Gly Ala Gly Val Val Thr Val Phe Lys Lys Leu Leu | |
| 115 120 125 | |
| aac ccc aaa tgt cgc gat gtc ttt gag cct gcc cgg gcc cag ttt aac | 432 |
| Asn Pro Lys Cys Arg Asp Val Phe Glu Pro Ala Arg Ala Gln Phe Asn | |
| 130 135 140 | |
| ggg aaa ggc tcc tat ggc aat gga ggt gcc atg cgg gtg gct ggc atc | 480 |
| Gly Lys Gly Ser Tyr Gly Asn Gly Gly Ala Met Arg Val Ala Gly Ile | |
| 145 150 155 160 | |
| tcc ctg gcc tat agc agt gtc cag gat gtg cag aag ttt gcc cgg ctc | 528 |
| Ser Leu Ala Tyr Ser Ser Val Gln Asp Val Gln Lys Phe Ala Arg Leu | |
| 165 170 175 | |
| tcg gcc cag ctg aca cac gcc tcc tcc ctg ggt tac aat ggc gcc atc | 576 |
| Ser Ala Gln Leu Thr His Ala Ser Ser Leu Gly Tyr Asn Gly Ala Ile | |
| 180 185 190 | |
| ctg cag gcc ctg gct gtg cac ctg gcc ttg cag ggc gag tct tcc agc | 624 |

383

| | |
|---|------|
| Leu Gln Ala Leu Ala Val His Leu Ala Leu Gln Gly Glu Ser Ser Ser | |
| 195 200 205 | |
| gag cac ttt ctc aag caa ctc ctg ggc cac atg gag gat ctg gag ggt | 672 |
| Glu His Phe Leu Lys Gln Leu Leu Gly His Met Glu Asp Leu Glu Gly | |
| 210 215 220 | |
| gat gcc cag tcc gtc ttg gat gcc agg gag ttg ggc atg gag gag cgt | 720 |
| Asp Ala Gln Ser Val Leu Asp Ala Arg Glu Leu Gly Met Glu Glu Arg | |
| 225 230 235 240 | |
| cca tac tcc agc cgc ctg aag aag att gga gag ctt cta gac cag gca | 768 |
| Pro Tyr Ser Ser Arg Leu Lys Lys Ile Gly Glu Leu Leu Asp Gln Ala | |
| 245 250 255 | |
| tcg gtg acc agg gag gaa gtg gtg tct gag cta ggg aat ggc att gct | 816 |
| Ser Val Thr Arg Glu Glu Val Val Ser Glu Leu Gly Asn Gly Ile Ala | |
| 260 265 270 | |
| gcc ttt gag tcg gta ccc acc gcc atc tac tgc ttc cta cgc tgc atg | 864 |
| Ala Phe Glu Ser Val Pro Thr Ala Ile Tyr Cys Phe Leu Arg Cys Met | |
| 275 280 285 | |
| gag cca gac cct gag atc cct tct gcc ttc aat agc ctc caa agg act | 912 |
| Glu Pro Asp Pro Glu Ile Pro Ser Ala Phe Asn Ser Leu Gln Arg Thr | |
| 290 295 300 | |
| ctc att tat tcc atc tca ctt ggt ggg gac aca gac acc att gcc acc | 960 |
| Leu Ile Tyr Ser Ile Ser Leu Gly Gly Asp Thr Asp Thr Ile Ala Thr | |
| 305 310 315 320 | |
| atg gct ggg gcc att gct ggt gcc tac tat ggg atg gat cag gtg cca | 1008 |
| Met Ala Gly Ala Ile Ala Gly Ala Tyr Tyr Gly Met Asp Gln Val Pro | |
| 325 330 335 | |
| gag agc tgg cag caa agc tgt gaa ggc tac gag gag aca gac atc ctg | 1056 |
| Glu Ser Trp Gln Gln Ser Cys Glu Gly Tyr Glu Glu Thr Asp Ile Leu | |
| 340 345 350 | |
| gcc caa agc ctg cac cgt gtc ttc cag aag agt tga | 1092 |
| Ala Gln Ser Leu His Arg Val Phe Gln Lys Ser * | |
| 355 360 | |

384

<210> 262
 <211> 363
 <212> PRT
 <213> Homo sapiens

<400> 262

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Met Ala Ala Ala Ala Met Ala Ala Ala Ala Gly Gly Gly Ala Gly Ala
 1           5           10          15
Ala Arg Ser Leu Ser Arg Phe Arg Gly Cys Leu Ala Gly Ala Leu Leu
      20           25           30
Gly Asp Cys Val Gly Ser Phe Tyr Glu Ala His Asp Thr Val Asp Leu
      35           40           45
Thr Ser Val Leu Arg His Val Gln Ser Leu Glu Pro Asp Pro Gly Thr
 50           55           60
Pro Gly Ser Glu Arg Thr Glu Ala Leu Tyr Tyr Thr Asp Asp Thr Ala
 65           70           75           80
Met Ala Arg Ala Leu Val Gln Ser Leu Leu Ala Lys Glu Ala Phe Asp
      85           90           95
Glu Val Asp Met Ala His Arg Phe Ala Gln Glu Tyr Lys Lys Asp Pro
     100          105          110
Asp Arg Gly Tyr Gly Ala Gly Val Val Thr Val Phe Lys Lys Leu Leu
     115          120          125
Asn Pro Lys Cys Arg Asp Val Phe Glu Pro Ala Arg Ala Gln Phe Asn
     130          135          140
Gly Lys Gly Ser Tyr Gly Asn Gly Gly Ala Met Arg Val Ala Gly Ile
 145          150          155          160
Ser Leu Ala Tyr Ser Ser Val Gln Asp Val Gln Lys Phe Ala Arg Leu
      165          170          175
Ser Ala Gln Leu Thr His Ala Ser Ser Leu Gly Tyr Asn Gly Ala Ile
     180          185          190
Leu Gln Ala Leu Ala Val His Leu Ala Leu Gln Gly Glu Ser Ser Ser
     195          200          205
Glu His Phe Leu Lys Gln Leu Leu Gly His Met Glu Asp Leu Glu Gly
     210          215          220
Asp Ala Gln Ser Val Leu Asp Ala Arg Glu Leu Gly Met Glu Glu Arg
 225          230          235          240
Pro Tyr Ser Ser Arg Leu Lys Lys Ile Gly Glu Leu Leu Asp Gln Ala
      245          250          255
Ser Val Thr Arg Glu Glu Val Val Ser Glu Leu Gly Asn Gly Ile Ala
     260          265          270
Ala Phe Glu Ser Val Pro Thr Ala Ile Tyr Cys Phe Leu Arg Cys Met
     275          280          285
Glu Pro Asp Pro Glu Ile Pro Ser Ala Phe Asn Ser Leu Gln Arg Thr
     290          295          300

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385

Leu Ile Tyr Ser Ile Ser Leu Gly Gly Asp Thr Asp Thr Ile Ala Thr
 305 310 315 320
 Met Ala Gly Ala Ile Ala Gly Ala Tyr Tyr Gly Met Asp Gln Val Pro
 325 330 335
 Glu Ser Trp Gln Gln Ser Cys Glu Gly Tyr Glu Glu Thr Asp Ile Leu
 340 345 350
 Ala Gln Ser Leu His Arg Val Phe Gln Lys Ser
 355 360

<210> 263

<211> 1239

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1239)

<400> 263

atg gcc ttg gcc ctg ctg agc cgg ctg ctg ccc gga agt gag tac ctc 48
 Met Ala Leu Ala Leu Leu Ser Arg Leu Leu Pro Gly Ser Glu Tyr Leu
 1 5 10 15

acc cat gag ctg ctg ctg agc tgt gta ttc cgg ctg gag ttc ctc ccg 96
 Thr His Glu Leu Leu Leu Ser Cys Val Phe Arg Leu Glu Phe Leu Pro
 20 25 30

gaa aga aca tca ggg ggt cca gag gca gcc gac ttc tct gac cag ctg 144
 Glu Arg Thr Ser Gly Gly Pro Glu Ala Ala Asp Phe Ser Asp Gln Leu
 35 40 45

tcg tta gga agc agc agg gtc cct cgg tgt ggg caa ggg act ctg ctg 192
 Ser Leu Gly Ser Ser Arg Val Pro Arg Cys Gly Gln Gly Thr Leu Leu
 50 55 60

gct cag gcc tgc cag gac ctc ccc agc atc cgc aac tgc tac ctg act 240
 Ala Gln Ala Cys Gln Asp Leu Pro Ser Ile Arg Asn Cys Tyr Leu Thr
 65 70 75 80

cat tgc tcg cca gcc cga gcc agt ctg ctg gcc tcc cag gct ctg cac 288
 His Cys Ser Pro Ala Arg Ala Ser Leu Leu Ala Ser Gln Ala Leu His
 85 90 95

cga ggg gag cta cag cga gtc cca acc ctg cta ctg ccc atg cct acg 336

386

| | |
|---|-----|
| Arg Gly Glu Leu Gln Arg Val Pro Thr Leu Leu Leu Pro Met Pro Thr | |
| 100 105 110 | |
| gag ccg ctg ctg ccc acc gac tgg ccc ttc ctg cca ctg att cgc ctc | 384 |
| Glu Pro Leu Leu Pro Thr Asp Trp Pro Phe Leu Pro Leu Ile Arg Leu | |
| 115 120 125 | |
| tac cac cgg gct tca gac acc ccc tcg gga ctc tct ccc aca gac acc | 432 |
| Tyr His Arg Ala Ser Asp Thr Pro Ser Gly Leu Ser Pro Thr Asp Thr | |
| 130 135 140 | |
| atg ggc aca gcc atg cgg gtc ctg cag tgg gtg cta gtt ttg gag agc | 480 |
| Met Gly Thr Ala Met Arg Val Leu Gln Trp Val Leu Val Leu Glu Ser | |
| 145 150 155 160 | |
| tgg cgc ccc cag gct ctc tgg gct gtg ccc cct gct gcc cgc ctg gca | 528 |
| Trp Arg Pro Gln Ala Leu Trp Ala Val Pro Pro Ala Ala Arg Leu Ala | |
| 165 170 175 | |
| cgg ctc atg tgt gtg ttc ctg gtg gac agt gag ctg ttc cgg gag tcc | 576 |
| Arg Leu Met Cys Val Phe Leu Val Asp Ser Glu Leu Phe Arg Glu Ser | |
| 180 185 190 | |
| cca gta cag cat ctg gtg gca gcc ctc ctc gcc cag ctc tgt cag cct | 624 |
| Pro Val Gln His Leu Val Ala Ala Leu Leu Ala Gln Leu Cys Gln Pro | |
| 195 200 205 | |
| caa gtc ttg cca aac ctc aac ctg gac tgc cga ctc cct ggc ctg acg | 672 |
| Gln Val Leu Pro Asn Leu Asn Leu Asp Cys Arg Leu Pro Gly Leu Thr | |
| 210 215 220 | |
| tct ttc cct gac ctc tat gcc aac ttc ctg gat cat ttt gag gct gtc | 720 |
| Ser Phe Pro Asp Leu Tyr Ala Asn Phe Leu Asp His Phe Glu Ala Val | |
| 225 230 235 240 | |
| tct ttt ggg gac cac ctc ttt ggg gcc ctg gtc ctc ctg ccc ctg cag | 768 |
| Ser Phe Gly Asp His Leu Phe Gly Ala Leu Val Leu Leu Pro Leu Gln | |
| 245 250 255 | |
| cgt cgg ttc agt gtc acc ttg cgc ctt gcc ctc ttt ggg gaa cac gtg | 816 |
| Arg Arg Phe Ser Val Thr Leu Arg Leu Ala Leu Phe Gly Glu His Val | |
| 260 265 270 | |
| gga gcc ttg cga gct ctg agc ctg cct ctg acc cag ttg cct gtg tcc | 864 |

387

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|------|
| Gly | Ala | Leu | Arg | Ala | Leu | Ser | Leu | Pro | Leu | Thr | Gln | Leu | Pro | Val | Ser | | |
| | 275 | | | | | | 280 | | | | | 285 | | | | | |
| ctg | gag | tgt | tac | aca | gtg | cct | cct | gaa | gac | aac | ctg | gcc | ctc | ctt | cag | | 912 |
| Leu | Glu | Cys | Tyr | Thr | Val | Pro | Pro | Glu | Asp | Asn | Leu | Ala | Leu | Leu | Gln | | |
| | 290 | | | | | 295 | | | | | 300 | | | | | | |
| ctc | tac | ttc | cgg | acc | ctg | gtt | act | ggt | gcg | ctc | cgc | cca | cgt | tgg | tgc | | 960 |
| Leu | Tyr | Phe | Arg | Thr | Leu | Val | Thr | Gly | Ala | Leu | Arg | Pro | Arg | Trp | Cys | | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | | |
| ccc | gtg | ctc | tat | gct | gtg | gct | gtg | gct | cat | gtc | aat | agc | ttc | atc | ttc | | 1008 |
| Pro | Val | Leu | Tyr | Ala | Val | Ala | Val | Ala | His | Val | Asn | Ser | Phe | Ile | Phe | | |
| | | | | 325 | | | | | 330 | | | | | 335 | | | |
| tct | cag | gac | cca | cag | agc | tca | gat | gag | gtc | aaa | gct | gcc | cgc | agg | agt | | 1056 |
| Ser | Gln | Asp | Pro | Gln | Ser | Ser | Asp | Glu | Val | Lys | Ala | Ala | Arg | Arg | Ser | | |
| | | | 340 | | | | | 345 | | | | | 350 | | | | |
| atg | ctg | cag | aaa | aca | tgg | ctg | ctg | gca | gat | gag | ggg | ctc | cgg | cag | cac | | 1104 |
| Met | Leu | Gln | Lys | Thr | Trp | Leu | Leu | Ala | Asp | Glu | Gly | Leu | Arg | Gln | His | | |
| | | | 355 | | | | 360 | | | | | 365 | | | | | |
| ctc | ctg | cac | tat | aag | ctt | ccc | aat | tcc | acg | ctc | cca | gag | ggc | ttt | gag | | 1152 |
| Leu | Leu | His | Tyr | Lys | Leu | Pro | Asn | Ser | Thr | Leu | Pro | Glu | Gly | Phe | Glu | | |
| | 370 | | | | | 375 | | | | | 380 | | | | | | |
| ctc | tat | tct | cag | ttg | ccc | cct | ctg | cgt | cag | cac | tac | ctc | cag | aga | ctg | | 1200 |
| Leu | Tyr | Ser | Gln | Leu | Pro | Pro | Leu | Arg | Gln | His | Tyr | Leu | Gln | Arg | Leu | | |
| 385 | | | | 390 | | | | | 395 | | | | | | 400 | | |
| act | tca | aca | gtg | ctc | caa | aat | ggg | gta | tca | gag | acc | tag | | | | | 1239 |
| Thr | Ser | Thr | Val | Leu | Gln | Asn | Gly | Val | Ser | Glu | Thr | * | | | | | |
| | | | 405 | | | | | 410 | | | | | | | | | |

<210> 264

<211> 412

<212> PRT

<213> Homo sapiens

<400> 264

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Leu | Ala | Leu | Leu | Ser | Arg | Leu | Leu | Pro | Gly | Ser | Glu | Tyr | Leu |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |

388

Thr His Glu Leu Leu Leu Ser Cys Val Phe Arg Leu Glu Phe Leu Pro
 20 25 30
 Glu Arg Thr Ser Gly Gly Pro Glu Ala Ala Asp Phe Ser Asp Gln Leu
 35 40 45
 Ser Leu Gly Ser Ser Arg Val Pro Arg Cys Gly Gln Gly Thr Leu Leu
 50 55 60
 Ala Gln Ala Cys Gln Asp Leu Pro Ser Ile Arg Asn Cys Tyr Leu Thr
 65 70 75 80
 His Cys Ser Pro Ala Arg Ala Ser Leu Leu Ala Ser Gln Ala Leu His
 85 90 95
 Arg Gly Glu Leu Gln Arg Val Pro Thr Leu Leu Leu Pro Met Pro Thr
 100 105 110
 Glu Pro Leu Leu Pro Thr Asp Trp Pro Phe Leu Pro Leu Ile Arg Leu
 115 120 125
 Tyr His Arg Ala Ser Asp Thr Pro Ser Gly Leu Ser Pro Thr Asp Thr
 130 135 140
 Met Gly Thr Ala Met Arg Val Leu Gln Trp Val Leu Val Leu Glu Ser
 145 150 155 160
 Trp Arg Pro Gln Ala Leu Trp Ala Val Pro Pro Ala Ala Arg Leu Ala
 165 170 175
 Arg Leu Met Cys Val Phe Leu Val Asp Ser Glu Leu Phe Arg Glu Ser
 180 185 190
 Pro Val Gln His Leu Val Ala Ala Leu Leu Ala Gln Leu Cys Gln Pro
 195 200 205
 Gln Val Leu Pro Asn Leu Asn Leu Asp Cys Arg Leu Pro Gly Leu Thr
 210 215 220
 Ser Phe Pro Asp Leu Tyr Ala Asn Phe Leu Asp His Phe Glu Ala Val
 225 230 235 240
 Ser Phe Gly Asp His Leu Phe Gly Ala Leu Val Leu Leu Pro Leu Gln
 245 250 255
 Arg Arg Phe Ser Val Thr Leu Arg Leu Ala Leu Phe Gly Glu His Val
 260 265 270
 Gly Ala Leu Arg Ala Leu Ser Leu Pro Leu Thr Gln Leu Pro Val Ser
 275 280 285
 Leu Glu Cys Tyr Thr Val Pro Pro Glu Asp Asn Leu Ala Leu Leu Gln
 290 295 300
 Leu Tyr Phe Arg Thr Leu Val Thr Gly Ala Leu Arg Pro Arg Trp Cys
 305 310 315 320
 Pro Val Leu Tyr Ala Val Ala Val Ala His Val Asn Ser Phe Ile Phe
 325 330 335
 Ser Gln Asp Pro Gln Ser Ser Asp Glu Val Lys Ala Ala Arg Arg Ser
 340 345 350
 Met Leu Gln Lys Thr Trp Leu Leu Ala Asp Glu Gly Leu Arg Gln His
 355 360 365

389

Leu Leu His Tyr Lys Leu Pro Asn Ser Thr Leu Pro Glu Gly Phe Glu
 370 375 380
 Leu Tyr Ser Gln Leu Pro Pro Leu Arg Gln His Tyr Leu Gln Arg Leu
 385 390 395 400
 Thr Ser Thr Val Leu Gln Asn Gly Val Ser Glu Thr
 405 410

<210> 265
 <211> 576
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(576)

<400> 265

atg gcg ggc gct gca gaa gat gcg cga gct ctt ttc cgg gct ggg gtc 48
 Met Ala Gly Ala Ala Glu Asp Ala Arg Ala Leu Phe Arg Ala Gly Val
 1 5 10 15

tgc gcg gcc ctg gag gcc tgg ccg gcc ttg cag atc gct gtg gag aat 96
 Cys Ala Ala Leu Glu Ala Trp Pro Ala Leu Gln Ile Ala Val Glu Asn
 20 25 30

ggc ttc ggg ggt gtg cac agc cag gag aag gcc aag tgg ctg ggg ggt 144
 Gly Phe Gly Gly Val His Ser Gln Glu Lys Ala Lys Trp Leu Gly Gly
 35 40 45

gca gtg gag gat tac ttc atg cgc aat gct gac ttg gag cta gat gag 192
 Ala Val Glu Asp Tyr Phe Met Arg Asn Ala Asp Leu Glu Leu Asp Glu
 50 55 60

gtg gaa gac ttc ctt gga gag ctg ttg acc aac gag ttt gat aca gtt 240
 Val Glu Asp Phe Leu Gly Glu Leu Leu Thr Asn Glu Phe Asp Thr Val
 65 70 75 80

gtg gaa gac ggg agt ctg ccc cag gtg agc cag caa ctg cag acc atg 288
 Val Glu Asp Gly Ser Leu Pro Gln Val Ser Gln Gln Leu Gln Thr Met
 85 90 95

ttc cac cac ttc cag agg ggt gat ggg gct gct ctg agg gag atg gcc 336
 Phe His His Phe Gln Arg Gly Asp Gly Ala Ala Leu Arg Glu Met Ala
 100 105 110

390

| | |
|---|-----|
| tcc tgc atc act cag aga aaa tgc aag gtc aca gcc act gca ctt aag | 384 |
| Ser Cys Ile Thr Gln Arg Lys Cys Lys Val Thr Ala Thr Ala Leu Lys | |
| 115 120 125 | |
| | |
| aca gct aga gag act gat gag gat gaa gat gat gtg gac agt gtg gaa | 432 |
| Thr Ala Arg Glu Thr Asp Glu Asp Glu Asp Asp Val Asp Ser Val Glu | |
| 130 135 140 | |
| | |
| gag atg gag gtc aca gct acg aat gat ggg gct gct aca gat ggg gtc | 480 |
| Glu Met Glu Val Thr Ala Thr Asn Asp Gly Ala Ala Thr Asp Gly Val | |
| 145 150 155 160 | |
| | |
| tgc ccc cag cct gaa ccc tct gat cca gac gct cag act att aag gaa | 528 |
| Cys Pro Gln Pro Glu Pro Ser Asp Pro Asp Ala Gln Thr Ile Lys Glu | |
| 165 170 175 | |
| | |
| gag gat ata gtg gaa gat ggc tgg acc att gtc cgg aga aaa aaa tga | 576 |
| Glu Asp Ile Val Glu Asp Gly Trp Thr Ile Val Arg Arg Lys Lys * | |
| 180 185 190 | |

<210> 266

<211> 191

<212> PRT

<213> Homo sapiens

<400> 266

| | |
|---|--|
| Met Ala Gly Ala Ala Glu Asp Ala Arg Ala Leu Phe Arg Ala Gly Val | |
| 1 5 10 15 | |
| Cys Ala Ala Leu Glu Ala Trp Pro Ala Leu Gln Ile Ala Val Glu Asn | |
| 20 25 30 | |
| Gly Phe Gly Gly Val His Ser Gln Glu Lys Ala Lys Trp Leu Gly Gly | |
| 35 40 45 | |
| Ala Val Glu Asp Tyr Phe Met Arg Asn Ala Asp Leu Glu Leu Asp Glu | |
| 50 55 60 | |
| Val Glu Asp Phe Leu Gly Glu Leu Leu Thr Asn Glu Phe Asp Thr Val | |
| 65 70 75 80 | |
| Val Glu Asp Gly Ser Leu Pro Gln Val Ser Gln Gln Leu Gln Thr Met | |
| 85 90 95 | |
| Phe His His Phe Gln Arg Gly Asp Gly Ala Ala Leu Arg Glu Met Ala | |
| 100 105 110 | |
| Ser Cys Ile Thr Gln Arg Lys Cys Lys Val Thr Ala Thr Ala Leu Lys | |
| 115 120 125 | |

391

Thr Ala Arg Glu Thr Asp Glu Asp Glu Asp Asp Val Asp Ser Val Glu
 130 135 140
 Glu Met Glu Val Thr Ala Thr Asn Asp Gly Ala Ala Thr Asp Gly Val
 145 150 155 160
 Cys Pro Gln Pro Glu Pro Ser Asp Pro Asp Ala Gln Thr Ile Lys Glu
 165 170 175
 Glu Asp Ile Val Glu Asp Gly Trp Thr Ile Val Arg Arg Lys Lys
 180 185 190

<210> 267
 <211> 567
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(567)

<400> 267

atg gtc ccc ggc gcc gcg ggc tgg tgt tgt ctc gtg ctc tgg ctc ccc 48
 Met Val Pro Gly Ala Ala Gly Trp Cys Cys Leu Val Leu Trp Leu Pro
 1 5 10 15

gcg tgc gtc gcg gcc cac ggc ttc cgt atc cat gat tat ttg tac ttt 96
 Ala Cys Val Ala Ala His Gly Phe Arg Ile His Asp Tyr Leu Tyr Phe
 20 25 30

caa gtg ctg agt cct ggg gac att cga tac atc ttc aca gcc aca cct 144
 Gln Val Leu Ser Pro Gly Asp Ile Arg Tyr Ile Phe Thr Ala Thr Pro
 35 40 45

gcc aag gac ttt ggt ggt atc ttt cac aca agg tat gag cag att cac 192
 Ala Lys Asp Phe Gly Gly Ile Phe His Thr Arg Tyr Glu Gln Ile His
 50 55 60

ctt gtc ccc gct gaa cct cca gag gcc tgc ggg gaa ctc agc aac ggt 240
 Leu Val Pro Ala Glu Pro Pro Glu Ala Cys Gly Glu Leu Ser Asn Gly
 65 70 75 80

ttc ttc atc cag gac cag att gct ctg gtg gag agg ggg ggc tgc tcc 288
 Phe Phe Ile Gln Asp Gln Ile Ala Leu Val Glu Arg Gly Gly Cys Ser
 85 90 95

ttc ctc tcc aag act cgg gtg gtc cag gag cac ggc ggg cgg gcg gtg 336

392

Phe Leu Ser Lys Thr Arg Val Val Gln Glu His Gly Gly Arg Ala Val
 100 105 110
 atc atc tct gac aac gca gtt gac aat gac agc ttc tac gtg gag atg 384
 Ile Ile Ser Asp Asn Ala Val Asp Asn Asp Ser Phe Tyr Val Glu Met
 115 120 125
 atc cag gac agt acc cag cgc aca gct gac atc ccc gcc ctc ttc ctg 432
 Ile Gln Asp Ser Thr Gln Arg Thr Ala Asp Ile Pro Ala Leu Phe Leu
 130 135 140
 ctc ggc cga gac ggc tac atg atc cgc cgc tct ctg gaa cag cat ggg 480
 Leu Gly Arg Asp Gly Tyr Met Ile Arg Arg Ser Leu Glu Gln His Gly
 145 150 155 160
 ctg cca tgg gcc atc att tcc atc cca gtc aat gtc acc agc atc ccc 528
 Leu Pro Trp Ala Ile Ile Ser Ile Pro Val Asn Val Thr Ser Ile Pro
 165 170 175
 acc ttt gag ctg ctg caa ccg ccc tgg acc ttc tgg tag 567
 Thr Phe Glu Leu Leu Gln Pro Pro Trp Thr Phe Trp *
 180 185

<210> 268
 <211> 188
 <212> PRT
 <213> Homo sapiens

<400> 268
 Met Val Pro Gly Ala Ala Gly Trp Cys Cys Leu Val Leu Trp Leu Pro
 1 5 10 15
 Ala Cys Val Ala Ala His Gly Phe Arg Ile His Asp Tyr Leu Tyr Phe
 20 25 30
 Gln Val Leu Ser Pro Gly Asp Ile Arg Tyr Ile Phe Thr Ala Thr Pro
 35 40 45
 Ala Lys Asp Phe Gly Gly Ile Phe His Thr Arg Tyr Glu Gln Ile His
 50 55 60
 Leu Val Pro Ala Glu Pro Pro Glu Ala Cys Gly Glu Leu Ser Asn Gly
 65 70 75 80
 Phe Phe Ile Gln Asp Gln Ile Ala Leu Val Glu Arg Gly Gly Cys Ser
 85 90 95
 Phe Leu Ser Lys Thr Arg Val Val Gln Glu His Gly Gly Arg Ala Val
 100 105 110

393

Ile Ile Ser Asp Asn Ala Val Asp Asn Asp Ser Phe Tyr Val Glu Met
 115 120 125
 Ile Gln Asp Ser Thr Gln Arg Thr Ala Asp Ile Pro Ala Leu Phe Leu
 130 135 140
 Leu Gly Arg Asp Gly Tyr Met Ile Arg Arg Ser Leu Glu Gln His Gly
 145 150 155 160
 Leu Pro Trp Ala Ile Ile Ser Ile Pro Val Asn Val Thr Ser Ile Pro
 165 170 175
 Thr Phe Glu Leu Leu Gln Pro Pro Trp Thr Phe Trp
 180 185

<210> 269
 <211> 1419
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1419)

<400> 269

| | |
|---|-----|
| atg gtg ctg gcc tcg gcg ctg ctg tgt gtg att gtg tct gtt ctg acc | 48 |
| Met Val Leu Ala Ser Ala Leu Leu Cys Val Ile Val Ser Val Leu Thr | |
| 1 5 10 15 | |
| aac gtg ctc gtg ggt gga aac acc cca agg aag aac ccc atg cat ccc | 96 |
| Asn Val Leu Val Gly Gly Asn Thr Pro Arg Lys Asn Pro Met His Pro | |
| 20 25 30 | |
| agc tca agg tgg tca gag cta gac ctt ctt att ctg ttg ggg acg gcg | 144 |
| Ser Ser Arg Trp Ser Glu Leu Asp Leu Leu Ile Leu Leu Gly Thr Ala | |
| 35 40 45 | |
| ggc cac gtc ttg agc ctg ggc gcc agc agc ttc gtg gag gag gag cac | 192 |
| Gly His Val Leu Ser Leu Gly Ala Ser Ser Phe Val Glu Glu Glu His | |
| 50 55 60 | |
| cag acc tgg tac ttc ctt gtg aac acc ctg tgt cta gct ctg agc caa | 240 |
| Gln Thr Trp Tyr Phe Leu Val Asn Thr Leu Cys Leu Ala Leu Ser Gln | |
| 65 70 75 80 | |
| gaa acc tac aga aac tac ttt ctg gga gat gac ggt gag cct ccg tgt | 288 |
| Glu Thr Tyr Arg Asn Tyr Phe Leu Gly Asp Asp Gly Glu Pro Pro Cys | |
| 85 90 95 | |

394

| | |
|---|-----|
| ggc ctc tgt gtg gaa caa ggg cat gac ggg gcc aca gca gcg tgg cag Gly Leu Cys Val Glu Gln Gly His Asp Gly Ala Thr Ala Ala Trp Gln 100 105 110 | 336 |
| gac ggg cct ggc tgt gat gtc ctg gag cga gac aaa ggc cac gga agc Asp Gly Pro Gly Cys Asp Val Leu Glu Arg Asp Lys Gly His Gly Ser 115 120 125 | 384 |
| ccc tct acc tcc gaa gtg ctc aga ggc cgc gag aag tgg atg gtg ctg Pro Ser Thr Ser Glu Val Leu Arg Gly Arg Glu Lys Trp Met Val Leu 130 135 140 | 432 |
| gcc agt ccg tgg cta ata ctg gcc tgc tgc cgg ctg ctg cgc tcc cta Ala Ser Pro Trp Leu Ile Leu Ala Cys Cys Arg Leu Leu Arg Ser Leu 145 150 155 160 | 480 |
| aac cag aca ggt gtg cag tgg gct cac cgg cct gac ctc ggc cac tgg Asn Gln Thr Gly Val Gln Trp Ala His Arg Pro Asp Leu Gly His Trp 165 170 175 | 528 |
| ctc acc agc tct gac cac aaa gcc gag ctc tct gtc ctg gct gcc ctc Leu Thr Ser Ser Asp His Lys Ala Glu Leu Ser Val Leu Ala Ala Leu 180 185 190 | 576 |
| tcc ctc ctc gta gtt ttt gtg ctg gtg cag agg ggg tgc tcc cct gtg Ser Leu Leu Val Val Phe Val Leu Val Gln Arg Gly Cys Ser Pro Val 195 200 205 | 624 |
| tcc aag gct gcc ctg gcg ctg ggg ctg ctg ggc gtc tac tgc tac cgg Ser Lys Ala Ala Leu Ala Leu Gly Leu Leu Gly Val Tyr Cys Tyr Arg 210 215 220 | 672 |
| gcg gcc atc ggg agt gtc cgg ttc ccg tgg cgg ccg gac agc aag gac Ala Ala Ile Gly Ser Val Arg Phe Pro Trp Arg Pro Asp Ser Lys Asp 225 230 235 240 | 720 |
| att tcc aag ggt att att gaa gct cgt ttt gtt tat gtc ttt gtc ctt Ile Ser Lys Gly Ile Ile Glu Ala Arg Phe Val Tyr Val Phe Val Leu 245 250 255 | 768 |
| ggc att ctg ttc acg ggc acc aaa gac tta ctt aaa tct caa gtc att Gly Ile Leu Phe Thr Gly Thr Lys Asp Leu Leu Lys Ser Gln Val Ile 260 265 270 | 816 |

395

| | |
|---|------|
| gct gca gac ttc aaa ctc aag act gta ggt tta tgg gag ata tat agt Ala Ala Asp Phe Lys Leu Lys Thr Val Gly Leu Trp Glu Ile Tyr Ser 275 280 285 | 864 |
| gga tta gtt ctt ctg gca gcc ttg ctc ttt aga cca cat aat ctt ccg Gly Leu Val Leu Leu Ala Ala Leu Leu Phe Arg Pro His Asn Leu Pro 290 295 300 | 912 |
| gtc tta gca ttt agc ctc ttg att cag act cta atg act aaa ttc atc Val Leu Ala Phe Ser Leu Leu Ile Gln Thr Leu Met Thr Lys Phe Ile 305 310 315 320 | 960 |
| tgg aag ccc ctg aga cac gat gca gct gag att act gtg atg cat tat Trp Lys Pro Leu Arg His Asp Ala Ala Glu Ile Thr Val Met His Tyr 325 330 335 | 1008 |
| tgg ttt ggt caa gca ttc ttc tat ttt cag ggc aac tcc aac aac att Trp Phe Gly Gln Ala Phe Phe Tyr Phe Gln Gly Asn Ser Asn Asn Ile 340 345 350 | 1056 |
| gcc acc gtg gac atc tcc gca ggc ttc gtg ggc tta gac acc tac gtg Ala Thr Val Asp Ile Ser Ala Gly Phe Val Gly Leu Asp Thr Tyr Val 355 360 365 | 1104 |
| gaa atc cca gcc gtg ctc ctg aca gcg ttt ggg acg tac gca ggg cct Glu Ile Pro Ala Val Leu Leu Thr Ala Phe Gly Thr Tyr Ala Gly Pro 370 375 380 | 1152 |
| gtg ctg tgg gcc agc cac tta gtg cac ttc ctg agc tca gaa aca cgc Val Leu Trp Ala Ser His Leu Val His Phe Leu Ser Ser Glu Thr Arg 385 390 395 400 | 1200 |
| agt ggt tca gca ctg agt cat gct tgc ttc tgc tac gca ctg att tgt Ser Gly Ser Ala Leu Ser His Ala Cys Phe Cys Tyr Ala Leu Ile Cys 405 410 415 | 1248 |
| tct att cca gtt ttc acg tac atc gtt ttg gtg aca tct ctg cgt tat Ser Ile Pro Val Phe Thr Tyr Ile Val Leu Val Thr Ser Leu Arg Tyr 420 425 430 | 1296 |
| cat tta ttt ata tgg agt gta ttt tct cca aaa ctt ctc tac gag gga His Leu Phe Ile Trp Ser Val Phe Ser Pro Lys Leu Leu Tyr Glu Gly 435 440 445 | 1344 |

396

atg cac ctg ctc att aca gct gct gtc tgt gta ttc ttc acg gca atg 1392
 Met His Leu Leu Ile Thr Ala Ala Val Cys Val Phe Phe Thr Ala Met
 450 455 460

gat caa acc aga ctc aca cag tct tag 1419
 Asp Gln Thr Arg Leu Thr Gln Ser *
 465 470

<210> 270
 <211> 472
 <212> PRT
 <213> Homo sapiens

<400> 270
 Met Val Leu Ala Ser Ala Leu Leu Cys Val Ile Val Ser Val Leu Thr
 1 5 10 15
 Asn Val Leu Val Gly Gly Asn Thr Pro Arg Lys Asn Pro Met His Pro
 20 25 30
 Ser Ser Arg Trp Ser Glu Leu Asp Leu Leu Ile Leu Leu Gly Thr Ala
 35 40 45
 Gly His Val Leu Ser Leu Gly Ala Ser Ser Phe Val Glu Glu Glu His
 50 55 60
 Gln Thr Trp Tyr Phe Leu Val Asn Thr Leu Cys Leu Ala Leu Ser Gln
 65 70 75 80
 Glu Thr Tyr Arg Asn Tyr Phe Leu Gly Asp Asp Gly Glu Pro Pro Cys
 85 90 95
 Gly Leu Cys Val Glu Gln Gly His Asp Gly Ala Thr Ala Ala Trp Gln
 100 105 110
 Asp Gly Pro Gly Cys Asp Val Leu Glu Arg Asp Lys Gly His Gly Ser
 115 120 125
 Pro Ser Thr Ser Glu Val Leu Arg Gly Arg Glu Lys Trp Met Val Leu
 130 135 140
 Ala Ser Pro Trp Leu Ile Leu Ala Cys Cys Arg Leu Leu Arg Ser Leu
 145 150 155 160
 Asn Gln Thr Gly Val Gln Trp Ala His Arg Pro Asp Leu Gly His Trp
 165 170 175
 Leu Thr Ser Ser Asp His Lys Ala Glu Leu Ser Val Leu Ala Ala Leu
 180 185 190
 Ser Leu Leu Val Val Phe Val Leu Val Gln Arg Gly Cys Ser Pro Val
 195 200 205
 Ser Lys Ala Ala Leu Ala Leu Gly Leu Leu Gly Val Tyr Cys Tyr Arg
 210 215 220

397

Ala Ala Ile Gly Ser Val Arg Phe Pro Trp Arg Pro Asp Ser Lys Asp
 225 230 235 240
 Ile Ser Lys Gly Ile Ile Glu Ala Arg Phe Val Tyr Val Phe Val Leu
 245 250 255
 Gly Ile Leu Phe Thr Gly Thr Lys Asp Leu Leu Lys Ser Gln Val Ile
 260 265 270
 Ala Ala Asp Phe Lys Leu Lys Thr Val Gly Leu Trp Glu Ile Tyr Ser
 275 280 285
 Gly Leu Val Leu Leu Ala Ala Leu Leu Phe Arg Pro His Asn Leu Pro
 290 295 300
 Val Leu Ala Phe Ser Leu Leu Ile Gln Thr Leu Met Thr Lys Phe Ile
 305 310 315 320
 Trp Lys Pro Leu Arg His Asp Ala Ala Glu Ile Thr Val Met His Tyr
 325 330 335
 Trp Phe Gly Gln Ala Phe Phe Tyr Phe Gln Gly Asn Ser Asn Asn Ile
 340 345 350
 Ala Thr Val Asp Ile Ser Ala Gly Phe Val Gly Leu Asp Thr Tyr Val
 355 360 365
 Glu Ile Pro Ala Val Leu Leu Thr Ala Phe Gly Thr Tyr Ala Gly Pro
 370 375 380
 Val Leu Trp Ala Ser His Leu Val His Phe Leu Ser Ser Glu Thr Arg
 385 390 395 400
 Ser Gly Ser Ala Leu Ser His Ala Cys Phe Cys Tyr Ala Leu Ile Cys
 405 410 415
 Ser Ile Pro Val Phe Thr Tyr Ile Val Leu Val Thr Ser Leu Arg Tyr
 420 425 430
 His Leu Phe Ile Trp Ser Val Phe Ser Pro Lys Leu Leu Tyr Glu Gly
 435 440 445
 Met His Leu Leu Ile Thr Ala Ala Val Cys Val Phe Phe Thr Ala Met
 450 455 460
 Asp Gln Thr Arg Leu Thr Gln Ser
 465 470

<210> 271
 <211> 1089
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1089)

<221> misc_feature
 <222> (1)...(1089)

398

<223> n = A,T,C or G

<400> 271

| | |
|---|-----|
| atg gac agc ccc gag gtg acc ttc act ctc gcc tat ctg gtg ttc gcc | 48 |
| Met Asp Ser Pro Glu Val Thr Phe Thr Leu Ala Tyr Leu Val Phe Ala | |
| 1 5 10 15 | |
| gtg tgc ttc gtg ttc acg ccc aac gag ttc cac gcg gcg ggg ctc acg | 96 |
| Val Cys Phe Val Phe Thr Pro Asn Glu Phe His Ala Ala Gly Leu Thr | |
| 20 25 30 | |
| gtg cag aac ctg ctg tcg ggc tgg ctg ggc agc gag gac gcc gcc ttc | 144 |
| Val Gln Asn Leu Leu Ser Gly Trp Leu Gly Ser Glu Asp Ala Ala Phe | |
| 35 40 45 | |
| gtg ccc ttc cac ttg cgc cgc acg gcc gcc acg ctg ttg tgc cac tcg | 192 |
| Val Pro Phe His Leu Arg Arg Thr Ala Ala Thr Leu Leu Cys His Ser | |
| 50 55 60 | |
| ctg ctg ccg ctc ggc tac tat gtg ggc atg tgc ctt gcg gct tca gaa | 240 |
| Leu Leu Pro Leu Gly Tyr Tyr Val Gly Met Cys Leu Ala Ala Ser Glu | |
| 65 70 75 80 | |
| aag cgg ctc cac gcc ctc agc cag gcc cct gag gcc tgg cgg ctc ttc | 288 |
| Lys Arg Leu His Ala Leu Ser Gln Ala Pro Glu Ala Trp Arg Leu Phe | |
| 85 90 95 | |
| ctg ctg ctg gcc gtg acc ctc ccc tcc atc gcc tgc atc ctg atc tac | 336 |
| Leu Leu Leu Ala Val Thr Leu Pro Ser Ile Ala Cys Ile Leu Ile Tyr | |
| 100 105 110 | |
| tac tgg tcc cgt gac cgg tgg gcc tgc cac cca ctg gcg cgc acc ctg | 384 |
| Tyr Trp Ser Arg Asp Arg Trp Ala Cys His Pro Leu Ala Arg Thr Leu | |
| 115 120 125 | |
| gcc ctc tac gcc ctc cca cag tct ggc tgg cag gct gtt gcc tcc tct | 432 |
| Ala Leu Tyr Ala Leu Pro Gln Ser Gly Trp Gln Ala Val Ala Ser Ser | |
| 130 135 140 | |
| gtc aac act gag ttc cgg cgg att gac aag ttt gcc acc ggt gca cca | 480 |
| Val Asn Thr Glu Phe Arg Arg Ile Asp Lys Phe Ala Thr Gly Ala Pro | |
| 145 150 155 160 | |
| ggg gcc cgt gtg att gtg aca gac acg tgg gtg atg aag gta acc acc | 528 |

399

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| Gly | Ala | Arg | Val | Ile | Val | Thr | Asp | Thr | Trp | Val | Met | Lys | Val | Thr | Thr | | |
| | | | 165 | | | | | | 170 | | | | | 175 | | | |
| tac | cga | gtg | cac | gtg | gcc | cag | cag | cag | gac | gtg | cac | ctg | act | gtg | acg | 576 | |
| Tyr | Arg | Val | His | Val | Ala | Gln | Gln | Gln | Asp | Val | His | Leu | Thr | Val | Thr | | |
| | | | 180 | | | | | 185 | | | | | 190 | | | | |
| gag | tct | cgg | cag | cat | gag | ctc | tcg | cca | gac | tcg | aac | ttg | ccc | gtg | cag | 624 | |
| Glu | Ser | Arg | Gln | His | Glu | Leu | Ser | Pro | Asp | Ser | Asn | Leu | Pro | Val | Gln | | |
| | | | 195 | | | | | 200 | | | | | 205 | | | | |
| ctc | ctc | acc | atc | cgt | gtg | gcc | agc | acc | aac | cct | gct | gtg | cag | gcc | ttt | 672 | |
| Leu | Leu | Thr | Ile | Arg | Val | Ala | Ser | Thr | Asn | Pro | Ala | Val | Gln | Ala | Phe | | |
| | | | 210 | | | 215 | | | | | | 220 | | | | | |
| gac | atc | tgg | ctg | aac | tcc | act | gag | tac | ggg | gag | ctc | tgc | gag | aag | ctc | 720 | |
| Asp | Ile | Trp | Leu | Asn | Ser | Thr | Glu | Tyr | Gly | Glu | Leu | Cys | Glu | Lys | Leu | | |
| | | | 225 | | | 230 | | | | | 235 | | | | 240 | | |
| cgg | gca | ccc | atc | cgc | agg | gca | gcc | cat | gtg | gtc | atc | cac | cag | agc | ctg | 768 | |
| Arg | Ala | Pro | Ile | Arg | Arg | Ala | Ala | His | Val | Val | Ile | His | Gln | Ser | Leu | | |
| | | | | 245 | | | | | 250 | | | | | 255 | | | |
| ggc | gac | ctg | ttc | ctg | gag | acn | ttt | gcc | tcc | ctg | gta | gag | gtc | aac | ccg | 816 | |
| Gly | Asp | Leu | Phe | Leu | Glu | Xaa | Phe | Ala | Ser | Leu | Val | Glu | Val | Asn | Pro | | |
| | | | 260 | | | | | 265 | | | | | 270 | | | | |
| gcc | tac | tca | gtg | ccc | agc | agc | cag | gag | ctg | gag | gcc | tgc | ata | ggc | tgc | 864 | |
| Ala | Tyr | Ser | Val | Pro | Ser | Ser | Gln | Glu | Leu | Glu | Ala | Cys | Ile | Gly | Cys | | |
| | | | 275 | | | | 280 | | | | | 285 | | | | | |
| atg | cag | aca | cgt | gcc | agc | gtg | aag | ctg | gtg | aag | acc | tgc | cag | gag | gca | 912 | |
| Met | Gln | Thr | Arg | Ala | Ser | Val | Lys | Leu | Val | Lys | Thr | Cys | Gln | Glu | Ala | | |
| | | | 290 | | | 295 | | | | | 300 | | | | | | |
| gcc | aca | ggc | gag | tgc | cag | cag | tgt | tac | tgc | cgc | ccc | atg | tgg | tgc | ctc | 960 | |
| Ala | Thr | Gly | Glu | Cys | Gln | Gln | Cys | Tyr | Cys | Arg | Pro | Met | Trp | Cys | Leu | | |
| | | | 305 | | | 310 | | | | 315 | | | | | 320 | | |
| acc | tgc | atg | ggc | aag | tgg | ttc | gcc | agc | cgc | cag | gac | ccc | ctg | cgc | cct | 1008 | |
| Thr | Cys | Met | Gly | Lys | Trp | Phe | Ala | Ser | Arg | Gln | Asp | Pro | Leu | Arg | Pro | | |
| | | | | 325 | | | | | 330 | | | | | 335 | | | |
| gac | acc | tgg | ctg | gcc | agc | cgc | gtg | ccc | tgc | ccc | acc | tgc | cgc | gca | cgc | 1056 | |

400

Asp Thr Trp Leu Ala Ser Arg Val Pro Cys Pro Thr Cys Arg Ala Arg
 340 345 350

ttc tgc atc ctg gat gtg tgc acc gtg cgc tga
 Phe Cys Ile Leu Asp Val Cys Thr Val Arg *
 355 360

1089

<210> 272

<211> 362

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(362)

<223> Xaa = Any Amino Acid

<400> 272

Met Asp Ser Pro Glu Val Thr Phe Thr Leu Ala Tyr Leu Val Phe Ala
 1 5 10 15
 Val Cys Phe Val Phe Thr Pro Asn Glu Phe His Ala Ala Gly Leu Thr
 20 25 30
 Val Gln Asn Leu Leu Ser Gly Trp Leu Gly Ser Glu Asp Ala Ala Phe
 35 40 45
 Val Pro Phe His Leu Arg Arg Thr Ala Ala Thr Leu Leu Cys His Ser
 50 55 60
 Leu Leu Pro Leu Gly Tyr Tyr Val Gly Met Cys Leu Ala Ala Ser Glu
 65 70 75 80
 Lys Arg Leu His Ala Leu Ser Gln Ala Pro Glu Ala Trp Arg Leu Phe
 85 90 95
 Leu Leu Leu Ala Val Thr Leu Pro Ser Ile Ala Cys Ile Leu Ile Tyr
 100 105 110
 Tyr Trp Ser Arg Asp Arg Trp Ala Cys His Pro Leu Ala Arg Thr Leu
 115 120 125
 Ala Leu Tyr Ala Leu Pro Gln Ser Gly Trp Gln Ala Val Ala Ser Ser
 130 135 140
 Val Asn Thr Glu Phe Arg Arg Ile Asp Lys Phe Ala Thr Gly Ala Pro
 145 150 155 160
 Gly Ala Arg Val Ile Val Thr Asp Thr Trp Val Met Lys Val Thr Thr
 165 170 175
 Tyr Arg Val His Val Ala Gln Gln Gln Asp Val His Leu Thr Val Thr
 180 185 190
 Glu Ser Arg Gln His Glu Leu Ser Pro Asp Ser Asn Leu Pro Val Gln

401

195 200 205
 Leu Leu Thr Ile Arg Val Ala Ser Thr Asn Pro Ala Val Gln Ala Phe
 210 215 220
 Asp Ile Trp Leu Asn Ser Thr Glu Tyr Gly Glu Leu Cys Glu Lys Leu
 225 230 235 240
 Arg Ala Pro Ile Arg Arg Ala Ala His Val Val Ile His Gln Ser Leu
 245 250 255
 Gly Asp Leu Phe Leu Glu Xaa Phe Ala Ser Leu Val Glu Val Asn Pro
 260 265 270
 Ala Tyr Ser Val Pro Ser Ser Gln Glu Leu Glu Ala Cys Ile Gly Cys
 275 280 285
 Met Gln Thr Arg Ala Ser Val Lys Leu Val Lys Thr Cys Gln Glu Ala
 290 295 300
 Ala Thr Gly Glu Cys Gln Gln Cys Tyr Cys Arg Pro Met Trp Cys Leu
 305 310 315 320
 Thr Cys Met Gly Lys Trp Phe Ala Ser Arg Gln Asp Pro Leu Arg Pro
 325 330 335
 Asp Thr Trp Leu Ala Ser Arg Val Pro Cys Pro Thr Cys Arg Ala Arg
 340 345 350
 Phe Cys Ile Leu Asp Val Cys Thr Val Arg
 355 360

<210> 273
 <211> 723
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(723)

<400> 273
 atg tcc cct ttg ctc ttt ggg gct ggg ctg gtc gtt ctg aat cta gtg 48
 Met Ser Pro Leu Leu Phe Gly Ala Gly Leu Val Val Leu Asn Leu Val
 1 5 10 15
 acg tct gcc agg agc cag aag aca gaa cct cta agt ggc tct ggg gac 96
 Thr Ser Ala Arg Ser Gln Lys Thr Glu Pro Leu Ser Gly Ser Gly Asp
 20 25 30
 cag cca ctc ttc cgt gga gct gat cga tat gac ttt gcc atc atg ata 144
 Gln Pro Leu Phe Arg Gly Ala Asp Arg Tyr Asp Phe Ala Ile Met Ile
 35 40 45

402

| | |
|---|-----|
| cct cca gga ggc acg gaa tgc ttt tgg caa ttt gcc cac cag act gga Pro Pro Gly Gly Thr Glu Cys Phe Trp Gln Phe Ala His Gln Thr Gly 50 55 60 | 192 |
| tac ttc tat ttc agt tac gag gtt cag cgg aca gtg ggg atg tca cat Tyr Phe Tyr Phe Ser Tyr Glu Val Gln Arg Thr Val Gly Met Ser His 65 70 75 80 | 240 |
| gac cgg cat gtt gct gcc acg gca cat aac cca cag gga ttt ctc ata Asp Arg His Val Ala Ala Thr Ala His Asn Pro Gln Gly Phe Leu Ile 85 90 95 | 288 |
| gac acc tcc cag ggt gtt cgg ggc cag att aac ttc tct acc caa gag Asp Thr Ser Gln Gly Val Arg Gly Gln Ile Asn Phe Ser Thr Gln Glu 100 105 110 | 336 |
| aca ggt ttt tat cag ctt tgt cta agt aat cag cat aat cac ttc ggt Thr Gly Phe Tyr Gln Leu Cys Leu Ser Asn Gln His Asn His Phe Gly 115 120 125 | 384 |
| tct gtg caa gtg tac ctc aac ttt ggg gtc ttc tat gag ggg cct gag Ser Val Gln Val Tyr Leu Asn Phe Gly Val Phe Tyr Glu Gly Pro Glu 130 135 140 | 432 |
| act gat cac aaa cag aag gaa aga aaa caa ctg aat gat act ctg gat Thr Asp His Lys Gln Lys Glu Arg Lys Gln Leu Asn Asp Thr Leu Asp 145 150 155 160 | 480 |
| gca att gag gac ggc aca caa aag gtg cag aac aat atc ttt cac atg Ala Ile Glu Asp Gly Thr Gln Lys Val Gln Asn Asn Ile Phe His Met 165 170 175 | 528 |
| tgg cga tac tac aac ttt gcc cgg atg agg aaa atg gct gac ttt ttc Trp Arg Tyr Tyr Asn Phe Ala Arg Met Arg Lys Met Ala Asp Phe Phe 180 185 190 | 576 |
| ctt atc caa tca aac tat aac tac gtg aac tgg tgg tcg aca gcc cag Leu Ile Gln Ser Asn Tyr Asn Tyr Val Asn Trp Trp Ser Thr Ala Gln 195 200 205 | 624 |
| agc ctt gtt att att ctt tct ggg atc ctg caa ctg tat ttc ttg aag Ser Leu Val Ile Ile Leu Ser Gly Ile Leu Gln Leu Tyr Phe Leu Lys 210 215 220 | 672 |

403

cgt ctc ttc aat gtt cca aca act aca gat aca aag aag cca aga tgc 720
 Arg Leu Phe Asn Val Pro Thr Thr Thr Asp Thr Lys Lys Pro Arg Cys
 225 230 235 240
 taa 723
 *

<210> 274
 <211> 240
 <212> PRT
 <213> Homo sapiens

<400> 274
 Met Ser Pro Leu Leu Phe Gly Ala Gly Leu Val Val Leu Asn Leu Val
 1 5 10 15
 Thr Ser Ala Arg Ser Gln Lys Thr Glu Pro Leu Ser Gly Ser Gly Asp
 20 25 30
 Gln Pro Leu Phe Arg Gly Ala Asp Arg Tyr Asp Phe Ala Ile Met Ile
 35 40 45
 Pro Pro Gly Gly Thr Glu Cys Phe Trp Gln Phe Ala His Gln Thr Gly
 50 55 60
 Tyr Phe Tyr Phe Ser Tyr Glu Val Gln Arg Thr Val Gly Met Ser His
 65 70 75 80
 Asp Arg His Val Ala Ala Thr Ala His Asn Pro Gln Gly Phe Leu Ile
 85 90 95
 Asp Thr Ser Gln Gly Val Arg Gly Gln Ile Asn Phe Ser Thr Gln Glu
 100 105 110
 Thr Gly Phe Tyr Gln Leu Cys Leu Ser Asn Gln His Asn His Phe Gly
 115 120 125
 Ser Val Gln Val Tyr Leu Asn Phe Gly Val Phe Tyr Glu Gly Pro Glu
 130 135 140
 Thr Asp His Lys Gln Lys Glu Arg Lys Gln Leu Asn Asp Thr Leu Asp
 145 150 155 160
 Ala Ile Glu Asp Gly Thr Gln Lys Val Gln Asn Asn Ile Phe His Met
 165 170 175
 Trp Arg Tyr Tyr Asn Phe Ala Arg Met Arg Lys Met Ala Asp Phe Phe
 180 185 190
 Leu Ile Gln Ser Asn Tyr Asn Tyr Val Asn Trp Trp Ser Thr Ala Gln
 195 200 205
 Ser Leu Val Ile Ile Leu Ser Gly Ile Leu Gln Leu Tyr Phe Leu Lys
 210 215 220
 Arg Leu Phe Asn Val Pro Thr Thr Thr Asp Thr Lys Lys Pro Arg Cys

404

| | | | | |
|--|-----|-----|-----|-----|
| 225 | 230 | 235 | 240 | |
| <210> 275 <211> 993 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (1)...(993) <221> misc_feature <222> (1)...(993) <223> n = A,T,C or G <400> 275 | | | | |
| atg gct gag cac gca ggg ccc cga ctc ccc ctg gtg ctg aag acg ctg | | | | 48 |
| Met Ala Glu His Ala Gly Pro Arg Leu Pro Leu Val Leu Lys Thr Leu | | | | |
| 1 5 10 15 | | | | |
| | | | | |
| gca tgc aca cac agc agt gcg tat gag aac cag agg gtg acc acc acc | | | | 96 |
| Ala Cys Thr His Ser Ser Ala Tyr Glu Asn Gln Arg Val Thr Thr Thr | | | | |
| 20 25 30 | | | | |
| | | | | |
| gcc ttc ctg gcc gag ctg ctg aac agc aac gtg gcc aac gac ctc atg | | | | 144 |
| Ala Phe Leu Ala Glu Leu Leu Asn Ser Asn Val Ala Asn Asp Leu Met | | | | |
| 35 40 45 | | | | |
| | | | | |
| ctc ttg gac tcg ctg ctg gag agc ctg gcg gct cgc cag aag gac aca | | | | 192 |
| Leu Leu Asp Ser Leu Leu Glu Ser Leu Ala Ala Arg Gln Lys Asp Thr | | | | |
| 50 55 60 | | | | |
| | | | | |
| tgc gcc anc gtg cgg agg ctg gtg ctc cgc ggc ctg gcc aac ctg gcc | | | | 240 |
| Cys Ala Xaa Val Arg Arg Leu Val Leu Arg Gly Leu Ala Asn Leu Ala | | | | |
| 65 70 75 80 | | | | |
| | | | | |
| tcc ggc tgc cct gac aag gtg cga acc cac ggc ccc cag ctc ctc aca | | | | 288 |
| Ser Gly Cys Pro Asp Lys Val Arg Thr His Gly Pro Gln Leu Leu Thr | | | | |
| 85 90 95 | | | | |
| | | | | |
| gcc atg att ggc ggg ctg gac gac ggg gac aac cct cac agc cca gtg | | | | 336 |
| Ala Met Ile Gly Gly Leu Asp Asp Gly Asp Asn Pro His Ser Pro Val | | | | |
| 100 105 110 | | | | |

405

| | |
|---|-----|
| gcc ctg gag gcc atg ctg ggc ctt gcg agg ctg gtg cac ctg gtg gag Ala Leu Glu Ala Met Leu Gly Leu Ala Arg Leu Val His Leu Val Glu 115 120 125 | 384 |
| tcc tgg gac ctg cgc tca ggg ctg ctg cac gtg gcc atc cgc atc cgg Ser Trp Asp Leu Arg Ser Gly Leu Leu His Val Ala Ile Arg Ile Arg 130 135 140 | 432 |
| cct ttc ttc gac agt gag aag atg gag ttc cgg acg gca tct atc cgc Pro Phe Phe Asp Ser Glu Lys Met Glu Phe Arg Thr Ala Ser Ile Arg 145 150 155 160 | 480 |
| ctc ttt ggg cac ctt aac aag gtc tgc cac gga gac tgt gag gac gtc Leu Phe Gly His Leu Asn Lys Val Cys His Gly Asp Cys Glu Asp Val 165 170 175 | 528 |
| ttc ctg gac cag gtg gtg ggc ggg ctg gcg ccc ctg ctg ctg cac ctg Phe Leu Asp Gln Val Val Gly Gly Leu Ala Pro Leu Leu Leu His Leu 180 185 190 | 576 |
| cag gac cct cag gcc acc gtg gcc agc gcc tgc agg ttt gcc ctg cgc Gln Asp Pro Gln Ala Thr Val Ala Ser Ala Cys Arg Phe Ala Leu Arg 195 200 205 | 624 |
| atg tgt ggc ccc aat ctg gca tgt gag gag ctc tca gct gct ttc cag Met Cys Gly Pro Asn Leu Ala Cys Glu Glu Leu Ser Ala Ala Phe Gln 210 215 220 | 672 |
| aaa cac ctg cag gag ggc cga gcc ctg cac ttc ggg gag ttc ctc aac Lys His Leu Gln Glu Gly Arg Ala Leu His Phe Gly Glu Phe Leu Asn 225 230 235 240 | 720 |
| acc acc tgc aag cac ctg atg cac cat ttc cca gac ctg ctg ggc cgt Thr Thr Cys Lys His Leu Met His His Phe Pro Asp Leu Leu Gly Arg 245 250 255 | 768 |
| ctc ctg acc acc tgc ctg ttc tac ttc aag agc agc tgg gag aac gtc Leu Leu Thr Thr Cys Leu Phe Tyr Phe Lys Ser Ser Trp Glu Asn Val 260 265 270 | 816 |
| cga gct gct gca ccc ctg ttc acc ggg ttc ctg gtg ctg cac tgc gag Arg Ala Ala Ala Pro Leu Phe Thr Gly Phe Leu Val Leu His Ser Glu 275 280 285 | 864 |

406

ccc agg cag cag ccg cag gtg gac ctg gac cag ctc att gcg gcg ctc 912
 Pro Arg Gln Gln Pro Gln Val Asp Leu Asp Gln Leu Ile Ala Ala Leu
 290 295 300

cag atc ctg ctg aag gac ccg gcc ccc gag gtg cgg acg agg gct gct 960
 Gln Ile Leu Leu Lys Asp Pro Ala Pro Glu Val Arg Thr Arg Ala Ala
 305 310 315 320

gag gcc ctg ggc cgc ctg gtg aag ctc gcc taa 993
 Glu Ala Leu Gly Arg Leu Val Lys Leu Ala *
 325 330

<210> 276

<211> 330

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(330)

<223> Xaa = Any Amino Acid

<400> 276

Met Ala Glu His Ala Gly Pro Arg Leu Pro Leu Val Leu Lys Thr Leu
 1 5 10 15
 Ala Cys Thr His Ser Ser Ala Tyr Glu Asn Gln Arg Val Thr Thr Thr
 20 25 30
 Ala Phe Leu Ala Glu Leu Leu Asn Ser Asn Val Ala Asn Asp Leu Met
 35 40 45
 Leu Leu Asp Ser Leu Leu Glu Ser Leu Ala Ala Arg Gln Lys Asp Thr
 50 55 60
 Cys Ala Xaa Val Arg Arg Leu Val Leu Arg Gly Leu Ala Asn Leu Ala
 65 70 75 80
 Ser Gly Cys Pro Asp Lys Val Arg Thr His Gly Pro Gln Leu Leu Thr
 85 90 95
 Ala Met Ile Gly Gly Leu Asp Asp Gly Asp Asn Pro His Ser Pro Val
 100 105 110
 Ala Leu Glu Ala Met Leu Gly Leu Ala Arg Leu Val His Leu Val Glu
 115 120 125
 Ser Trp Asp Leu Arg Ser Gly Leu Leu His Val Ala Ile Arg Ile Arg
 130 135 140
 Pro Phe Phe Asp Ser Glu Lys Met Glu Phe Arg Thr Ala Ser Ile Arg
 145 150 155 160

407

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<210> 277
<211> 642
<212> DNA
<213> Homo sapiens
```

| | | | | | | | | | | | | | | | | |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> 277 | | | | | | | | | | | | | | | | |
| atg | gat | caa | caa | ctg | cgt | ggg | aag | ccg | gaa | tta | ttg | gtc | ttc | ttc | agc | 48 |
| Met | Asp | Gln | Gln | Leu | Arg | Gly | Lys | Pro | Glu | Leu | Leu | Val | Phe | Phe | Ser | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| | | | | | | | | | | | | | | | | |
| act | gtg | gcc | tcg | gcc | aca | gct | ggc | atg | ctc | tgc | ctg | atc | gcc | atc | ctg | 96 |
| Thr | Val | Ala | Ser | Ala | Thr | Ala | Gly | Met | Leu | Cys | Leu | Ile | Ala | Ile | Leu | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| | | | | | | | | | | | | | | | | |
| ctg | tat | gtc | ctc | gtc | cag | tac | ctc | gtg | aac | ccc | ggg | gtg | ctc | cgc | acg | 144 |
| Leu | Tyr | Val | Leu | Val | Gln | Tyr | Leu | Val | Asn | Pro | Gly | Val | Leu | Arg | Thr | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |

408

| | |
|---|-----|
| gac ccc aga gat gtc aag aat atg aac acg tgg ctg ctg ttc ctc ccc | 192 |
| Asp Pro Arg Asp Val Lys Asn Met Asn Thr Trp Leu Leu Phe Leu Pro | |
| 50 55 60 | |
| ctg ttc ccg gtg cag gtg cag acc ctg ata gtc gtg atc atc ggg atg | 240 |
| Leu Phe Pro Val Gln Val Gln Thr Leu Ile Val Val Ile Ile Gly Met | |
| 65 70 75 80 | |
| ctc gtg ctc ctg ctg gac ttt ctt ggc ttg gtg cac ctg ggc cag ctg | 288 |
| Leu Val Leu Leu Leu Asp Phe Leu Gly Leu Val His Leu Gly Gln Leu | |
| 85 90 95 | |
| ctc atc ttc cac atc tac ctg aag gcc aag aag atg acc acc ttt gag | 336 |
| Leu Ile Phe His Ile Tyr Leu Lys Ala Lys Lys Met Thr Thr Phe Glu | |
| 100 105 110 | |
| tat ctc att aat aac cgc aaa gaa gag agt tca aaa cat caa gca gtg | 384 |
| Tyr Leu Ile Asn Asn Arg Lys Glu Glu Ser Ser Lys His Gln Ala Val | |
| 115 120 125 | |
| agg aaa gat cca tac gtg caa atg gac aaa gga gtt ctc cag caa gga | 432 |
| Arg Lys Asp Pro Tyr Val Gln Met Asp Lys Gly Val Leu Gln Gln Gly | |
| 130 135 140 | |
| gct ggc gcc ctg ggc tca tct gca cag gga gtc aaa gcc aag agc tcc | 480 |
| Ala Gly Ala Leu Gly Ser Ser Ala Gln Gly Val Lys Ala Lys Ser Ser | |
| 145 150 155 160 | |
| ctg ctg att cac aag cac tta tgt cac ttc tgc act tca gta aac cag | 528 |
| Leu Leu Ile His Lys His Leu Cys His Phe Cys Thr Ser Val Asn Gln | |
| 165 170 175 | |
| gac ggg gat tcg aag gca cag gaa gca gat gat gcc ccg agt aca tct | 576 |
| Asp Gly Asp Ser Lys Ala Gln Glu Ala Asp Asp Ala Pro Ser Thr Ser | |
| 180 185 190 | |
| aca ctt ggg ctg caa caa gaa aca aca gag ccc atg aaa act gac agt | 624 |
| Thr Leu Gly Leu Gln Gln Glu Thr Thr Glu Pro Met Lys Thr Asp Ser | |
| 195 200 205 | |
| gct gaa agt gaa gac tga | 642 |
| Ala Glu Ser Glu Asp * | |
| 210 | |

409

<210> 278
 <211> 213
 <212> PRT
 <213> Homo sapiens

<400> 278
 Met Asp Gln Gln Leu Arg Gly Lys Pro Glu Leu Leu Val Phe Phe Ser
 1 5 10 15
 Thr Val Ala Ser Ala Thr Ala Gly Met Leu Cys Leu Ile Ala Ile Leu
 20 25 30
 Leu Tyr Val Leu Val Gln Tyr Leu Val Asn Pro Gly Val Leu Arg Thr
 35 40 45
 Asp Pro Arg Asp Val Lys Asn Met Asn Thr Trp Leu Leu Phe Leu Pro
 50 55 60
 Leu Phe Pro Val Gln Val Gln Thr Leu Ile Val Val Ile Ile Gly Met
 65 70 75 80
 Leu Val Leu Leu Leu Asp Phe Leu Gly Leu Val His Leu Gly Gln Leu
 85 90 95
 Leu Ile Phe His Ile Tyr Leu Lys Ala Lys Lys Met Thr Thr Phe Glu
 100 105 110
 Tyr Leu Ile Asn Asn Arg Lys Glu Glu Ser Ser Lys His Gln Ala Val
 115 120 125
 Arg Lys Asp Pro Tyr Val Gln Met Asp Lys Gly Val Leu Gln Gln Gly
 130 135 140
 Ala Gly Ala Leu Gly Ser Ser Ala Gln Gly Val Lys Ala Lys Ser Ser
 145 150 155 160
 Leu Leu Ile His Lys His Leu Cys His Phe Cys Thr Ser Val Asn Gln
 165 170 175
 Asp Gly Asp Ser Lys Ala Gln Glu Ala Asp Asp Ala Pro Ser Thr Ser
 180 185 190
 Thr Leu Gly Leu Gln Gln Glu Thr Thr Glu Pro Met Lys Thr Asp Ser
 195 200 205
 Ala Glu Ser Glu Asp
 210

<210> 279
 <211> 1194
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> (1)...(1194)

atg agc tgg ctt ttt ccc ctg acc aag agc gcc tcc tcc tcc gcg gct 48
Met Ser Trp Leu Phe Pro Leu Thr Lys Ser Ala Ser Ser Ser Ala Ala
1 5 10 15

ggg tcc ccc ggt ggc ctc acc agc ctc cag cag cag aag cag cgc ctg 96
Gly Ser Pro Gly Gly Leu Thr Ser Leu Gln Gln Gln Lys Gln Arg Leu
20 25 30

atc gag tcc ctc cgg aac tca cac tcc agt ata gcc gaa ata cag aaa 144
Ile Glu Ser Leu Arg Asn Ser His Ser Ser Ile Ala Glu Ile Gln Lys
35 40 45

gat gtg gaa tac aga ttg cca ttc acc ata aac aac ctg aca att aac 192
Asp Val Glu Tyr Arg Leu Pro Phe Thr Ile Asn Asn Leu Thr Ile Asn
50 55 60

att aat ata ttg ctt cct cca cag ttt cct cag gaa aaa cca gtg atc 240
Ile Asn Ile Leu Leu Pro Pro Gln Phe Pro Gln Glu Lys Pro Val Ile
65 70 75 80

agt gtt tat cca cca ata cga cat cac tta atg gat aaa caa gga gtg 288
Ser Val Tyr Pro Pro Ile Arg His His Leu Met Asp Lys Gln Gly Val
85 90 95

tat gtt acc tct cca tta gta aac aat ttt aca atg cac tca gat ctt 336
Tyr Val Thr Ser Pro Leu Val Asn Asn Phe Thr Met His Ser Asp Leu
100 105 110

gga aaa att att cag agt ctg ttg gat gag ttt tgg aag aat cct cca 384
Gly Lys Ile Ile Gln Ser Leu Leu Asp Glu Phe Trp Lys Asn Pro Pro
115 120 125

ggt tta gct cct act tca aca gca ttt cct tat cta tac agt aac cca 432
Val Leu Ala Pro Thr Ser Thr Ala Phe Pro Tyr Leu Tyr Ser Asn Pro
130 135 140

agt ggg atg tct cct tat gct tct cag ggt ttt cca ttt ctt cct cca 480
Ser Gly Met Ser Pro Tyr Ala Ser Gln Gly Phe Pro Phe Leu Pro Pro
145 150 155 160

tat cct cca caa gaa gca aac agg agt atc act tct tta tct gtt gct 528

411

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| Tyr | Pro | Pro | Gln | Glu | Ala | Asn | Arg | Ser | Ile | Thr | Ser | Leu | Ser | Val | Ala | | |
| | | | | 165 | | | | | 170 | | | | | 175 | | | |
| gac | act | gtt | tct | tct | tca | aca | aca | agt | cat | acc | aca | gcc | aag | cct | gcc | 576 | |
| Asp | Thr | Val | Ser | Ser | Ser | Thr | Thr | Ser | His | Thr | Thr | Ala | Lys | Pro | Ala | | |
| | | | 180 | | | | | 185 | | | | | 190 | | | | |
| gct | cct | tca | ttt | ggt | gtc | ctt | tca | aat | ctg | cca | tta | ccc | att | ccc | aca | 624 | |
| Ala | Pro | Ser | Phe | Gly | Val | Leu | Ser | Asn | Leu | Pro | Leu | Pro | Ile | Pro | Thr | | |
| | | 195 | | | | | 200 | | | | | 205 | | | | | |
| gtg | gat | gct | tca | ata | ccg | aca | agc | caa | aat | ggt | ttt | ggg | tac | aag | atg | 672 | |
| Val | Asp | Ala | Ser | Ile | Pro | Thr | Ser | Gln | Asn | Gly | Phe | Gly | Tyr | Lys | Met | | |
| | 210 | | | | | 215 | | | | | 220 | | | | | | |
| cca | gat | gtc | cct | gat | gca | ttt | cca | gaa | ctc | tca | gaa | cta | agt | gtg | tca | 720 | |
| Pro | Asp | Val | Pro | Asp | Ala | Phe | Pro | Glu | Leu | Ser | Glu | Leu | Ser | Val | Ser | | |
| 225 | | | | | 230 | | | | 235 | | | | | 240 | | | |
| caa | ctc | aca | gat | atg | aat | gaa | caa | gag | gag | gta | tta | cta | gaa | cag | ttt | 768 | |
| Gln | Leu | Thr | Asp | Met | Asn | Glu | Gln | Glu | Glu | Val | Leu | Leu | Glu | Gln | Phe | | |
| | | | 245 | | | | | 250 | | | | | | 255 | | | |
| ctg | act | ttg | cct | caa | cta | aaa | caa | att | att | acc | gac | aaa | gat | gac | tta | 816 | |
| Leu | Thr | Leu | Pro | Gln | Leu | Lys | Gln | Ile | Ile | Thr | Asp | Lys | Asp | Asp | Leu | | |
| | | 260 | | | | | 265 | | | | | | 270 | | | | |
| gta | aaa | agt | att | gag | gaa | cta | gca | aga | aaa | aat | ctc | ctt | ttg | gag | ccc | 864 | |
| Val | Lys | Ser | Ile | Glu | Glu | Leu | Ala | Arg | Lys | Asn | Leu | Leu | Leu | Glu | Pro | | |
| | | 275 | | | | | 280 | | | | | 285 | | | | | |
| agc | ttg | gaa | gcc | aaa | aga | caa | act | gtt | tta | gat | aag | tat | gaa | tta | ctt | 912 | |
| Ser | Leu | Glu | Ala | Lys | Arg | Gln | Thr | Val | Leu | Asp | Lys | Tyr | Glu | Leu | Leu | | |
| | 290 | | | | | 295 | | | | | 300 | | | | | | |
| aca | cag | atg | aag | tcc | act | ttc | gaa | aag | aag | atg | caa | agg | cag | cat | gaa | 960 | |
| Thr | Gln | Met | Lys | Ser | Thr | Phe | Glu | Lys | Lys | Met | Gln | Arg | Gln | His | Glu | | |
| 305 | | | | | 310 | | | | | 315 | | | | 320 | | | |
| ctt | agt | gag | agc | tgt | agt | gca | agt | gcc | ctt | cag | gca | aga | ttg | aaa | gta | 1008 | |
| Leu | Ser | Glu | Ser | Cys | Ser | Ala | Ser | Ala | Leu | Gln | Ala | Arg | Leu | Lys | Val | | |
| | | | 325 | | | | | 330 | | | | | 335 | | | | |
| gct | gca | cat | gaa | gct | gag | gaa | gaa | tct | gat | aat | att | gca | gaa | gac | ttc | 1056 | |

412

Ala Ala His Glu Ala Glu Glu Glu Ser Asp Asn Ile Ala Glu Asp Phe
 340 345 350

ttg gag gga aag atg gaa ata gat gat ttt ctc agt agc ttc atg gaa 1104
 Leu Glu Gly Lys Met Glu Ile Asp Asp Phe Leu Ser Ser Phe Met Glu
 355 360 365

aag aga aca att tgc cac tgt aga aga gcc aag gaa gag aaa ctt cag 1152
 Lys Arg Thr Ile Cys His Cys Arg Arg Ala Lys Glu Glu Lys Leu Gln
 370 375 380

cag gcg ata gca atg cac agc caa ttt cat gct cca cta tag 1194
 Gln Ala Ile Ala Met His Ser Gln Phe His Ala Pro Leu *
 385 390 395

<210> 280
 <211> 397
 <212> PRT
 <213> Homo sapiens

<400> 280

Met Ser Trp Leu Phe Pro Leu Thr Lys Ser Ala Ser Ser Ser Ala Ala
 1 5 10 15
 Gly Ser Pro Gly Gly Leu Thr Ser Leu Gln Gln Gln Lys Gln Arg Leu
 20 25 30
 Ile Glu Ser Leu Arg Asn Ser His Ser Ser Ile Ala Glu Ile Gln Lys
 35 40 45
 Asp Val Glu Tyr Arg Leu Pro Phe Thr Ile Asn Asn Leu Thr Ile Asn
 50 55 60
 Ile Asn Ile Leu Leu Pro Pro Gln Phe Pro Gln Glu Lys Pro Val Ile
 65 70 75 80
 Ser Val Tyr Pro Pro Ile Arg His His Leu Met Asp Lys Gln Gly Val
 85 90 95
 Tyr Val Thr Ser Pro Leu Val Asn Asn Phe Thr Met His Ser Asp Leu
 100 105 110
 Gly Lys Ile Ile Gln Ser Leu Leu Asp Glu Phe Trp Lys Asn Pro Pro
 115 120 125
 Val Leu Ala Pro Thr Ser Thr Ala Phe Pro Tyr Leu Tyr Ser Asn Pro
 130 135 140
 Ser Gly Met Ser Pro Tyr Ala Ser Gln Gly Phe Pro Phe Leu Pro Pro
 145 150 155 160
 Tyr Pro Pro Gln Glu Ala Asn Arg Ser Ile Thr Ser Leu Ser Val Ala
 165 170 175

413

Asp Thr Val Ser Ser Ser Thr Thr Ser His Thr Thr Ala Lys Pro Ala
 180 185 190
 Ala Pro Ser Phe Gly Val Leu Ser Asn Leu Pro Leu Pro Ile Pro Thr
 195 200 205
 Val Asp Ala Ser Ile Pro Thr Ser Gln Asn Gly Phe Gly Tyr Lys Met
 210 215 220
 Pro Asp Val Pro Asp Ala Phe Pro Glu Leu Ser Glu Leu Ser Val Ser
 225 230 235 240
 Gln Leu Thr Asp Met Asn Glu Gln Glu Glu Val Leu Leu Glu Gln Phe
 245 250 255
 Leu Thr Leu Pro Gln Leu Lys Gln Ile Ile Thr Asp Lys Asp Asp Leu
 260 265 270
 Val Lys Ser Ile Glu Glu Leu Ala Arg Lys Asn Leu Leu Leu Glu Pro
 275 280 285
 Ser Leu Glu Ala Lys Arg Gln Thr Val Leu Asp Lys Tyr Glu Leu Leu
 290 295 300
 Thr Gln Met Lys Ser Thr Phe Glu Lys Lys Met Gln Arg Gln His Glu
 305 310 315 320
 Leu Ser Glu Ser Cys Ser Ala Ser Ala Leu Gln Ala Arg Leu Lys Val
 325 330 335
 Ala Ala His Glu Ala Glu Glu Glu Ser Asp Asn Ile Ala Glu Asp Phe
 340 345 350
 Leu Glu Gly Lys Met Glu Ile Asp Asp Phe Leu Ser Ser Phe Met Glu
 355 360 365
 Lys Arg Thr Ile Cys His Cys Arg Arg Ala Lys Glu Glu Lys Leu Gln
 370 375 380
 Gln Ala Ile Ala Met His Ser Gln Phe His Ala Pro Leu
 385 390 395

<210> 281

<211> 579

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(579)

<400> 281

atg gcg gcg caa att cca att gtg gcc acc act tcc act ccc gga ata
 Met Ala Ala Gln Ile Pro Ile Val Ala Thr Thr Ser Thr Pro Gly Ile
 1 5 10 15

48

gtc cgg aac agc aag aag agg ccg gcc agc cct tcc cac aat ggc agc

96

415

*

<210> 282
 <211> 192
 <212> PRT
 <213> Homo sapiens

<400> 282
 Met Ala Ala Gln Ile Pro Ile Val Ala Thr Thr Ser Thr Pro Gly Ile
 1 5 10 15
 Val Arg Asn Ser Lys Lys Arg Pro Ala Ser Pro Ser His Asn Gly Ser
 20 25 30
 Ser Gly Gly Gly Tyr Gly Ala Ser Lys Lys Lys Lys Ala Ser Ala Ser
 35 40 45
 Ser Phe Ala Gln Gly Ile Ser Met Glu Ala Met Ser Glu Asn Lys Met
 50 55 60
 Val Pro Ser Glu Phe Ser Thr Gly Pro Val Glu Lys Ala Ala Lys Pro
 65 70 75 80
 Leu Pro Phe Lys Asp Pro Asn Phe Val His Ser Gly His Gly Gly Ala
 85 90 95
 Val Ala Gly Lys Lys Asn Arg Thr Trp Lys Asn Leu Lys Gln Ile Leu
 100 105 110
 Ala Ser Glu Arg Ala Leu Pro Trp Gln Leu Asn Asp Pro Asn Tyr Phe
 115 120 125
 Ser Ile Asp Ala Pro Pro Ser Phe Lys Pro Ala Lys Lys Tyr Ser Asp
 130 135 140
 Val Ser Gly Leu Leu Ala Asn Tyr Thr Asp Pro Gln Ser Lys Leu Arg
 145 150 155 160
 Phe Ser Thr Ile Glu Glu Phe Ser Tyr Ile Arg Arg Leu Pro Ser Asp
 165 170 175
 Val Val Thr Gly Tyr Leu Ala Leu Arg Lys Ala Thr Ser Ile Val Pro
 180 185 190

<210> 283
 <211> 948
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(948)

416

<400> 283

| | |
|---|-----|
| atg gcc tca gca gta ctt agt tct gtt ccc acc acc gct tct cgt ttt | 48 |
| Met Ala Ser Ala Val Leu Ser Ser Val Pro Thr Thr Ala Ser Arg Phe | |
| 1 5 10 15 | |
| gcc ctg tta caa gtg gat agt ggc agt ggc tct gat tct gaa cct gga | 96 |
| Ala Leu Leu Gln Val Asp Ser Gly Ser Gly Ser Asp Ser Glu Pro Gly | |
| 20 25 30 | |
| aaa ggt aaa ggt cga aat act gga aag tct caa act tta gga agc aag | 144 |
| Lys Gly Lys Gly Arg Asn Thr Gly Lys Ser Gln Thr Leu Gly Ser Lys | |
| 35 40 45 | |
| tca act aca aat gag aaa aaa aga gag aaa aga aga aaa aag aag gaa | 192 |
| Ser Thr Thr Asn Glu Lys Lys Arg Glu Lys Arg Arg Lys Lys Lys Glu | |
| 50 55 60 | |
| cag caa cag agt gaa gca aat gag ctc agg aat ctt gct ttt aag aaa | 240 |
| Gln Gln Gln Ser Glu Ala Asn Glu Leu Arg Asn Leu Ala Phe Lys Lys | |
| 65 70 75 80 | |
| att ccc cag aaa tcc tcc cat gct gtt tgt aac gct caa cat gat ctt | 288 |
| Ile Pro Gln Lys Ser Ser His Ala Val Cys Asn Ala Gln His Asp Leu | |
| 85 90 95 | |
| cca ttg tca aac cca gta cag aag gat tca cga gaa gaa aat tgg caa | 336 |
| Pro Leu Ser Asn Pro Val Gln Lys Asp Ser Arg Glu Glu Asn Trp Gln | |
| 100 105 110 | |
| gag tgg aga caa aga gat gag cag ctg aca tct gaa atg ttt gaa gca | 384 |
| Glu Trp Arg Gln Arg Asp Glu Gln Leu Thr Ser Glu Met Phe Glu Ala | |
| 115 120 125 | |
| gat ctt gag aag gca ttg tta cta agt aaa cta gaa tat gaa gag cac | 432 |
| Asp Leu Glu Lys Ala Leu Leu Leu Ser Lys Leu Glu Tyr Glu Glu His | |
| 130 135 140 | |
| aaa aag gag tat gaa gat gct gaa aat act tca act cag tcc aaa gtt | 480 |
| Lys Lys Glu Tyr Glu Asp Ala Glu Asn Thr Ser Thr Gln Ser Lys Val | |
| 145 150 155 160 | |
| atg aat aaa aaa gat aaa aga aag aat cat cag gga aaa gac aga cct | 528 |
| Met Asn Lys Lys Asp Lys Arg Lys Asn His Gln Gly Lys Asp Arg Pro | |
| 165 170 175 | |

417

| | |
|---|-----|
| ctc aca gta tca cta aaa gat ttt cat tcg gaa gat cac att agt aaa | 576 |
| Leu Thr Val Ser Leu Lys Asp Phe His Ser Glu Asp His Ile Ser Lys | |
| 180 185 190 | |
| aag act gag gaa gtg gtt ctg aaa gat gga aga att gaa aga cta aag | 624 |
| Lys Thr Glu Glu Val Val Leu Lys Asp Gly Arg Ile Glu Arg Leu Lys | |
| 195 200 205 | |
| tta gag ctt gaa agg aaa gat gct gaa atc cag aag ctg aaa aat gta | 672 |
| Leu Glu Leu Glu Arg Lys Asp Ala Glu Ile Gln Lys Leu Lys Asn Val | |
| 210 215 220 | |
| atc act caa tgg gag gca aag tat aag gaa gta aag gca aga aat gca | 720 |
| Ile Thr Gln Trp Glu Ala Lys Tyr Lys Glu Val Lys Ala Arg Asn Ala | |
| 225 230 235 240 | |
| caa tta ttg aaa atg ctt cag gaa ggt gaa atg aaa gat aag gca gaa | 768 |
| Gln Leu Leu Lys Met Leu Gln Glu Gly Glu Met Lys Asp Lys Ala Glu | |
| 245 250 255 | |
| ata ctt ctg caa gtt gat gaa tca caa agt atc aag aat gag ctc act | 816 |
| Ile Leu Leu Gln Val Asp Glu Ser Gln Ser Ile Lys Asn Glu Leu Thr | |
| 260 265 270 | |
| att cag gtg act tca ctt cat gct gca tta gaa caa gaa aga tct aaa | 864 |
| Ile Gln Val Thr Ser Leu His Ala Ala Leu Glu Gln Glu Arg Ser Lys | |
| 275 280 285 | |
| gtg aaa gta tta caa gca gag tta gcc aaa tac cag ggt ggc aga aaa | 912 |
| Val Lys Val Leu Gln Ala Glu Leu Ala Lys Tyr Gln Gly Gly Arg Lys | |
| 290 295 300 | |
| ggg aaa aga aac tct gaa tcc gac cag tgt agg tga | 948 |
| Gly Lys Arg Asn Ser Glu Ser Asp Gln Cys Arg * | |
| 305 310 315 | |

<210> 284

<211> 315

<212> PRT

<213> Homo sapiens

<400> 284

418

Met Ala Ser Ala Val Leu Ser Ser Val Pro Thr Thr Ala Ser Arg Phe
 1 5 10 15
 Ala Leu Leu Gln Val Asp Ser Gly Ser Gly Ser Asp Ser Glu Pro Gly
 20 25 30
 Lys Gly Lys Gly Arg Asn Thr Gly Lys Ser Gln Thr Leu Gly Ser Lys
 35 40 45
 Ser Thr Thr Asn Glu Lys Lys Arg Glu Lys Arg Arg Lys Lys Lys Glu
 50 55 60
 Gln Gln Gln Ser Glu Ala Asn Glu Leu Arg Asn Leu Ala Phe Lys Lys
 65 70 75 80
 Ile Pro Gln Lys Ser Ser His Ala Val Cys Asn Ala Gln His Asp Leu
 85 90 95
 Pro Leu Ser Asn Pro Val Gln Lys Asp Ser Arg Glu Glu Asn Trp Gln
 100 105 110
 Glu Trp Arg Gln Arg Asp Glu Gln Leu Thr Ser Glu Met Phe Glu Ala
 115 120 125
 Asp Leu Glu Lys Ala Leu Leu Leu Ser Lys Leu Glu Tyr Glu Glu His
 130 135 140
 Lys Lys Glu Tyr Glu Asp Ala Glu Asn Thr Ser Thr Gln Ser Lys Val
 145 150 155 160
 Met Asn Lys Lys Asp Lys Arg Lys Asn His Gln Gly Lys Asp Arg Pro
 165 170 175
 Leu Thr Val Ser Leu Lys Asp Phe His Ser Glu Asp His Ile Ser Lys
 180 185 190
 Lys Thr Glu Glu Val Val Leu Lys Asp Gly Arg Ile Glu Arg Leu Lys
 195 200 205
 Leu Glu Leu Glu Arg Lys Asp Ala Glu Ile Gln Lys Leu Lys Asn Val
 210 215 220
 Ile Thr Gln Trp Glu Ala Lys Tyr Lys Glu Val Lys Ala Arg Asn Ala
 225 230 235 240
 Gln Leu Leu Lys Met Leu Gln Glu Gly Glu Met Lys Asp Lys Ala Glu
 245 250 255
 Ile Leu Leu Gln Val Asp Glu Ser Gln Ser Ile Lys Asn Glu Leu Thr
 260 265 270
 Ile Gln Val Thr Ser Leu His Ala Ala Leu Glu Gln Glu Arg Ser Lys
 275 280 285
 Val Lys Val Leu Gln Ala Glu Leu Ala Lys Tyr Gln Gly Gly Arg Lys
 290 295 300
 Gly Lys Arg Asn Ser Glu Ser Asp Gln Cys Arg
 305 310 315

<210> 285

<211> 1308

<212> DNA

419

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1308)

<400> 285

| | |
|---|-----|
| atg ggc acc tct gtc acc ggc ttg tat cca gag ctg ttc act ctc ctc | 48 |
| Met Gly Thr Ser Val Thr Gly Leu Tyr Pro Glu Leu Phe Thr Leu Leu | |
| 1 5 10 15 | |
| ctg aag ctg gtt agc tgc aca ctg ggc cag aag atg ccc act tgt ccc | 96 |
| Leu Lys Leu Val Ser Cys Thr Leu Gly Gln Lys Met Pro Thr Cys Pro | |
| 20 25 30 | |
| tgg agc cat agg cgg cat gtg atg cag cag gga gaa cag cag cag atc | 144 |
| Trp Ser His Arg Arg His Val Met Gln Gln Gly Glu Gln Gln Gln Ile | |
| 35 40 45 | |
| cca gac ccc tgc agg ctt tca act gct act tta aaa tgt ttg caa gcc | 192 |
| Pro Asp Pro Cys Arg Leu Ser Thr Ala Thr Leu Lys Cys Leu Gln Ala | |
| 50 55 60 | |
| caa gcc atg aga gaa ggc ctt gca aag gaa tct gat gag ggg gac aac | 240 |
| Gln Ala Met Arg Glu Gly Leu Ala Lys Glu Ser Asp Glu Gly Asp Asn | |
| 65 70 75 80 | |
| tta tgg act cta ctc agc agt cct agt acc cac cac ata ggc gta tgt | 288 |
| Leu Trp Thr Leu Leu Ser Ser Pro Ser Thr His His Ile Gly Val Cys | |
| 85 90 95 | |
| tca ctg gcc agg agc atg gca gtg tgg caa cac gga gtc ata ctg gac | 336 |
| Ser Leu Ala Arg Ser Met Ala Val Trp Gln His Gly Val Ile Leu Asp | |
| 100 105 110 | |
| atc atg gaa cag ctg ctc tca tct ctt acc tcc tcc tcg gag aac tac | 384 |
| Ile Met Glu Gln Leu Leu Ser Ser Leu Thr Ser Ser Ser Glu Asn Tyr | |
| 115 120 125 | |
| cgg ata acc ggc gca gct ttc ttc tct gag ctc atg aag gaa cca atc | 432 |
| Arg Ile Thr Gly Ala Ala Phe Phe Ser Glu Leu Met Lys Glu Pro Ile | |
| 130 135 140 | |
| ctt tgg aag cat ggg aat ctg cga aat gtg ctg atc ttg atg gat caa | 480 |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| Leu | Trp | Lys | His | Gly | Asn | Leu | Arg | Asn | Val | Leu | Ile | Leu | Met | Asp | Gln | |
| 145 | | | | | 150 | | | | 155 | | | | | | 160 | |
| agt | gcc | tgg | gac | tcc | aac | gcc | act | ctg | agg | cag | atg | gcc | atc | cga | ggg | 528 |
| Ser | Ala | Trp | Asp | Ser | Asn | Ala | Thr | Leu | Arg | Gln | Met | Ala | Ile | Arg | Gly | |
| | | | | 165 | | | | 170 | | | | | | 175 | | |
| ctc | ggc | aac | aca | gca | tcc | ggg | gct | cct | cac | aag | gtg | aag | aaa | cat | aag | 576 |
| Leu | Gly | Asn | Thr | Ala | Ser | Gly | Ala | Pro | His | Lys | Val | Lys | Lys | His | Lys | |
| | | | | 180 | | | | 185 | | | | | | 190 | | |
| cag | tta | atg | cta | gaa | tct | atc | atc | aga | ggc | ctg | tat | cac | cta | gct | cgc | 624 |
| Gln | Leu | Met | Leu | Glu | Ser | Ile | Ile | Arg | Gly | Leu | Tyr | His | Leu | Ala | Arg | |
| | | | | 195 | | | | 200 | | | | | | 205 | | |
| act | gaa | gtc | gtc | tgt | gaa | agc | ttg | aag | gct | cta | aaa | aaa | atc | ctg | gag | 672 |
| Thr | Glu | Val | Val | Cys | Glu | Ser | Leu | Lys | Ala | Leu | Lys | Lys | Ile | Leu | Glu | |
| | | | | 210 | | | | 215 | | | | | | 220 | | |
| ctg | ctg | aca | gac | cga | gac | gtg | agc | ttc | tac | ttc | aag | gaa | ata | gtg | ctg | 720 |
| Leu | Leu | Thr | Asp | Arg | Asp | Val | Ser | Phe | Tyr | Phe | Lys | Glu | Ile | Val | Leu | |
| | | | | | 225 | | | | | 235 | | | | | 240 | |
| caa | aca | agg | acc | ttc | ttt | gaa | gat | gag | cag | gat | gat | gtg | aga | ttg | act | 768 |
| Gln | Thr | Arg | Thr | Phe | Phe | Glu | Asp | Glu | Gln | Asp | Asp | Val | Arg | Leu | Thr | |
| | | | | 245 | | | | | 250 | | | | | | 255 | |
| gcc | atc | ttc | tta | ttt | gag | gac | ctg | gca | ccc | cta | aca | gga | aga | agg | tgg | 816 |
| Ala | Ile | Phe | Leu | Phe | Glu | Asp | Leu | Ala | Pro | Leu | Thr | Gly | Arg | Arg | Trp | |
| | | | | 260 | | | | 265 | | | | | | 270 | | |
| aag | att | ttt | ttt | gct | gaa | gaa | ata | aaa | aag | agc | ctg | att | tca | ttc | ctt | 864 |
| Lys | Ile | Phe | Phe | Ala | Glu | Glu | Ile | Lys | Lys | Ser | Leu | Ile | Ser | Phe | Leu | |
| | | | | 275 | | | | 280 | | | | | | 285 | | |
| ctg | cac | ctt | tgg | gat | ccc | aac | ccc | aag | att | gga | gtt | gct | tgc | cgt | gat | 912 |
| Leu | His | Leu | Trp | Asp | Pro | Asn | Pro | Lys | Ile | Gly | Val | Ala | Cys | Arg | Asp | |
| | | | | 290 | | | | 295 | | | | | | 300 | | |
| gtc | ttg | atg | gtc | tgc | att | ccc | ttt | ttg | ggc | ctc | cag | gag | ctc | tat | ggg | 960 |
| Val | Leu | Met | Val | Cys | Ile | Pro | Phe | Leu | Gly | Leu | Gln | Glu | Leu | Tyr | Gly | |
| | | | | | 305 | | | | | 315 | | | | | 320 | |
| gtg | tta | gac | cgt | ctc | ctt | gat | cag | gat | cta | cca | agg | gcc | agg | gat | ttc | 1008 |

[illegible]

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<210> 286
<211> 435
<212> PRT
<213> Homo sapiens
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<400> 286

Met Gly Thr Ser Val Thr Gly Leu Tyr Pro Glu Leu Phe Thr Leu Leu
1 5 10 15
Leu Lys Leu Val Ser Cys Thr Leu Gly Gln Lys Met Pro Thr Cys Pro
20 25 30
Trp Ser His Arg Arg His Val Met Gln Gln Gly Glu Gln Gln Ile
35 40 45

422

Pro Asp Pro Cys Arg Leu Ser Thr Ala Thr Leu Lys Cys Leu Gln Ala
 50 55 60
 Gln Ala Met Arg Glu Gly Leu Ala Lys Glu Ser Asp Glu Gly Asp Asn
 65 70 75 80
 Leu Trp Thr Leu Leu Ser Ser Pro Ser Thr His His Ile Gly Val Cys
 85 90 95
 Ser Leu Ala Arg Ser Met Ala Val Trp Gln His Gly Val Ile Leu Asp
 100 105 110
 Ile Met Glu Gln Leu Leu Ser Ser Leu Thr Ser Ser Ser Glu Asn Tyr
 115 120 125
 Arg Ile Thr Gly Ala Ala Phe Phe Ser Glu Leu Met Lys Glu Pro Ile
 130 135 140
 Leu Trp Lys His Gly Asn Leu Arg Asn Val Leu Ile Leu Met Asp Gln
 145 150 155 160
 Ser Ala Trp Asp Ser Asn Ala Thr Leu Arg Gln Met Ala Ile Arg Gly
 165 170 175
 Leu Gly Asn Thr Ala Ser Gly Ala Pro His Lys Val Lys Lys His Lys
 180 185 190
 Gln Leu Met Leu Glu Ser Ile Ile Arg Gly Leu Tyr His Leu Ala Arg
 195 200 205
 Thr Glu Val Val Cys Glu Ser Leu Lys Ala Leu Lys Lys Ile Leu Glu
 210 215 220
 Leu Leu Thr Asp Arg Asp Val Ser Phe Tyr Phe Lys Glu Ile Val Leu
 225 230 235 240
 Gln Thr Arg Thr Phe Phe Glu Asp Glu Gln Asp Asp Val Arg Leu Thr
 245 250 255
 Ala Ile Phe Leu Phe Glu Asp Leu Ala Pro Leu Thr Gly Arg Arg Trp
 260 265 270
 Lys Ile Phe Phe Ala Glu Glu Ile Lys Lys Ser Leu Ile Ser Phe Leu
 275 280 285
 Leu His Leu Trp Asp Pro Asn Pro Lys Ile Gly Val Ala Cys Arg Asp
 290 295 300
 Val Leu Met Val Cys Ile Pro Phe Leu Gly Leu Gln Glu Leu Tyr Gly
 305 310 315 320
 Val Leu Asp Arg Leu Leu Asp Gln Asp Leu Pro Arg Ala Arg Asp Phe
 325 330 335
 Tyr Arg Gln Phe Cys Val Lys Leu Ala Lys Lys Asn Gln Glu Ile Leu
 340 345 350
 Trp Ile Leu His Thr His Ser Phe Thr Phe Phe Thr Ser Thr Trp Glu
 355 360 365
 Val Ile Arg Ser Ala Ala Val Lys Leu Thr Asp Ala Val Val Leu Asn
 370 375 380
 Leu Thr Ser Gln Tyr Val Glu Leu Leu Asp Arg Glu Gln Leu Thr Thr
 385 390 395 400

423

Arg Leu Gln Ala Leu Arg Gln Asp Pro Cys Ile Ser Val Gln Arg Ala
405 410 415
Ala Glu Ala Ala Leu Gln Thr Leu Leu Arg Arg Cys Lys Glu Thr Ser
420 425 430
Ile Pro Leu
435

<210> 287
<211> 822
<212> DNA
<213> Homo sapiens

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<220>  
<221> CDS  
<222> (1)...(822)
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| | | | | | | | | | | | | | | | | |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> 287 | | | | | | | | | | | | | | | | |
| atg | gat | ccc | gta | ccc | ggg | aca | gac | tcg | gcg | ccg | ctg | gct | ggc | ctg | gcc | 48 |
| Met | Asp | Pro | Val | Pro | Gly | Thr | Asp | Ser | Ala | Pro | Leu | Ala | Gly | Leu | Ala | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| | | | | | | | | | | | | | | | | |
| tgg | tcg | tcg | gcc | tct | gca | ccc | ccg | ccg | cgg | ggg | ttc | agc | gcg | atc | tcc | 96 |
| Trp | Ser | Ser | Ala | Ser | Ala | Pro | Pro | Pro | Arg | Gly | Phe | Ser | Ala | Ile | Ser | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| | | | | | | | | | | | | | | | | |
| tgc | acc | gtc | gag | ggg | gca | ccc | gcc | agc | ttt | ggc | aag | agc | ttc | gcg | cag | 144 |
| Cys | Thr | Val | Glu | Gly | Ala | Pro | Ala | Ser | Phe | Gly | Lys | Ser | Phe | Ala | Gln | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| | | | | | | | | | | | | | | | | |
| aaa | tct | ggc | tac | ttc | ctg | tgc | ctt | agt | tct | ctg | ggc | agc | cta | gag | aac | 192 |
| Lys | Ser | Gly | Tyr | Phe | Leu | Cys | Leu | Ser | Ser | Leu | Gly | Ser | Leu | Glu | Asn | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| | | | | | | | | | | | | | | | | |
| ccg | cag | gag | aac | gtg | gtg | gcc | gat | atc | cag | atc | gtg | gtg | gac | aag | agc | 240 |
| Pro | Gln | Glu | Asn | Val | Val | Ala | Asp | Ile | Gln | Ile | Val | Val | Asp | Lys | Ser | |
| 65 | | | | | 70 | | | | | 75 | | | | 80 | | |
| | | | | | | | | | | | | | | | | |
| ccc | ctg | ccg | ctg | ggc | ttc | tcc | ccc | gtc | tgc | gac | ccc | atg | gat | tcc | aag | 288 |
| Pro | Leu | Pro | Leu | Gly | Phe | Ser | Pro | Val | Cys | Asp | Pro | Met | Asp | Ser | Lys | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| | | | | | | | | | | | | | | | | |
| gcc | tct | gtg | tcc | aag | aag | aaa | cgc | atg | tgt | gtg | aag | ctg | ttg | ccc | ctg | 336 |
| Ala | Ser | Val | Ser | Lys | Lys | Lys | Arg | Met | Cys | Val | Lys | Leu | Leu | Pro | Leu | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |

424

| | |
|---|-----|
| gga gcc acg gac acg gct gtg ttt gat gtc cgg ctg agt ggg aag acc Gly Ala Thr Asp Thr Ala Val Phe Asp Val Arg Leu Ser Gly Lys Thr 115 120 125 | 384 |
| aag aca gtg cct gga tac ctt cga ata ggg gac atg ggc ggc ttt gcc Lys Thr Val Pro Gly Tyr Leu Arg Ile Gly Asp Met Gly Gly Phe Ala 130 135 140 | 432 |
| atc tgg tgc aag aag gcc aag gcc ccg agg cca gtg ccc aag ccc cga Ile Trp Cys Lys Lys Ala Lys Ala Pro Arg Pro Val Pro Lys Pro Arg 145 150 155 160 | 480 |
| ggc ctc agc cgg gac atg cag ggc ctc tct ctg gat gca gcc agc cag Gly Leu Ser Arg Asp Met Gln Gly Leu Ser Leu Asp Ala Ala Ser Gln 165 170 175 | 528 |
| cca agt aag ggc ggc ctc ctg gag cgg aca gcg tca agg ctg ggc tct Pro Ser Lys Gly Gly Leu Leu Glu Arg Thr Ala Ser Arg Leu Gly Ser 180 185 190 | 576 |
| cgg gca tcc act ctg cgg agg aat gac tcc atc tac gag gcc tcc agc Arg Ala Ser Thr Leu Arg Arg Asn Asp Ser Ile Tyr Glu Ala Ser Ser 195 200 205 | 624 |
| ctc tat ggc atc tca gcc atg gat ggg gtt ccc ttc aca ctc cac cca Leu Tyr Gly Ile Ser Ala Met Asp Gly Val Pro Phe Thr Leu His Pro 210 215 220 | 672 |
| cga ttt gag ggc aag agc tgc agc ccc ctg gcc ttc tct gct ttt ggg Arg Phe Glu Gly Lys Ser Cys Ser Pro Leu Ala Phe Ser Ala Phe Gly 225 230 235 240 | 720 |
| gac ctg acc atc aag tct ctg gcg gac att gag gag gag tat aac tac Asp Leu Thr Ile Lys Ser Leu Ala Asp Ile Glu Glu Glu Tyr Asn Tyr 245 250 255 | 768 |
| ggc ttc gtg gtg gag aag acc gcg gct gcc cgc ctg ccc ccc agc gtc Gly Phe Val Val Glu Lys Thr Ala Ala Ala Arg Leu Pro Pro Ser Val 260 265 270 | 816 |
| tca tag Ser * | 822 |

425

<210> 288
 <211> 273
 <212> PRT
 <213> Homo sapiens

<400> 288

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Met Asp Pro Val Pro Gly Thr Asp Ser Ala Pro Leu Ala Gly Leu Ala
 1          5          10          15
Trp Ser Ser Ala Ser Ala Pro Pro Pro Arg Gly Phe Ser Ala Ile Ser
          20          25          30
Cys Thr Val Glu Gly Ala Pro Ala Ser Phe Gly Lys Ser Phe Ala Gln
          35          40          45
Lys Ser Gly Tyr Phe Leu Cys Leu Ser Ser Leu Gly Ser Leu Glu Asn
          50          55          60
Pro Gln Glu Asn Val Val Ala Asp Ile Gln Ile Val Val Asp Lys Ser
65          70          75          80
Pro Leu Pro Leu Gly Phe Ser Pro Val Cys Asp Pro Met Asp Ser Lys
          85          90          95
Ala Ser Val Ser Lys Lys Lys Arg Met Cys Val Lys Leu Leu Pro Leu
          100          105          110
Gly Ala Thr Asp Thr Ala Val Phe Asp Val Arg Leu Ser Gly Lys Thr
          115          120          125
Lys Thr Val Pro Gly Tyr Leu Arg Ile Gly Asp Met Gly Gly Phe Ala
          130          135          140
Ile Trp Cys Lys Lys Ala Lys Ala Pro Arg Pro Val Pro Lys Pro Arg
          145          150          155          160
Gly Leu Ser Arg Asp Met Gln Gly Leu Ser Leu Asp Ala Ala Ser Gln
          165          170          175
Pro Ser Lys Gly Gly Leu Leu Glu Arg Thr Ala Ser Arg Leu Gly Ser
          180          185          190
Arg Ala Ser Thr Leu Arg Arg Asn Asp Ser Ile Tyr Glu Ala Ser Ser
          195          200          205
Leu Tyr Gly Ile Ser Ala Met Asp Gly Val Pro Phe Thr Leu His Pro
          210          215          220
Arg Phe Glu Gly Lys Ser Cys Ser Pro Leu Ala Phe Ser Ala Phe Gly
          225          230          235          240
Asp Leu Thr Ile Lys Ser Leu Ala Asp Ile Glu Glu Glu Tyr Asn Tyr
          245          250          255
Gly Phe Val Val Glu Lys Thr Ala Ala Ala Arg Leu Pro Pro Ser Val
          260          265          270
Ser

```

426

<210> 289
 <211> 744
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(744)

<400> 289
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 Met Pro Gly Arg Ser Ser Ser Asn Ser Gly Ser Thr Gly Phe Ile Ser
 1 5 10 15
 ttc agt ggt gta gag tct gct ctc tcc tcc ttg aaa aac ttc caa gcc 96
 Phe Ser Gly Val Glu Ser Ala Leu Ser Ser Leu Lys Asn Phe Gln Ala
 20 25 30
 tgt atc aac tct ggt atg gac aca gct tct agt gtt gct ttg gat ctt 144
 Cys Ile Asn Ser Gly Met Asp Thr Ala Ser Ser Val Ala Leu Asp Leu
 35 40 45
 gtg gaa agt cag act gaa gtg agt agt gaa tat agt atg gac aag gca 192
 Val Glu Ser Gln Thr Glu Val Ser Ser Glu Tyr Ser Met Asp Lys Ala
 50 55 60
 atg gtt gaa ttt gct aca ttg gat cgg caa cta aac cat tat gta aag 240
 Met Val Glu Phe Ala Thr Leu Asp Arg Gln Leu Asn His Tyr Val Lys
 65 70 75 80
 gct gtt caa tct aca ata aat cat gtg aaa gaa gaa cgt cca gaa aaa 288
 Ala Val Gln Ser Thr Ile Asn His Val Lys Glu Glu Arg Pro Glu Lys
 85 90 95
 ata cca gat tta aaa tta ttg gta gag aag aaa ttt ttg gct tta cag 336
 Ile Pro Asp Leu Lys Leu Leu Val Glu Lys Lys Phe Leu Ala Leu Gln
 100 105 110
 agc aag aat tct gat gca gac ttt caa aat aat gaa aaa ttt gta cag 384
 Ser Lys Asn Ser Asp Ala Asp Phe Gln Asn Asn Glu Lys Phe Val Gln
 115 120 125
 ttt aaa caa cag ctg aaa gaa cta aag aag caa tgt ggt ctt caa gct 432

427

Phe Lys Gln Gln Leu Lys Glu Leu Lys Lys Gln Cys Gly Leu Gln Ala
 130 135 140
 gac aga gaa gct gac gga aca gaa gga gtg gat gaa gat ata att gtg 480
 Asp Arg Glu Ala Asp Gly Thr Glu Gly Val Asp Glu Asp Ile Ile Val
 145 150 155 160
 acc caa agt cag acc aac ttc acc tgc ccc att aca aag gag gaa atg 528
 Thr Gln Ser Gln Thr Asn Phe Thr Cys Pro Ile Thr Lys Glu Glu Met
 165 170 175
 aag aag cca gtg aaa aat aaa gtg tgt ggc cac acc tat gaa gag gac 576
 Lys Lys Pro Val Lys Asn Lys Val Cys Gly His Thr Tyr Glu Glu Asp
 180 185 190
 gcc att gtt cgc atg att gag tcc agg caa aag cgg aag aaa aag gcc 624
 Ala Ile Val Arg Met Ile Glu Ser Arg Gln Lys Arg Lys Lys Lys Ala
 195 200 205
 tat tgc cct caa att ggc tgt agc cac acg gat ata aga aag tca gat 672
 Tyr Cys Pro Gln Ile Gly Cys Ser His Thr Asp Ile Arg Lys Ser Asp
 210 215 220
 ctt atc cag gat gaa gca ctt aga agg gca att gag aac cat aac aag 720
 Leu Ile Gln Asp Glu Ala Leu Arg Arg Ala Ile Glu Asn His Asn Lys
 225 230 235 240
 aaa aga cat cgt cat tcc gag tag 744
 Lys Arg His Arg His Ser Glu *
 245

<210> 290

<211> 247

<212> PRT

<213> Homo sapiens

<400> 290

Met Pro Gly Arg Ser Ser Ser Asn Ser Gly Ser Thr Gly Phe Ile Ser
 1 5 10 15
 Phe Ser Gly Val Glu Ser Ala Leu Ser Ser Leu Lys Asn Phe Gln Ala
 20 25 30
 Cys Ile Asn Ser Gly Met Asp Thr Ala Ser Ser Val Ala Leu Asp Leu
 35 40 45

428

Val Glu Ser Gln Thr Glu Val Ser Ser Glu Tyr Ser Met Asp Lys Ala
 50 55 60
 Met Val Glu Phe Ala Thr Leu Asp Arg Gln Leu Asn His Tyr Val Lys
 65 70 75 80
 Ala Val Gln Ser Thr Ile Asn His Val Lys Glu Glu Arg Pro Glu Lys
 85 90 95
 Ile Pro Asp Leu Lys Leu Leu Val Glu Lys Lys Phe Leu Ala Leu Gln
 100 105 110
 Ser Lys Asn Ser Asp Ala Asp Phe Gln Asn Asn Glu Lys Phe Val Gln
 115 120 125
 Phe Lys Gln Gln Leu Lys Glu Leu Lys Lys Gln Cys Gly Leu Gln Ala
 130 135 140
 Asp Arg Glu Ala Asp Gly Thr Glu Gly Val Asp Glu Asp Ile Ile Val
 145 150 155 160
 Thr Gln Ser Gln Thr Asn Phe Thr Cys Pro Ile Thr Lys Glu Glu Met
 165 170 175
 Lys Lys Pro Val Lys Asn Lys Val Cys Gly His Thr Tyr Glu Glu Asp
 180 185 190
 Ala Ile Val Arg Met Ile Glu Ser Arg Gln Lys Arg Lys Lys Lys Ala
 195 200 205
 Tyr Cys Pro Gln Ile Gly Cys Ser His Thr Asp Ile Arg Lys Ser Asp
 210 215 220
 Leu Ile Gln Asp Glu Ala Leu Arg Arg Ala Ile Glu Asn His Asn Lys
 225 230 235 240
 Lys Arg His Arg His Ser Glu
 245

<210> 291

<211> 957

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(957)

<221> misc_feature

<222> (1)...(957)

<223> n = A,T,C or G

<400> 291

atg gct gag cac gca ggg ccc cga ctc ccc ctg gtg ctg aag acg ctg
 Met Ala Glu His Ala Gly Pro Arg Leu Pro Leu Val Leu Lys Thr Leu
 1 5 10 15

48

429

| | |
|---|-----|
| gca tgc aca cac agc agt gcg tat gag aac cag agg gtg acc acc acc Ala Cys Thr His Ser Ser Ala Tyr Glu Asn Gln Arg Val Thr Thr Thr 20 25 30 | 96 |
| gcc ttc ctg gcc gag ctg ctg aac agc aac gtg gcc aac gac ctc atg Ala Phe Leu Ala Glu Leu Leu Asn Ser Asn Val Ala Asn Asp Leu Met 35 40 45 | 144 |
| ctc ttg gac tcg ctg ctg gag agc ctg gcg gct cgc cag aag gac aca Leu Leu Asp Ser Leu Leu Glu Ser Leu Ala Ala Arg Gln Lys Asp Thr 50 55 60 | 192 |
| tgc gcc anc gtg cgg agg ctg gtg ctc cgc ggc ctg gcc aac ctg gcc Cys Ala Xaa Val Arg Arg Leu Val Leu Arg Gly Leu Ala Asn Leu Ala 65 70 75 80 | 240 |
| tcc ggc tgc cct gac aag gtg cga acc cac ggc ccc cag ctc ctc aca Ser Gly Cys Pro Asp Lys Val Arg Thr His Gly Pro Gln Leu Leu Thr 85 90 95 | 288 |
| gcc atg att ggc ggg ctg gac gac ggg gac aac cct cac agc cca gtg Ala Met Ile Gly Gly Leu Asp Asp Gly Asp Asn Pro His Ser Pro Val 100 105 110 | 336 |
| gcc ctg gag gcc atg ctg ggc ctt gcg agg ctg gtg cac ctg gtg gag Ala Leu Glu Ala Met Leu Gly Leu Ala Arg Leu Val His Leu Val Glu 115 120 125 | 384 |
| tcc tgg gac ctg cgc tca ggg ctg ctg cac gtg gcc atc cgc atc cgg Ser Trp Asp Leu Arg Ser Gly Leu Leu His Val Ala Ile Arg Ile Arg 130 135 140 | 432 |
| cct ttc ttc gac agt gag aag atg gag ttc cgg acg gca tct atc cgc Pro Phe Phe Asp Ser Glu Lys Met Glu Phe Arg Thr Ala Ser Ile Arg 145 150 155 160 | 480 |
| ctc ttt ggg cac ctt aac aag gtc tgc cac gga gac tgt gag gac gtc Leu Phe Gly His Leu Asn Lys Val Cys His Gly Asp Cys Glu Asp Val 165 170 175 | 528 |
| ttc ctg gac cag gtg gtg ggc ggg ctg gcg ccc ctg ctg ctg cac ctg Phe Leu Asp Gln Val Val Gly Gly Leu Ala Pro Leu Leu Leu His Leu 180 185 190 | 576 |

430

| | |
|---|-----|
| cag gac cct cag gcc acc gtg gcc agc gcc tgc agg ttt gcc ctg cgc | 624 |
| Gln Asp Pro Gln Ala Thr Val Ala Ser Ala Cys Arg Phe Ala Leu Arg | |
| 195 200 205 | |
| atg tgt ggc ccc aat ctg gca tgt gag gag ctc tca gct gct ttc cag | 672 |
| Met Cys Gly Pro Asn Leu Ala Cys Glu Glu Leu Ser Ala Ala Phe Gln | |
| 210 215 220 | |
| aaa cac ctg cag gag ggc cga gcc ctg cac ttc ggg gag ttc ctc aac | 720 |
| Lys His Leu Gln Glu Gly Arg Ala Leu His Phe Gly Glu Phe Leu Asn | |
| 225 230 235 240 | |
| acc acc tgc aag cac ctg atg cac cat ttc cca gac ctg ctg ggc cgt | 768 |
| Thr Thr Cys Lys His Leu Met His His Phe Pro Asp Leu Leu Gly Arg | |
| 245 250 255 | |
| ctc ctg acc acc tgc ctg ttc tac ttc aag agc agc tgg gag aac gtc | 816 |
| Leu Leu Thr Thr Cys Leu Phe Tyr Phe Lys Ser Ser Trp Glu Asn Val | |
| 260 265 270 | |
| cga gct gct gca ccc ctg ttc acc ggg ttc ctg gtg ctg cac tcg gag | 864 |
| Arg Ala Ala Ala Pro Leu Phe Thr Gly Phe Leu Val Leu His Ser Glu | |
| 275 280 285 | |
| ccc agg cag cag ccg cag gtg gac ctg gac cag ctc att gcg ggt gag | 912 |
| Pro Arg Gln Gln Pro Gln Val Asp Leu Asp Gln Leu Ile Ala Gly Glu | |
| 290 295 300 | |
| cac ccc tcc acg ggg ccc ctc cgc tgg gcc ctg ctg acc ctg tag | 957 |
| His Pro Ser Thr Gly Pro Leu Arg Trp Ala Leu Leu Thr Leu * | |
| 305 310 315 | |

<210> 292

<211> 318

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

431

<400> 292

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Met Ala Glu His Ala Gly Pro Arg Leu Pro Leu Val Leu Lys Thr Leu
 1           5           10           15
Ala Cys Thr His Ser Ser Ala Tyr Glu Asn Gln Arg Val Thr Thr Thr
          20           25           30
Ala Phe Leu Ala Glu Leu Leu Asn Ser Asn Val Ala Asn Asp Leu Met
          35           40           45
Leu Leu Asp Ser Leu Leu Glu Ser Leu Ala Ala Arg Gln Lys Asp Thr
          50           55           60
Cys Ala Xaa Val Arg Arg Leu Val Leu Arg Gly Leu Ala Asn Leu Ala
65           70           75           80
Ser Gly Cys Pro Asp Lys Val Arg Thr His Gly Pro Gln Leu Leu Thr
          85           90           95
Ala Met Ile Gly Gly Leu Asp Asp Gly Asp Asn Pro His Ser Pro Val
          100          105          110
Ala Leu Glu Ala Met Leu Gly Leu Ala Arg Leu Val His Leu Val Glu
          115          120          125
Ser Trp Asp Leu Arg Ser Gly Leu Leu His Val Ala Ile Arg Ile Arg
          130          135          140
Pro Phe Phe Asp Ser Glu Lys Met Glu Phe Arg Thr Ala Ser Ile Arg
145           150           155           160
Leu Phe Gly His Leu Asn Lys Val Cys His Gly Asp Cys Glu Asp Val
          165          170          175
Phe Leu Asp Gln Val Val Gly Gly Leu Ala Pro Leu Leu Leu His Leu
          180          185          190
Gln Asp Pro Gln Ala Thr Val Ala Ser Ala Cys Arg Phe Ala Leu Arg
          195          200          205
Met Cys Gly Pro Asn Leu Ala Cys Glu Glu Leu Ser Ala Ala Phe Gln
          210          215          220
Lys His Leu Gln Glu Gly Arg Ala Leu His Phe Gly Glu Phe Leu Asn
225           230           235           240
Thr Thr Cys Lys His Leu Met His His Phe Pro Asp Leu Leu Gly Arg
          245          250          255
Leu Leu Thr Thr Cys Leu Phe Tyr Phe Lys Ser Ser Trp Glu Asn Val
          260          265          270
Arg Ala Ala Ala Pro Leu Phe Thr Gly Phe Leu Val Leu His Ser Glu
          275          280          285
Pro Arg Gln Gln Pro Gln Val Asp Leu Asp Gln Leu Ile Ala Gly Glu
          290          295          300
His Pro Ser Thr Gly Pro Leu Arg Trp Ala Leu Leu Thr Leu
305           310           315

```

<210> 293

<211> 1107

432

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1107)

<400> 293

| | |
|---|-----|
| atg cag cct gga tcc agc cgg tgt gaa gag gag acc cct tcc ctc ttg | 48 |
| Met Gln Pro Gly Ser Ser Arg Cys Glu Glu Glu Thr Pro Ser Leu Leu | |
| 1 5 10 15 | |
| tggttg gat cct gtgttt cta gcc ttt gca aaa ctc tac atc agg | 96 |
| Trp Gly Leu Asp Pro Val Phe Leu Ala Phe Ala Lys Leu Tyr Ile Arg | |
| 20 25 30 | |
| gat atc ctg gac atg aag gag tcc cgc cag gtg cca ggt gta ttt ttg | 144 |
| Asp Ile Leu Asp Met Lys Glu Ser Arg Gln Val Pro Gly Val Phe Leu | |
| 35 40 45 | |
| tac aat gga cat cca ata aaa cag gta gat gtc ttg gga act gtc att | 192 |
| Tyr Asn Gly His Pro Ile Lys Gln Val Asp Val Leu Gly Thr Val Ile | |
| 50 55 60 | |
| gga gtg aga gaa aga gat gct ttc tac agt tat gga gtg gat gac agc | 240 |
| Gly Val Arg Glu Arg Asp Ala Phe Tyr Ser Tyr Gly Val Asp Asp Ser | |
| 65 70 75 80 | |
| act gga gtt ata aac tgc atc tgc tgg aaa aag ttg aat act gag tct | 288 |
| Thr Gly Val Ile Asn Cys Ile Cys Trp Lys Lys Leu Asn Thr Glu Ser | |
| 85 90 95 | |
| gta tca gct gct cca agt gca gca aga gag ctc agc tta acc tca caa | 336 |
| Val Ser Ala Ala Pro Ser Ala Ala Arg Glu Leu Ser Leu Thr Ser Gln | |
| 100 105 110 | |
| ctt aag aag cta caa gag acc att gag cag aaa aca aag ata gag atc | 384 |
| Leu Lys Lys Leu Gln Glu Thr Ile Glu Gln Lys Thr Lys Ile Glu Ile | |
| 115 120 125 | |
| ggg gac acg atc cga gtc aga ggc agt atc cgc aca tac aga gaa gag | 432 |
| Gly Asp Thr Ile Arg Val Arg Gly Ser Ile Arg Thr Tyr Arg Glu Glu | |
| 130 135 140 | |

| | |
|---|-----|
| cga gag att cat gcc acc gct tac tat aaa gtg gac cca gtg tgg | 480 |
| Arg Glu Ile His Ala Thr Ala Tyr Tyr Lys Val Asp Asp Pro Val Trp | |
| 145 150 155 160 | |
| aac att caa att gca agg atg ctt gag ctg ccc act atc tac agg aaa | 528 |
| Asn Ile Gln Ile Ala Arg Met Leu Glu Leu Pro Thr Ile Tyr Arg Lys | |
| 165 170 175 | |
| gtt tat gac cag cct ttt cac agc tca gcc cta gag aaa gaa gag gca | 576 |
| Val Tyr Asp Gln Pro Phe His Ser Ser Ala Leu Glu Lys Glu Glu Ala | |
| 180 185 190 | |
| cta agc aat cca ggc gcc ctg gac ctc ccc agt ctc acg agt ttg ctg | 624 |
| Leu Ser Asn Pro Gly Ala Leu Asp Leu Pro Ser Leu Thr Ser Leu Leu | |
| 195 200 205 | |
| agt gaa aaa gcc aaa gaa ttc ctc atg gag aac aga gtg cag agc ttt | 672 |
| Ser Glu Lys Ala Lys Glu Phe Leu Met Glu Asn Arg Val Gln Ser Phe | |
| 210 215 220 | |
| tac cag cag gag ctg gaa atg gtg gag tct ttg ctg tcc ctt gcc aat | 720 |
| Tyr Gln Gln Glu Leu Glu Met Val Glu Ser Leu Leu Ser Leu Ala Asn | |
| 225 230 235 240 | |
| cag cct gtg att cac agt gcc tgc tcc gac caa gtg aat ttt aag aag | 768 |
| Gln Pro Val Ile His Ser Ala Cys Ser Asp Gln Val Asn Phe Lys Lys | |
| 245 250 255 | |
| gac acc act tcc aag gca att cat agt ata ttt aag aat gct ata caa | 816 |
| Asp Thr Thr Ser Lys Ala Ile His Ser Ile Phe Lys Asn Ala Ile Gln | |
| 260 265 270 | |
| ctg ctg cag gaa aaa gga ctt gtt ttc cag aaa gat gat ggt ttt gat | 864 |
| Leu Leu Gln Glu Lys Gly Leu Val Phe Gln Lys Asp Asp Gly Phe Asp | |
| 275 280 285 | |
| aac cta tac tat gta acc aga gaa gac aaa gac ctg cac aga aag atc | 912 |
| Asn Leu Tyr Tyr Val Thr Arg Glu Asp Lys Asp Leu His Arg Lys Ile | |
| 290 295 300 | |
| cac cgg atc att cag cag gac tgc cag aaa cca aat cac atg gag aag | 960 |
| His Arg Ile Ile Gln Gln Asp Cys Gln Lys Pro Asn His Met Glu Lys | |
| 305 310 315 320 | |

434

ggc tgt cac ttc ctg cac atc ttg gcc tgt gct cgc ctg agc atc cgc 1008
 Gly Cys His Phe Leu His Ile Leu Ala Cys Ala Arg Leu Ser Ile Arg
 325 330 335

 ccg ggc ctg agc gag gct gtg ctg cag caa gtt ctg gag ctc ctg gag 1056
 Pro Gly Leu Ser Glu Ala Val Leu Gln Gln Val Leu Glu Leu Leu Glu
 340 345 350

 gac cag agt gac att gtc agc aca atg gag cac tac tac aca gcg ttc 1104
 Asp Gln Ser Asp Ile Val Ser Thr Met Glu His Tyr Tyr Thr Ala Phe
 355 360 365

 tga 1107
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<210> 294
 <211> 368
 <212> PRT
 <213> Homo sapiens

<400> 294
 Met Gln Pro Gly Ser Ser Arg Cys Glu Glu Glu Thr Pro Ser Leu Leu
 1 5 10 15
 Trp Gly Leu Asp Pro Val Phe Leu Ala Phe Ala Lys Leu Tyr Ile Arg
 20 25 30
 Asp Ile Leu Asp Met Lys Glu Ser Arg Gln Val Pro Gly Val Phe Leu
 35 40 45
 Tyr Asn Gly His Pro Ile Lys Gln Val Asp Val Leu Gly Thr Val Ile
 50 55 60
 Gly Val Arg Glu Arg Asp Ala Phe Tyr Ser Tyr Gly Val Asp Asp Ser
 65 70 75 80
 Thr Gly Val Ile Asn Cys Ile Cys Trp Lys Lys Leu Asn Thr Glu Ser
 85 90 95
 Val Ser Ala Ala Pro Ser Ala Ala Arg Glu Leu Ser Leu Thr Ser Gln
 100 105 110
 Leu Lys Lys Leu Gln Glu Thr Ile Glu Gln Lys Thr Lys Ile Glu Ile
 115 120 125
 Gly Asp Thr Ile Arg Val Arg Gly Ser Ile Arg Thr Tyr Arg Glu Glu
 130 135 140
 Arg Glu Ile His Ala Thr Ala Tyr Tyr Lys Val Asp Asp Pro Val Trp
 145 150 155 160
 Asn Ile Gln Ile Ala Arg Met Leu Glu Leu Pro Thr Ile Tyr Arg Lys

435

165 170 175
 Val Tyr Asp Gln Pro Phe His Ser Ser Ala Leu Glu Lys Glu Glu Ala
 180 185 190
 Leu Ser Asn Pro Gly Ala Leu Asp Leu Pro Ser Leu Thr Ser Leu Leu
 195 200 205
 Ser Glu Lys Ala Lys Glu Phe Leu Met Glu Asn Arg Val Gln Ser Phe
 210 215 220
 Tyr Gln Gln Glu Leu Glu Met Val Glu Ser Leu Leu Ser Leu Ala Asn
 225 230 235 240
 Gln Pro Val Ile His Ser Ala Cys Ser Asp Gln Val Asn Phe Lys Lys
 245 250 255
 Asp Thr Thr Ser Lys Ala Ile His Ser Ile Phe Lys Asn Ala Ile Gln
 260 265 270
 Leu Leu Gln Glu Lys Gly Leu Val Phe Gln Lys Asp Asp Gly Phe Asp
 275 280 285
 Asn Leu Tyr Tyr Val Thr Arg Glu Asp Lys Asp Leu His Arg Lys Ile
 290 295 300
 His Arg Ile Ile Gln Gln Asp Cys Gln Lys Pro Asn His Met Glu Lys
 305 310 315 320
 Gly Cys His Phe Leu His Ile Leu Ala Cys Ala Arg Leu Ser Ile Arg
 325 330 335
 Pro Gly Leu Ser Glu Ala Val Leu Gln Gln Val Leu Glu Leu Leu Glu
 340 345 350
 Asp Gln Ser Asp Ile Val Ser Thr Met Glu His Tyr Tyr Thr Ala Phe
 355 360 365

<210> 295

<211> 558

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(558)

<400> 295

atg att aaa agc gcc cct gtg ggt cct gtg gct gga ggg atc atg gga
 Met Ile Lys Ser Ala Pro Val Gly Pro Val Ala Gly Gly Ile Met Gly
 1 5 10 15

48

tgc atc atg gtc ttg gtc ctg gcg gtg tat gcc tac cgc cac cag att
 Cys Ile Met Val Leu Val Leu Ala Val Tyr Ala Tyr Arg His Gln Ile
 20 25 30

96

436

| | |
|---|-----|
| cat cgc cgg agc cat cag cat atg tct cct ctt gct gcc caa gaa atg His Arg Arg Ser His Gln His Met Ser Pro Leu Ala Ala Gln Glu Met 35 40 45 | 144 |
| tca gtg cgt atg tcc aac ctg gag aat gac aga gat gaa agg gac gac Ser Val Arg Met Ser Asn Leu Glu Asn Asp Arg Asp Glu Arg Asp Asp 50 55 60 | 192 |
| gac agc cac gaa gac aga ggc atc atc agc aac act cgg ttt ata gct Asp Ser His Glu Asp Arg Gly Ile Ile Ser Asn Thr Arg Phe Ile Ala 65 70 75 80 | 240 |
| gcg gtc atc gaa cga cat gca cac agt cca gaa aga agg cgc cgc tac Ala Val Ile Glu Arg His Ala His Ser Pro Glu Arg Arg Arg Arg Tyr 85 90 95 | 288 |
| tgg ggt cga tca gga aca gaa agt gat cat ggt tac agc acc atg agc Trp Gly Arg Ser Gly Thr Glu Ser Asp His Gly Tyr Ser Thr Met Ser 100 105 110 | 336 |
| cca cag gag gac agt gaa aat cct cca tgc aac aat gac ccc ttg tca Pro Gln Glu Asp Ser Glu Asn Pro Pro Cys Asn Asn Asp Pro Leu Ser 115 120 125 | 384 |
| gcc ggg gtc gat gtg gga aac cat gat gag gac tta gac ctg gat acc Ala Gly Val Asp Val Gly Asn His Asp Glu Asp Leu Asp Leu Asp Thr 130 135 140 | 432 |
| ccc cct cag act gct gcc cta cta agt cac aag ttc cac cac tac cgg Pro Pro Gln Thr Ala Ala Leu Leu Ser His Lys Phe His His Tyr Arg 145 150 155 160 | 480 |
| tca cac cac cct aca ctt cat cat agc cac cac tta cag gcg gcc gtc Ser His His Pro Thr Leu His His Ser His His Leu Gln Ala Ala Val 165 170 175 | 528 |
| acg gta cac act gtc gat gca gaa tgc taa Thr Val His Thr Val Asp Ala Glu Cys * | 558 |
| 180 185 | |

<210> 296

<211> 185

<212> PRT

437

<213> Homo sapiens

<400> 296

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Met Ile Lys Ser Ala Pro Val Gly Pro Val Ala Gly Gly Ile Met Gly
 1           5           10           15
Cys Ile Met Val Leu Val Leu Ala Val Tyr Ala Tyr Arg His Gln Ile
          20           25           30
His Arg Arg Ser His Gln His Met Ser Pro Leu Ala Ala Gln Glu Met
          35           40           45
Ser Val Arg Met Ser Asn Leu Glu Asn Asp Arg Asp Glu Arg Asp Asp
          50           55           60
Asp Ser His Glu Asp Arg Gly Ile Ile Ser Asn Thr Arg Phe Ile Ala
65           70           75           80
Ala Val Ile Glu Arg His Ala His Ser Pro Glu Arg Arg Arg Arg Tyr
          85           90           95
Trp Gly Arg Ser Gly Thr Glu Ser Asp His Gly Tyr Ser Thr Met Ser
          100          105          110
Pro Gln Glu Asp Ser Glu Asn Pro Pro Cys Asn Asn Asp Pro Leu Ser
          115          120          125
Ala Gly Val Asp Val Gly Asn His Asp Glu Asp Leu Asp Leu Asp Thr
          130          135          140
Pro Pro Gln Thr Ala Ala Leu Leu Ser His Lys Phe His His Tyr Arg
          145          150          155          160
Ser His His Pro Thr Leu His His Ser His His Leu Gln Ala Ala Val
          165          170          175
Thr Val His Thr Val Asp Ala Glu Cys
          180          185

```

<210> 297

<211> 501

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(501)

<400> 297

```

atg gat gat att gtg gtt gta gct cag ggc tcc cag gcc tca cgg aac
Met Asp Asp Ile Val Val Val Ala Gln Gly Ser Gln Ala Ser Arg Asn
 1           5           10           15

gtc agc aac gat ccc gat gtc atc aag ttg caa gag att cca acc ttc
Val Ser Asn Asp Pro Asp Val Ile Lys Leu Gln Glu Ile Pro Thr Phe

```

48

96

438

| 20 | 25 | 30 | |
|---|-----|-----|-----|
| cag ccc ctt ttg aaa ggg cta ttg agt ggc cag act tcc cca aca aat | | | 144 |
| Gln Pro Leu Leu Lys Gly Leu Leu Ser Gly Gln Thr Ser Pro Thr Asn | | | |
| 35 | 40 | 45 | |
| gcc aaa ttg gag aaa ctg gac tct cag cag gtg ttg cag ctc tgc ctc | | | 192 |
| Ala Lys Leu Glu Lys Leu Asp Ser Gln Gln Val Leu Gln Leu Cys Leu | | | |
| 50 | 55 | 60 | |
| cga tat caa gat cac ctg cat cag tgt gca gag gcc gtt gct ttt gac | | | 240 |
| Arg Tyr Gln Asp His Leu His Gln Cys Ala Glu Ala Val Ala Phe Asp | | | |
| 65 | 70 | 75 | 80 |
| cag aat gct ttg gtt aaa cga atc aaa gag atg gat ctg tct gta gaa | | | 288 |
| Gln Asn Ala Leu Val Lys Arg Ile Lys Glu Met Asp Leu Ser Val Glu | | | |
| 85 | 90 | 95 | |
| act ctg ttc agc ttc atg cag gag cgc cag aaa aga tac gcc aag tat | | | 336 |
| Thr Leu Phe Ser Phe Met Gln Glu Arg Gln Lys Arg Tyr Ala Lys Tyr | | | |
| 100 | 105 | 110 | |
| gcc gag cag atc cag aaa gtg aac gag atg tcc gcc atc ctc cgc cgc | | | 384 |
| Ala Glu Gln Ile Gln Lys Val Asn Glu Met Ser Ala Ile Leu Arg Arg | | | |
| 115 | 120 | 125 | |
| ata cag atg ggc atc gac cag act gtg ccc ctg ctg gac agg ctc aac | | | 432 |
| Ile Gln Met Gly Ile Asp Gln Thr Val Pro Leu Leu Asp Arg Leu Asn | | | |
| 130 | 135 | 140 | |
| agc atg ctg ccc gag ggc gag cgg ctg gag ccc ttc agc atg aag ccc | | | 480 |
| Ser Met Leu Pro Glu Gly Glu Arg Leu Glu Pro Phe Ser Met Lys Pro | | | |
| 145 | 150 | 155 | 160 |
| gac cgc gag ctc agg ctg tag | | | 501 |
| Asp Arg Glu Leu Arg Leu * | | | |
| 165 | | | |

<210> 298

<211> 166

<212> PRT

<213> Homo sapiens

439

<400> 298

```

Met Asp Asp Ile Val Val Val Ala Gln Gly Ser Gln Ala Ser Arg Asn
 1           5           10           15
Val Ser Asn Asp Pro Asp Val Ile Lys Leu Gln Glu Ile Pro Thr Phe
          20           25           30
Gln Pro Leu Leu Lys Gly Leu Leu Ser Gly Gln Thr Ser Pro Thr Asn
          35           40           45
Ala Lys Leu Glu Lys Leu Asp Ser Gln Gln Val Leu Gln Leu Cys Leu
          50           55           60
Arg Tyr Gln Asp His Leu His Gln Cys Ala Glu Ala Val Ala Phe Asp
65           70           75           80
Gln Asn Ala Leu Val Lys Arg Ile Lys Glu Met Asp Leu Ser Val Glu
          85           90           95
Thr Leu Phe Ser Phe Met Gln Glu Arg Gln Lys Arg Tyr Ala Lys Tyr
          100          105          110
Ala Glu Gln Ile Gln Lys Val Asn Glu Met Ser Ala Ile Leu Arg Arg
          115          120          125
Ile Gln Met Gly Ile Asp Gln Thr Val Pro Leu Leu Asp Arg Leu Asn
          130          135          140
Ser Met Leu Pro Glu Gly Glu Arg Leu Glu Pro Phe Ser Met Lys Pro
145          150          155          160
Asp Arg Glu Leu Arg Leu
          165

```

<210> 299

<211> 828

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(828)

<221> misc_feature

<222> (1)...(828)

<223> n = A,T,C or G

<400> 299

```

atg agt gaa gag cct gac gct cta tcg gta gtt aac cag tta cgg gat
Met Ser Glu Glu Pro Asp Ala Leu Ser Val Val Asn Gln Leu Arg Asp
 1           5           10           15

```

48

```

cta gca gca gat ccg tta aac aga aga gcc atc gtc cag gat cag gga
Leu Ala Ala Asp Pro Leu Asn Arg Arg Ala Ile Val Gln Asp Gln Gly

```

96

440

| 20 | 25 | 30 | |
|---|-----|-----|-----|
| tgt ctg cct ggc ctt att tta ttt atg gac cat ccc aac cct cca gtc | | | 144 |
| Cys Leu Pro Gly Leu Ile Leu Phe Met Asp His Pro Asn Pro Pro Val | | | |
| 35 | 40 | 45 | |
| gtc cac tcc gct ttg ctt gct ctt cga tac ttg gca gaa tgc cgt gca | | | 192 |
| Val His Ser Ala Leu Leu Ala Leu Arg Tyr Leu Ala Glu Cys Arg Ala | | | |
| 50 | 55 | 60 | |
| aac aga gaa aag atg aaa gga gaa ctg ggt atg atg ttg agc tta caa | | | 240 |
| Asn Arg Glu Lys Met Lys Gly Glu Leu Gly Met Met Leu Ser Leu Gln | | | |
| 65 | 70 | 75 | 80 |
| aat gtt ata cag aaa act aca act cca gga gaa aca aaa ctt ctg gcc | | | 288 |
| Asn Val Ile Gln Lys Thr Thr Thr Pro Gly Glu Thr Lys Leu Leu Ala | | | |
| 85 | 90 | 95 | |
| tct gaa atc tat gac att ctt cag tcc tcc aat atg gca gat ggt gat | | | 336 |
| Ser Glu Ile Tyr Asp Ile Leu Gln Ser Ser Asn Met Ala Asp Gly Asp | | | |
| 100 | 105 | 110 | |
| agt ttt aat gag atg aat tca cgt cga agg aaa gct can ttt ttt ctg | | | 384 |
| Ser Phe Asn Glu Met Asn Ser Arg Arg Arg Lys Ala Xaa Phe Phe Leu | | | |
| 115 | 120 | 125 | |
| gga act aca aac aaa cgt gcc aaa aca gtg gtt ttg cat ata gat ggc | | | 432 |
| Gly Thr Thr Asn Lys Arg Ala Lys Thr Val Val Leu His Ile Asp Gly | | | |
| 130 | 135 | 140 | |
| ctt gat gat acg tct cgg aga aat cta tgt gaa gag gct ttg tta aaa | | | 480 |
| Leu Asp Asp Thr Ser Arg Arg Asn Leu Cys Glu Glu Ala Leu Leu Lys | | | |
| 145 | 150 | 155 | 160 |
| att aaa ggt gtt att agc ttt act ttt caa atg gct gtt caa agg tgt | | | 528 |
| Ile Lys Gly Val Ile Ser Phe Thr Phe Gln Met Ala Val Gln Arg Cys | | | |
| 165 | 170 | 175 | |
| gtg gtg cga atc cgt tca gat ttg aaa gct gag gct ttg gca tca gca | | | 576 |
| Val Val Arg Ile Arg Ser Asp Leu Lys Ala Glu Ala Leu Ala Ser Ala | | | |
| 180 | 185 | 190 | |
| ata gca tca acc aag gtt atg aaa gct cag caa gtt gtg aaa agt gaa | | | 624 |
| Ile Ala Ser Thr Lys Val Met Lys Ala Gln Gln Val Val Lys Ser Glu | | | |

441

| 195 | 200 | 205 | |
|---|-----|-----|-----|
| agt gga gaa gag atg ttg gtc cca ttc caa gat act cct gtg gaa gtt | | | 672 |
| Ser Gly Glu Glu Met Leu Val Pro Phe Gln Asp Thr Pro Val Glu Val | | | |
| 210 | 215 | 220 | |
| gaa cag aac aca gag cta cct gac tac ctg cct gag gat gag agt ccc | | | 720 |
| Glu Gln Asn Thr Glu Leu Pro Asp Tyr Leu Pro Glu Asp Glu Ser Pro | | | |
| 225 | 230 | 235 | 240 |
| aca aag gaa cag gac aaa gcg gtg tcc cgg gtc ggc tca cac cca gaa | | | 768 |
| Thr Lys Glu Gln Asp Lys Ala Val Ser Arg Val Gly Ser His Pro Glu | | | |
| | 245 | 250 | 255 |
| ggg gga gct agc tgg ctt agc aca gct gca aac ttt tta tcc aga tca | | | 816 |
| Gly Gly Ala Ser Trp Leu Ser Thr Ala Ala Asn Phe Leu Ser Arg Ser | | | |
| | 260 | 265 | 270 |
| ttt tat tgg tga | | | 828 |
| Phe Tyr Trp * | | | |
| 275 | | | |

<210> 300
 <211> 275
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(275)
 <223> Xaa = Any Amino Acid

<400> 300

| | |
|---|--|
| Met Ser Glu Glu Pro Asp Ala Leu Ser Val Val Asn Gln Leu Arg Asp | |
| 1 5 10 15 | |
| Leu Ala Ala Asp Pro Leu Asn Arg Arg Ala Ile Val Gln Asp Gln Gly | |
| 20 25 30 | |
| Cys Leu Pro Gly Leu Ile Leu Phe Met Asp His Pro Asn Pro Pro Val | |
| 35 40 45 | |
| Val His Ser Ala Leu Leu Ala Leu Arg Tyr Leu Ala Glu Cys Arg Ala | |
| 50 55 60 | |
| Asn Arg Glu Lys Met Lys Gly Glu Leu Gly Met Met Leu Ser Leu Gln | |
| 65 70 75 80 | |

442

Asn Val Ile Gln Lys Thr Thr Thr Pro Gly Glu Thr Lys Leu Leu Ala
 85 90 95
 Ser Glu Ile Tyr Asp Ile Leu Gln Ser Ser Asn Met Ala Asp Gly Asp
 100 105 110
 Ser Phe Asn Glu Met Asn Ser Arg Arg Arg Lys Ala Xaa Phe Phe Leu
 115 120 125
 Gly Thr Thr Asn Lys Arg Ala Lys Thr Val Val Leu His Ile Asp Gly
 130 135 140
 Leu Asp Asp Thr Ser Arg Arg Asn Leu Cys Glu Glu Ala Leu Leu Lys
 145 150 155 160
 Ile Lys Gly Val Ile Ser Phe Thr Phe Gln Met Ala Val Gln Arg Cys
 165 170 175
 Val Val Arg Ile Arg Ser Asp Leu Lys Ala Glu Ala Leu Ala Ser Ala
 180 185 190
 Ile Ala Ser Thr Lys Val Met Lys Ala Gln Gln Val Val Lys Ser Glu
 195 200 205
 Ser Gly Glu Glu Met Leu Val Pro Phe Gln Asp Thr Pro Val Glu Val
 210 215 220
 Glu Gln Asn Thr Glu Leu Pro Asp Tyr Leu Pro Glu Asp Glu Ser Pro
 225 230 235 240
 Thr Lys Glu Gln Asp Lys Ala Val Ser Arg Val Gly Ser His Pro Glu
 245 250 255
 Gly Gly Ala Ser Trp Leu Ser Thr Ala Ala Asn Phe Leu Ser Arg Ser
 260 265 270
 Phe Tyr Trp
 275

<210> 301
 <211> 1101
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1101)

<221> misc_feature
 <222> (1)...(1101)
 <223> n = A,T,C or G

<400> 301
 atg gcc tca gca gta ctt agt tct gtt ccc acc acc gct tct cgt ttt
 Met Ala Ser Ala Val Leu Ser Ser Val Pro Thr Thr Ala Ser Arg Phe
 1 5 10 15

443

| | |
|---|-----|
| gcc ctg tta caa gtg gat agt ggc agt ggc tct gat tct gaa cct gga Ala Leu Leu Gln Val Asp Ser Gly Ser Gly Ser Asp Ser Glu Pro Gly 20 25 30 | 96 |
| aaa ggt aaa ggt cga aat act gga aag tct caa act tta gga agc aag Lys Gly Lys Gly Arg Asn Thr Gly Lys Ser Gln Thr Leu Gly Ser Lys 35 40 45 | 144 |
| tca act aca aat gag aaa aaa aga gag aaa aga aga aaa aag aag gaa Ser Thr Thr Asn Glu Lys Lys Arg Glu Lys Arg Arg Lys Lys Lys Glu 50 55 60 | 192 |
| cag caa cag agt gaa gca aat gag ctc agg aat ctt gct ttt aag aaa Gln Gln Gln Ser Glu Ala Asn Glu Leu Arg Asn Leu Ala Phe Lys Lys 65 70 75 80 | 240 |
| att ccc cag aaa tcc tcc cat gct gtt tgt aac gct caa cat gat ctt Ile Pro Gln Lys Ser Ser His Ala Val Cys Asn Ala Gln His Asp Leu 85 90 95 | 288 |
| cca ttg tca aac cca gta cag aag gat tca cga gaa gaa aat tgg caa Pro Leu Ser Asn Pro Val Gln Lys Asp Ser Arg Glu Glu Asn Trp Gln 100 105 110 | 336 |
| gag tgg aga caa aga gat gag cag ctg aca tct gaa atg ttt gaa gca Glu Trp Arg Gln Arg Asp Glu Gln Leu Thr Ser Glu Met Phe Glu Ala 115 120 125 | 384 |
| gat ctt gag aag gca ttg tta cta agt aaa cta gaa tat gaa gag cac Asp Leu Glu Lys Ala Leu Leu Leu Ser Lys Leu Glu Tyr Glu Glu His 130 135 140 | 432 |
| aaa aag gag tat gaa gat gct gaa aat act tca act cag tcc aaa gtt Lys Lys Glu Tyr Glu Asp Ala Glu Asn Thr Ser Thr Gln Ser Lys Val 145 150 155 160 | 480 |
| atg aat ann aaa gat aaa aga aag aat cat cag gga aaa gac aga cct Met Asn Xaa Lys Asp Lys Arg Lys Asn His Gln Gly Lys Asp Arg Pro 165 170 175 | 528 |
| ctc aca gta tca cta aaa gat ttt cat tcg gaa gat cac att agt aaa Leu Thr Val Ser Leu Lys Asp Phe His Ser Glu Asp His Ile Ser Lys 180 185 190 | 576 |

444

| | |
|---|------|
| aag act gag gaa ttg agt tct tct cag act tta tca cat gat gga gga Lys Thr Glu Glu Leu Ser Ser Ser Gln Thr Leu Ser His Asp Gly Gly 195 200 205 | 624 |
| ttc ttc aat aga ctg gaa gat gat gtt cat aaa att ctt att aga gaa Phe Phe Asn Arg Leu Glu Asp Asp Val His Lys Ile Leu Ile Arg Glu 210 215 220 | 672 |
| aaa cga aga gaa cag ctt aca gaa tat aat gga aca gat aat tgt aca Lys Arg Arg Glu Gln Leu Thr Glu Tyr Asn Gly Thr Asp Asn Cys Thr 225 230 235 240 | 720 |
| gct cat gaa cac aac cag gaa gtg gtt ctg aaa gat gga aga att gaa Ala His Glu His Asn Gln Glu Val Val Leu Lys Asp Gly Arg Ile Glu 245 250 255 | 768 |
| aga cta aag tta gag ctt gaa agg aaa gat gct gaa atc cag aag ctg Arg Leu Lys Leu Glu Leu Glu Arg Lys Asp Ala Glu Ile Gln Lys Leu 260 265 270 | 816 |
| aaa aat gta atc act caa tgg gag gca aag tat aag gaa gta aag gca Lys Asn Val Ile Thr Gln Trp Glu Ala Lys Tyr Lys Glu Val Lys Ala 275 280 285 | 864 |
| aga aat gca caa tta ttg aaa atg ctt cag gaa ggt gaa atg aaa gat Arg Asn Ala Gln Leu Leu Lys Met Leu Gln Glu Gly Glu Met Lys Asp 290 295 300 | 912 |
| aag gca gaa ata ctt ctg caa gtt gat gaa tca caa agt atc aag aat Lys Ala Glu Ile Leu Leu Gln Val Asp Glu Ser Gln Ser Ile Lys Asn 305 310 315 320 | 960 |
| gag ctc act att cag gtg act tca ctt cat gct gca tta gaa caa gaa Glu Leu Thr Ile Gln Val Thr Ser Leu His Ala Ala Leu Glu Gln Glu 325 330 335 | 1008 |
| aga tct aaa gtg aaa gta tta caa gca gag tta gcc aaa tac cag ggt Arg Ser Lys Val Lys Val Leu Gln Ala Glu Leu Ala Lys Tyr Gln Gly 340 345 350 | 1056 |
| ggc aga aaa ggg aaa aga aac tct gaa tcc gac cag tgt agg tga Gly Arg Lys Gly Lys Arg Asn Ser Glu Ser Asp Gln Cys Arg * 355 360 365 | 1101 |

445

<210> 302
 <211> 366
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(366)
 <223> Xaa = Any Amino Acid

<400> 302
 Met Ala Ser Ala Val Leu Ser Ser Val Pro Thr Thr Ala Ser Arg Phe
 1 5 10 15
 Ala Leu Leu Gln Val Asp Ser Gly Ser Gly Ser Asp Ser Glu Pro Gly
 20 25 30
 Lys Gly Lys Gly Arg Asn Thr Gly Lys Ser Gln Thr Leu Gly Ser Lys
 35 40 45
 Ser Thr Thr Asn Glu Lys Lys Arg Glu Lys Arg Arg Lys Lys Lys Glu
 50 55 60
 Gln Gln Gln Ser Glu Ala Asn Glu Leu Arg Asn Leu Ala Phe Lys Lys
 65 70 75 80
 Ile Pro Gln Lys Ser Ser His Ala Val Cys Asn Ala Gln His Asp Leu
 85 90 95
 Pro Leu Ser Asn Pro Val Gln Lys Asp Ser Arg Glu Glu Asn Trp Gln
 100 105 110
 Glu Trp Arg Gln Arg Asp Glu Gln Leu Thr Ser Glu Met Phe Glu Ala
 115 120 125
 Asp Leu Glu Lys Ala Leu Leu Ser Lys Leu Glu Tyr Glu Glu His
 130 135 140
 Lys Lys Glu Tyr Glu Asp Ala Glu Asn Thr Ser Thr Gln Ser Lys Val
 145 150 155 160
 Met Asn Xaa Lys Asp Lys Arg Lys Asn His Gln Gly Lys Asp Arg Pro
 165 170 175
 Leu Thr Val Ser Leu Lys Asp Phe His Ser Glu Asp His Ile Ser Lys
 180 185 190
 Lys Thr Glu Glu Leu Ser Ser Ser Gln Thr Leu Ser His Asp Gly Gly
 195 200 205
 Phe Phe Asn Arg Leu Glu Asp Asp Val His Lys Ile Leu Ile Arg Glu
 210 215 220
 Lys Arg Arg Glu Gln Leu Thr Glu Tyr Asn Gly Thr Asp Asn Cys Thr
 225 230 235 240
 Ala His Glu His Asn Gln Glu Val Val Leu Lys Asp Gly Arg Ile Glu

446

245 250 255
 Arg Leu Lys Leu Glu Leu Glu Arg Lys Asp Ala Glu Ile Gln Lys Leu
 260 265 270
 Lys Asn Val Ile Thr Gln Trp Glu Ala Lys Tyr Lys Glu Val Lys Ala
 275 280 285
 Arg Asn Ala Gln Leu Leu Lys Met Leu Gln Glu Gly Glu Met Lys Asp
 290 295 300
 Lys Ala Glu Ile Leu Leu Gln Val Asp Glu Ser Gln Ser Ile Lys Asn
 305 310 315 320
 Glu Leu Thr Ile Gln Val Thr Ser Leu His Ala Ala Leu Glu Gln Glu
 325 330 335
 Arg Ser Lys Val Lys Val Leu Gln Ala Glu Leu Ala Lys Tyr Gln Gly
 340 345 350
 Gly Arg Lys Gly Lys Arg Asn Ser Glu Ser Asp Gln Cys Arg
 355 360 365

<210> 303
 <211> 807
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(807)

<400> 303
 atg cta agg aag ctg tgg caa gaa aat aaa gca acc aac aca gac cat 48
 Met Leu Arg Lys Leu Trp Gln Glu Asn Lys Ala Thr Asn Thr Asp His
 1 5 10 15
 tta acc acg gta ctc tac ctc cag ctt gct att tgt tca agt ttg cag 96
 Leu Thr Thr Val Leu Tyr Leu Gln Leu Ala Ile Cys Ser Ser Leu Gln
 20 25 30
 aac ttg gag aaa aca att ttc tgc ctg cag aaa ctg att tct ttg cat 144
 Asn Leu Glu Lys Thr Ile Phe Cys Leu Gln Lys Leu Ile Ser Leu His
 35 40 45
 cct ttt aat cct tgg aac tgg ggc aaa ttg gca gag gct tac ctg aat 192
 Pro Phe Asn Pro Trp Asn Trp Gly Lys Leu Ala Glu Ala Tyr Leu Asn
 50 55 60
 ctg ggg cca gct ctt tca gca gca ctt gcg tca tct cag aaa cag cac 240
 Leu Gly Pro Ala Leu Ser Ala Ala Leu Ala Ser Ser Gln Lys Gln His

447

| 65 | 70 | 75 | 80 | |
|-----------------|---------------------|---------------------|-----------------|-----|
| agt ttc acc tca | agt gac aaa act atc | aaa tcc ttc ttt cca | cac tca | 288 |
| Ser Phe Thr Ser | Ser Asp Lys Thr Ile | Lys Ser Phe Phe | Pro His Ser | |
| | 85 | 90 | 95 | |
| gga aaa gac tgt | ctt ttg tgt ttt cct | gaa acc ttg cct | gag agc tct | 336 |
| Gly Lys Asp Cys | Leu Leu Cys Phe | Pro Glu Thr Leu | Pro Glu Ser Ser | |
| | 100 | 105 | 110 | |
| tta ttt tct gtg | gaa gcg aat agc agt | aat agc cag aaa | aat gag aaa | 384 |
| Leu Phe Ser Val | Glu Ala Asn Ser Ser | Asn Ser Gln Lys | Asn Glu Lys | |
| | 115 | 120 | 125 | |
| gct ctg aca aat | atc caa aac tgt atg | gca gaa aag aga | gaa aca gtg | 432 |
| Ala Leu Thr Asn | Ile Gln Asn Cys | Met Ala Glu Lys | Arg Glu Thr Val | |
| | 130 | 135 | 140 | |
| ttg ata gag act | cag ctg aaa gca | tgt gcc tct ttt | ata cga acc agg | 480 |
| Leu Ile Glu Thr | Gln Leu Lys Ala | Cys Ala Ser Phe | Ile Arg Thr Arg | |
| | 145 | 150 | 155 | 160 |
| ctt ctg ctt cag | ttt acc caa cct | cag caa aca tcg | ttt gct ttg gag | 528 |
| Leu Leu Leu Gln | Phe Thr Gln Pro | Gln Gln Thr Ser | Phe Ala Leu Glu | |
| | 165 | 170 | 175 | |
| agg aac tta agg | act cag cag gaa | att gaa gat aaa | atg aaa ggg ttc | 576 |
| Arg Asn Leu Arg | Thr Gln Gln Glu | Ile Glu Asp Lys | Met Lys Gly Phe | |
| | 180 | 185 | 190 | |
| agc ttc aaa gaa | gac act ttg ctg | ttg ata gct gag | gtt atg gga gaa | 624 |
| Ser Phe Lys Glu | Asp Thr Leu Leu | Ile Ala Glu Val | Met Gly Glu | |
| | 195 | 200 | 205 | |
| gat atc cca gaa | aaa ata aaa gat | gaa gtt cac cca | gag gtg aag tgt | 672 |
| Asp Ile Pro Glu | Lys Ile Lys Asp | Glu Val His Pro | Glu Val Lys Cys | |
| | 210 | 215 | 220 | |
| gtt ggc tcc gta | gcc ctg act gcc | ttg gtg act gta | tcc tca gaa gaa | 720 |
| Val Gly Ser Val | Ala Leu Thr Ala | Leu Val Thr Val | Ser Ser Glu Glu | |
| | 225 | 230 | 240 | |
| ttt gaa gac aag | tgg ttc aga aag | atc aaa gac cat | ttc tgt cca ttt | 768 |
| Phe Glu Asp Lys | Trp Phe Arg Lys | Ile Lys Asp His | Phe Cys Pro Phe | |

448

245

250

255

gaa aat cag ttc cat aca gag ata caa atc ttg gct tag
 Glu Asn Gln Phe His Thr Glu Ile Gln Ile Leu Ala *
 260 265

807

<210> 304

<211> 268

<212> PRT

<213> Homo sapiens

<400> 304

Met Leu Arg Lys Leu Trp Gln Glu Asn Lys Ala Thr Asn Thr Asp His
 1 5 10 15
 Leu Thr Thr Val Leu Tyr Leu Gln Leu Ala Ile Cys Ser Ser Leu Gln
 20 25 30
 Asn Leu Glu Lys Thr Ile Phe Cys Leu Gln Lys Leu Ile Ser Leu His
 35 40 45
 Pro Phe Asn Pro Trp Asn Trp Gly Lys Leu Ala Glu Ala Tyr Leu Asn
 50 55 60
 Leu Gly Pro Ala Leu Ser Ala Ala Leu Ala Ser Ser Gln Lys Gln His
 65 70 75 80
 Ser Phe Thr Ser Ser Asp Lys Thr Ile Lys Ser Phe Phe Pro His Ser
 85 90 95
 Gly Lys Asp Cys Leu Leu Cys Phe Pro Glu Thr Leu Pro Glu Ser Ser
 100 105 110
 Leu Phe Ser Val Glu Ala Asn Ser Ser Asn Ser Gln Lys Asn Glu Lys
 115 120 125
 Ala Leu Thr Asn Ile Gln Asn Cys Met Ala Glu Lys Arg Glu Thr Val
 130 135 140
 Leu Ile Glu Thr Gln Leu Lys Ala Cys Ala Ser Phe Ile Arg Thr Arg
 145 150 155 160
 Leu Leu Leu Gln Phe Thr Gln Pro Gln Gln Thr Ser Phe Ala Leu Glu
 165 170 175
 Arg Asn Leu Arg Thr Gln Gln Glu Ile Glu Asp Lys Met Lys Gly Phe
 180 185 190
 Ser Phe Lys Glu Asp Thr Leu Leu Leu Ile Ala Glu Val Met Gly Glu
 195 200 205
 Asp Ile Pro Glu Lys Ile Lys Asp Glu Val His Pro Glu Val Lys Cys
 210 215 220
 Val Gly Ser Val Ala Leu Thr Ala Leu Val Thr Val Ser Ser Glu Glu
 225 230 235 240
 Phe Glu Asp Lys Trp Phe Arg Lys Ile Lys Asp His Phe Cys Pro Phe

449

| | | | | |
|---|-----|-----|-----|-----|
| | 245 | 250 | 255 | |
| Glu Asn Gln Phe His Thr Glu Ile Gln Ile Leu Ala | | | | |
| | 260 | 265 | | |
| <210> 305 | | | | |
| <211> 810 | | | | |
| <212> DNA | | | | |
| <213> Homo sapiens | | | | |
| <220> | | | | |
| <221> CDS | | | | |
| <222> (1)...(810) | | | | |
| <400> 305 | | | | |
| atg gcc ata ttt ctg cag cat gcc gca gga ctc tta cat gca atg tgt | | | | 48 |
| Met Ala Ile Phe Leu Gln His Ala Ala Gly Leu Leu His Ala Met Cys | | | | |
| 1 5 10 15 | | | | |
| aca ctg tgc ttt gct gtc act gga agg tca tac agc ata ttt gac aat | | | | 96 |
| Thr Leu Cys Phe Ala Val Thr Gly Arg Ser Tyr Ser Ile Phe Asp Asn | | | | |
| 20 25 30 | | | | |
| aat cgc cag gat ccc aca ggg ctg aca gct gct ctt cag gca acc gac | | | | 144 |
| Asn Arg Gln Asp Pro Thr Gly Leu Thr Ala Ala Leu Gln Ala Thr Asp | | | | |
| 35 40 45 | | | | |
| ctg gct gga gtt ctt cat atg ctc tac tgt gtc ctc ttc cat ggc acc | | | | 192 |
| Leu Ala Gly Val Leu His Met Leu Tyr Cys Val Leu Phe His Gly Thr | | | | |
| 50 55 60 | | | | |
| atc ttg gac ccc agc act gcc agt ccc aag gag aat tac act caa aat | | | | 240 |
| Ile Leu Asp Pro Ser Thr Ala Ser Pro Lys Glu Asn Tyr Thr Gln Asn | | | | |
| 65 70 75 80 | | | | |
| acc atc caa gtg gcc att cag agt tta cgt ttc ttc aac agc ttt gca | | | | 288 |
| Thr Ile Gln Val Ala Ile Gln Ser Leu Arg Phe Phe Asn Ser Phe Ala | | | | |
| 85 90 95 | | | | |
| gct ctt cat ctg cct gct ttt cag tct att gta ggg gca gag ggc ttg | | | | 336 |
| Ala Leu His Leu Pro Ala Phe Gln Ser Ile Val Gly Ala Glu Gly Leu | | | | |
| 100 105 110 | | | | |
| tcc ctt gca ttc cgg cac atg gcc agc tcc ctg ctg ggc cac tgc agc | | | | 384 |
| Ser Leu Ala Phe Arg His Met Ala Ser Ser Leu Leu Gly His Cys Ser | | | | |

450

| 115 | 120 | 125 | |
|---|-----|-----|-----|
| caa gtc tcc tgt gaa agc ctc ctt cat gag gtc atc gtc tgt gtg ggc | | | 432 |
| Gln Val Ser Cys Glu Ser Leu Leu His Glu Val Ile Val Cys Val Gly | | | |
| 130 | 135 | 140 | |
| tac ttc act gtc aac cac cca gat aac cag gtg atc gtg cag tcc ggc | | | 480 |
| Tyr Phe Thr Val Asn His Pro Asp Asn Gln Val Ile Val Gln Ser Gly | | | |
| 145 | 150 | 155 | 160 |
| cgc cac ccc aca gtg ctg cag aag ctc tgc cag ttg ccc ttc cag tat | | | 528 |
| Arg His Pro Thr Val Leu Gln Lys Leu Cys Gln Leu Pro Phe Gln Tyr | | | |
| | 165 | 170 | 175 |
| ttc agt gac cca cgg ctg atc aaa gta ctg ttc cct tca ctt atc gct | | | 576 |
| Phe Ser Asp Pro Arg Leu Ile Lys Val Leu Phe Pro Ser Leu Ile Ala | | | |
| | 180 | 185 | 190 |
| gct tgt tac aac aac cat cag aac aag atc att ctg gag caa gag atg | | | 624 |
| Ala Cys Tyr Asn Asn His Gln Asn Lys Ile Ile Leu Glu Gln Glu Met | | | |
| | 195 | 200 | 205 |
| agc tgt gtt tta ctg gcc act ttc att cag gat ttg gca cag act cca | | | 672 |
| Ser Cys Val Leu Leu Ala Thr Phe Ile Gln Asp Leu Ala Gln Thr Pro | | | |
| | 210 | 215 | 220 |
| ggt caa gcg gaa aac cag cct tac caa ccc aaa ggg aaa tgc ctt ggt | | | 720 |
| Gly Gln Ala Glu Asn Gln Pro Tyr Gln Pro Lys Gly Lys Cys Leu Gly | | | |
| | 225 | 230 | 235 |
| tcc caa gac tat ctt gag ctg gct aac aga ttt cct cag cag gcc tgg | | | 768 |
| Ser Gln Asp Tyr Leu Glu Leu Ala Asn Arg Phe Pro Gln Gln Ala Trp | | | |
| | 245 | 250 | 255 |
| gaa gaa gct cga cag ttt ttc ttg aaa aaa gag aaa aaa taa | | | 810 |
| Glu Glu Ala Arg Gln Phe Phe Leu Lys Lys Glu Lys Lys * | | | |
| | 260 | 265 | |

<210> 306

<211> 269

<212> PRT

<213> Homo sapiens

451

<400> 306

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Met Ala Ile Phe Leu Gln His Ala Ala Gly Leu Leu His Ala Met Cys
 1              5              10              15
Thr Leu Cys Phe Ala Val Thr Gly Arg Ser Tyr Ser Ile Phe Asp Asn
      20              25              30
Asn Arg Gln Asp Pro Thr Gly Leu Thr Ala Ala Leu Gln Ala Thr Asp
      35              40              45
Leu Ala Gly Val Leu His Met Leu Tyr Cys Val Leu Phe His Gly Thr
      50              55              60
Ile Leu Asp Pro Ser Thr Ala Ser Pro Lys Glu Asn Tyr Thr Gln Asn
65              70              75              80
Thr Ile Gln Val Ala Ile Gln Ser Leu Arg Phe Phe Asn Ser Phe Ala
      85              90              95
Ala Leu His Leu Pro Ala Phe Gln Ser Ile Val Gly Ala Glu Gly Leu
      100             105             110
Ser Leu Ala Phe Arg His Met Ala Ser Ser Leu Leu Gly His Cys Ser
      115             120             125
Gln Val Ser Cys Glu Ser Leu Leu His Glu Val Ile Val Cys Val Gly
      130             135             140
Tyr Phe Thr Val Asn His Pro Asp Asn Gln Val Ile Val Gln Ser Gly
145             150             155             160
Arg His Pro Thr Val Leu Gln Lys Leu Cys Gln Leu Pro Phe Gln Tyr
      165             170             175
Phe Ser Asp Pro Arg Leu Ile Lys Val Leu Phe Pro Ser Leu Ile Ala
      180             185             190
Ala Cys Tyr Asn Asn His Gln Asn Lys Ile Ile Leu Glu Gln Glu Met
      195             200             205
Ser Cys Val Leu Leu Ala Thr Phe Ile Gln Asp Leu Ala Gln Thr Pro
      210             215             220
Gly Gln Ala Glu Asn Gln Pro Tyr Gln Pro Lys Gly Lys Cys Leu Gly
225             230             235             240
Ser Gln Asp Tyr Leu Glu Leu Ala Asn Arg Phe Pro Gln Gln Ala Trp
      245             250             255
Glu Glu Ala Arg Gln Phe Phe Leu Lys Lys Glu Lys Lys
      260             265

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<210> 307

<211> 831

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(831)

452

<400> 307

| | |
|---|-----|
| atg cag aac aag gtg act cag cta gtc ctg tct gcc ttg cag tcc ctg | 48 |
| Met Gln Asn Lys Val Thr Gln Leu Val Leu Ser Ala Leu Gln Ser Leu | |
| 1 5 10 15 | |
| act gac acc ttg ctt ttt ccc ttt tat tct ggg ccg agt ggt acc ctg | 96 |
| Thr Asp Thr Leu Leu Phe Pro Phe Tyr Ser Gly Pro Ser Gly Thr Leu | |
| 20 25 30 | |
| aaa aca gcc ctg ctg gac tac atc aaa cgc tgc cgt cct gga gac agt | 144 |
| Lys Thr Ala Leu Leu Asp Tyr Ile Lys Arg Cys Arg Pro Gly Asp Ser | |
| 35 40 45 | |
| gaa aag cac aat atg att gcc ctg tgc ttc agc atg tgc cgg gag att | 192 |
| Glu Lys His Asn Met Ile Ala Leu Cys Phe Ser Met Cys Arg Glu Ile | |
| 50 55 60 | |
| ggc gag aac cac gag gca gct gcc cgc atc caa ctg aaa ttg att gag | 240 |
| Gly Glu Asn His Glu Ala Ala Ala Arg Ile Gln Leu Lys Leu Ile Glu | |
| 65 70 75 80 | |
| tct cag ccc tgg gag gac agc ctc aag gat ggg cac cag ctg aaa caa | 288 |
| Ser Gln Pro Trp Glu Asp Ser Leu Lys Asp Gly His Gln Leu Lys Gln | |
| 85 90 95 | |
| ctg ctg ctg aag gcc ctg act ctg atg ttg gat gca gca gag agt tat | 336 |
| Leu Leu Leu Lys Ala Leu Thr Leu Met Leu Asp Ala Ala Glu Ser Tyr | |
| 100 105 110 | |
| gcc aag gac tcc tgt gtg cga cag gcc cag cac tgt cag cgg ctc acc | 384 |
| Ala Lys Asp Ser Cys Val Arg Gln Ala Gln His Cys Gln Arg Leu Thr | |
| 115 120 125 | |
| aag ttg ata act ctg cag att cac ttt ctg aac act ggc cag aac aca | 432 |
| Lys Leu Ile Thr Leu Gln Ile His Phe Leu Asn Thr Gly Gln Asn Thr | |
| 130 135 140 | |
| atg ctc atc aac ttg ggc cgc cac aag ctg atg gac tgt att ctg gcc | 480 |
| Met Leu Ile Asn Leu Gly Arg His Lys Leu Met Asp Cys Ile Leu Ala | |
| 145 150 155 160 | |
| cta cct cgg ttc tac cag gct tct att gtg gct gag gcc tac gat ttt | 528 |
| Leu Pro Arg Phe Tyr Gln Ala Ser Ile Val Ala Glu Ala Tyr Asp Phe | |

453

165

170

175

gtt cca gat tgg gct gaa att tta tac cag caa gtg att ctt aaa gga 576
 Val Pro Asp Trp Ala Glu Ile Leu Tyr Gln Gln Val Ile Leu Lys Gly
 180 185 190

gac ttt aat tac ttg gaa gaa ttt aag cag caa agg tta tta aag tcc 624
 Asp Phe Asn Tyr Leu Glu Glu Phe Lys Gln Gln Arg Leu Leu Lys Ser
 195 200 205

agt ata ttt gaa gag att tcc aaa aaa tat aaa caa cat cag cct act 672
 Ser Ile Phe Glu Glu Ile Ser Lys Lys Tyr Lys Gln His Gln Pro Thr
 210 215 220

gac atg gtc atg gaa aac ctg aag aaa tta ctc aca tat tgt gaa gat 720
 Asp Met Val Met Glu Asn Leu Lys Lys Leu Leu Thr Tyr Cys Glu Asp
 225 230 235 240

gtt tac ctg tat tac aag ttg gca tac gaa cac aag ttt tat gaa att 768
 Val Tyr Leu Tyr Tyr Lys Leu Ala Tyr Glu His Lys Phe Tyr Glu Ile
 245 250 255

gta aat gtg ctt ctg aag gac cct cag aca ggt tgc tgt cta aag gac 816
 Val Asn Val Leu Leu Lys Asp Pro Gln Thr Gly Cys Cys Leu Lys Asp
 260 265 270

atg cta gca ggt tag 831
 Met Leu Ala Gly *
 275

<210> 308

<211> 276

<212> PRT

<213> Homo sapiens

<400> 308

Met Gln Asn Lys Val Thr Gln Leu Val Leu Ser Ala Leu Gln Ser Leu
 1 5 10 15
 Thr Asp Thr Leu Leu Phe Pro Phe Tyr Ser Gly Pro Ser Gly Thr Leu
 20 25 30
 Lys Thr Ala Leu Leu Asp Tyr Ile Lys Arg Cys Arg Pro Gly Asp Ser
 35 40 45
 Glu Lys His Asn Met Ile Ala Leu Cys Phe Ser Met Cys Arg Glu Ile

454

50 55 60
 Gly Glu Asn His Glu Ala Ala Arg Ile Gln Leu Lys Leu Ile Glu
 65 70 75 80
 Ser Gln Pro Trp Glu Asp Ser Leu Lys Asp Gly His Gln Leu Lys Gln
 85 90 95
 Leu Leu Leu Lys Ala Leu Thr Leu Met Leu Asp Ala Ala Glu Ser Tyr
 100 105 110
 Ala Lys Asp Ser Cys Val Arg Gln Ala Gln His Cys Gln Arg Leu Thr
 115 120 125
 Lys Leu Ile Thr Leu Gln Ile His Phe Leu Asn Thr Gly Gln Asn Thr
 130 135 140
 Met Leu Ile Asn Leu Gly Arg His Lys Leu Met Asp Cys Ile Leu Ala
 145 150 155 160
 Leu Pro Arg Phe Tyr Gln Ala Ser Ile Val Ala Glu Ala Tyr Asp Phe
 165 170 175
 Val Pro Asp Trp Ala Glu Ile Leu Tyr Gln Gln Val Ile Leu Lys Gly
 180 185 190
 Asp Phe Asn Tyr Leu Glu Glu Phe Lys Gln Gln Arg Leu Leu Lys Ser
 195 200 205
 Ser Ile Phe Glu Glu Ile Ser Lys Lys Tyr Lys Gln His Gln Pro Thr
 210 215 220
 Asp Met Val Met Glu Asn Leu Lys Lys Leu Leu Thr Tyr Cys Glu Asp
 225 230 235 240
 Val Tyr Leu Tyr Tyr Lys Leu Ala Tyr Glu His Lys Phe Tyr Glu Ile
 245 250 255
 Val Asn Val Leu Lys Asp Pro Gln Thr Gly Cys Cys Leu Lys Asp
 260 265 270
 Met Leu Ala Gly
 275

<210> 309
 <211> 369
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(369)

<400> 309

atg agg aca att gat gac aga ata gta cat gaa tta aac act acg gtt
 Met Arg Thr Ile Asp Asp Arg Ile Val His Glu Leu Asn Thr Thr Val
 1 5 10 15

48

455

| | |
|---|-----|
| cca aca gct tcc ttt gca ggg aaa att gat gcc agc caa acc tgt aaa | 96 |
| Pro Thr Ala Ser Phe Ala Gly Lys Ile Asp Ala Ser Gln Thr Cys Lys | |
| 20 25 30 | |
| caa ctt tat gag tct ttg atg gca gct cat gcc agt aga gac aga gtc | 144 |
| Gln Leu Tyr Glu Ser Leu Met Ala Ala His Ala Ser Arg Asp Arg Val | |
| 35 40 45 | |
| ata aaa aac tgt ata gcc cag act tca gca gta gta aaa aac ctc cga | 192 |
| Ile Lys Asn Cys Ile Ala Gln Thr Ser Ala Val Val Lys Asn Leu Arg | |
| 50 55 60 | |
| gaa gag aga gaa aag aat ttg gac gat tta acg tta tta aaa caa ctt | 240 |
| Glu Glu Arg Glu Lys Asn Leu Asp Asp Leu Thr Leu Leu Lys Gln Leu | |
| 65 70 75 80 | |
| aga aaa gag cag aca aag ttg aaa tgg atg cag tca gaa ctg aat gtt | 288 |
| Arg Lys Glu Gln Thr Lys Leu Lys Trp Met Gln Ser Glu Leu Asn Val | |
| 85 90 95 | |
| gaa gaa gtg gta aat gac agg agc tgg aag gtg ttt aat gaa cgc tgc | 336 |
| Glu Glu Val Val Asn Asp Arg Ser Trp Lys Val Phe Asn Glu Arg Cys | |
| 100 105 110 | |
| cga att cac ttc aag cct cca aag aat gaa taa | 369 |
| Arg Ile His Phe Lys Pro Pro Lys Asn Glu * | |
| 115 120 | |

<210> 310

<211> 122

<212> PRT

<213> Homo sapiens

<400> 310

| | |
|---|--|
| Met Arg Thr Ile Asp Asp Arg Ile Val His Glu Leu Asn Thr Thr Val | |
| 1 5 10 15 | |
| Pro Thr Ala Ser Phe Ala Gly Lys Ile Asp Ala Ser Gln Thr Cys Lys | |
| 20 25 30 | |
| Gln Leu Tyr Glu Ser Leu Met Ala Ala His Ala Ser Arg Asp Arg Val | |
| 35 40 45 | |
| Ile Lys Asn Cys Ile Ala Gln Thr Ser Ala Val Val Lys Asn Leu Arg | |
| 50 55 60 | |
| Glu Glu Arg Glu Lys Asn Leu Asp Asp Leu Thr Leu Leu Lys Gln Leu | |

65 70 75 80
Arg Lys Glu Gln Thr Lys Leu Lys Trp Met Gln Ser Glu Leu Asn Val
 85 90 95
Glu Glu Val Val Asn Asp Arg Ser Trp Lys Val Phe Asn Glu Arg Cys
 100 105 110
Arg Ile His Phe Lys Pro Pro Lys Asn Glu
 115 120

```
<210> 311
<211> 549
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (1)...(549)

| | | | | | | | | | | | | | | | | | |
|---|-----|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|
| <400> 311 | | | | | | | | | | | | | | | | | |
| atg gtc ccc gcc gcc ggc gcg ctg ctg tgg gtc ctg ctg ctg aat ctg | 48 | | | | | | | | | | | | | | | | |
| Met Val Pro Ala Ala Gly Ala Leu Leu Trp Val Leu Leu Leu Asn Leu | | | | | | | | | | | | | | | | | |
| 1 5 10 15 | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | |
| ggt ccc cgg gcg gcg ggg gcc caa ggc ctg acc cag act ccg acc gaa | 96 | | | | | | | | | | | | | | | | |
| Gly Pro Arg Ala Ala Gly Ala Gln Gly Leu Thr Gln Thr Pro Thr Glu | | | | | | | | | | | | | | | | | |
| 20 25 30 | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | |
| atg cag cgg gtc agt tta cgc ttt ggg ggc ccc atg acc cgc agc tac | 144 | | | | | | | | | | | | | | | | |
| Met Gln Arg Val Ser Leu Arg Phe Gly Gly Pro Met Thr Arg Ser Tyr | | | | | | | | | | | | | | | | | |
| 35 40 45 | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | |
| cgg agc acc gcc cgg act ggt ctt ccc cgg aag aca agg ata atc cta | 192 | | | | | | | | | | | | | | | | |
| Arg Ser Thr Ala Arg Thr Gly Leu Pro Arg Lys Thr Arg Ile Ile Leu | | | | | | | | | | | | | | | | | |
| 50 55 60 | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | |
| gag gac gag aat gat gcc atg gcc gac gcc gac cgc ctg gct gga cca | 240 | | | | | | | | | | | | | | | | |
| Glu Asp Glu Asn Asp Ala Met Ala Asp Ala Asp Arg Leu Ala Gly Pro | | | | | | | | | | | | | | | | | |
| 65 70 75 80 | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | |
| gcg gct gcc gag ctc ttg gcc gcc acg gtg tcc acc ggc ttt agc cgg | 288 | | | | | | | | | | | | | | | | |
| Ala Ala Ala Glu Leu Leu Ala Ala Thr Val Ser Thr Gly Phe Ser Arg | | | | | | | | | | | | | | | | | |
| 85 90 95 | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | |
| tcg tcc gcc att aac gag gag gat ggg tct tca gaa gag ggg gtt gtg | 336 | | | | | | | | | | | | | | | | |
| Ser Ser Ala Ile Asn Glu Glu Asp Gly Ser Ser Glu Glu Gly Val Val | | | | | | | | | | | | | | | | | |

457

| 100 | 105 | 110 | |
|---|-----|-----|-----|
| att aat gct gat gcc ctg ggg ccc gtg gca ctg cca ctg caa gtc ggg | | | 384 |
| Ile Asn Ala Asp Ala Leu Gly Pro Val Ala Leu Pro Leu Gln Val Gly | | | |
| 115 | 120 | 125 | |
| cac cat gag ccg gag ccg gtc tgg gaa gct gca cgg cct ttc cgg gcg | | | 432 |
| His His Glu Pro Glu Pro Val Trp Glu Ala Ala Arg Pro Phe Arg Ala | | | |
| 130 | 135 | 140 | |
| cct tcg agt tgg ggc gct gag cca gct ccg cac gga gca caa gcc ttg | | | 480 |
| Pro Ser Ser Trp Gly Ala Glu Pro Ala Pro His Gly Ala Gln Ala Leu | | | |
| 145 | 150 | 155 | 160 |
| cac cta tca aca atg tcc ctg caa ccg act tcg gga aga gtg ccc cct | | | 528 |
| His Leu Ser Thr Met Ser Leu Gln Pro Thr Ser Gly Arg Val Pro Pro | | | |
| 165 | 170 | 175 | |
| gga cac aag tct ctg tac tga | | | 549 |
| Gly His Lys Ser Leu Tyr * | | | |
| 180 | | | |

<210> 312
 <211> 182
 <212> PRT
 <213> Homo sapiens

<400> 312

| | | | |
|---|-----|-----|----|
| Met Val Pro Ala Ala Gly Ala Leu Leu Trp Val Leu Leu Leu Asn Leu | | | |
| 1 | 5 | 10 | 15 |
| Gly Pro Arg Ala Ala Gly Ala Gln Gly Leu Thr Gln Thr Pro Thr Glu | | | |
| 20 | 25 | 30 | |
| Met Gln Arg Val Ser Leu Arg Phe Gly Gly Pro Met Thr Arg Ser Tyr | | | |
| 35 | 40 | 45 | |
| Arg Ser Thr Ala Arg Thr Gly Leu Pro Arg Lys Thr Arg Ile Ile Leu | | | |
| 50 | 55 | 60 | |
| Glu Asp Glu Asn Asp Ala Met Ala Asp Ala Asp Arg Leu Ala Gly Pro | | | |
| 65 | 70 | 75 | 80 |
| Ala Ala Ala Glu Leu Leu Ala Ala Thr Val Ser Thr Gly Phe Ser Arg | | | |
| 85 | 90 | 95 | |
| Ser Ser Ala Ile Asn Glu Glu Asp Gly Ser Ser Glu Glu Gly Val Val | | | |
| 100 | 105 | 110 | |
| Ile Asn Ala Asp Ala Leu Gly Pro Val Ala Leu Pro Leu Gln Val Gly | | | |

458

```

      115              120              125
His His Glu Pro Glu Pro Val Trp Glu Ala Ala Arg Pro Phe Arg Ala
      130              135              140
Pro Ser Ser Trp Gly Ala Glu Pro Ala Pro His Gly Ala Gln Ala Leu
145              150              155              160
His Leu Ser Thr Met Ser Leu Gln Pro Thr Ser Gly Arg Val Pro Pro
      165              170              175
Gly His Lys Ser Leu Tyr
      180

```

```

<210> 313
<211> 225
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (1)...(225)

<221> misc_feature
<222> (1)...(225)
<223> n = A,T,C or G

```

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<400> 313
atg cac cca gct aag act ggc ttg acc gnn agc ctg gcc ttt ggt ggg      48
Met His Pro Ala Lys Thr Gly Leu Thr Xaa Ser Leu Ala Phe Gly Gly
  1              5              10              15

ggg ctt cct ggg gcc tgg gga aag ctg gcc acc ttc aac agc tgg tac      96
Gly Leu Pro Gly Ala Trp Gly Lys Leu Ala Thr Phe Asn Ser Trp Tyr
      20              25              30

ctc ttc aac agt gtg gcc ttt caa aat gca gat gcc acc agg aga aca      144
Leu Phe Asn Ser Val Ala Phe Gln Asn Ala Asp Ala Thr Arg Arg Thr
      35              40              45

tgc cca cag ctc acc acc tat gga tgc cat ggc tct ggg cag ctt tca      192
Cys Pro Gln Leu Thr Thr Tyr Gly Cys His Gly Ser Gly Gln Leu Ser
      50              55              60

aag cag gtt cct gtg gtc tcc tca gct gtt tga      225
Lys Gln Val Pro Val Val Ser Ser Ala Val *
  65              70

```

459

<210> 314
 <211> 74
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(74)
 <223> Xaa = Any Amino Acid

<400> 314
 Met His Pro Ala Lys Thr Gly Leu Thr Xaa Ser Leu Ala Phe Gly Gly
 1 5 10 15
 Gly Leu Pro Gly Ala Trp Gly Lys Leu Ala Thr Phe Asn Ser Trp Tyr
 20 25 30
 Leu Phe Asn Ser Val Ala Phe Gln Asn Ala Asp Ala Thr Arg Arg Thr
 35 40 45
 Cys Pro Gln Leu Thr Thr Tyr Gly Cys His Gly Ser Gly Gln Leu Ser
 50 55 60
 Lys Gln Val Pro Val Val Ser Ser Ala Val
 65 70

<210> 315
 <211> 1086
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1086)

<400> 315
 atg gcc agc ctg ggg ctg ctg ctc ctg ctc tta ctg aca gca ctg cca 48
 Met Ala Ser Leu Gly Leu Leu Leu Leu Leu Leu Thr Ala Leu Pro
 1 5 10 15
 ccg ctg tgg tcc tcc tca ctg cct ggg ctg gac act gct gaa agt aaa 96
 Pro Leu Trp Ser Ser Ser Leu Pro Gly Leu Asp Thr Ala Glu Ser Lys
 20 25 30
 gcc acc att gca gac ctg atc ctg tct gcg ctg gag aga gcc acc gtc 144
 Ala Thr Ile Ala Asp Leu Ile Leu Ser Ala Leu Glu Arg Ala Thr Val
 35 40 45

460

| | |
|---|-----|
| ttc cta gaa cag agg ctg cct gaa atc aac ctg gat ggc atg gtg ggg Phe Leu Glu Gln Arg Leu Pro Glu Ile Asn Leu Asp Gly Met Val Gly 50 55 60 | 192 |
| gtc cga gtg ctg gaa gag cag cta aaa agt gtc cgg gag aag tgg gcc Val Arg Val Leu Glu Glu Gln Leu Lys Ser Val Arg Glu Lys Trp Ala 65 70 75 80 | 240 |
| cag gag ccc ctg ctg cag ccg ctg agc ctg cgc gtg ggg atg ctg ggg Gln Glu Pro Leu Leu Gln Pro Leu Ser Leu Arg Val Gly Met Leu Gly 85 90 95 | 288 |
| gag aag ctg gag gct gcc atc cag aga tcc ctc cac tac ctc aag ctg Glu Lys Leu Glu Ala Ala Ile Gln Arg Ser Leu His Tyr Leu Lys Leu 100 105 110 | 336 |
| agt gat ccc aag tac cta aga gag ttc cag ctg acc ctc cag ccc ggg Ser Asp Pro Lys Tyr Leu Arg Glu Phe Gln Leu Thr Leu Gln Pro Gly 115 120 125 | 384 |
| ttt tgg aag ctc cca cat gcc tgg atc cac act gat gcc tcc ttg gtg Phe Trp Lys Leu Pro His Ala Trp Ile His Thr Asp Ala Ser Leu Val 130 135 140 | 432 |
| tac ccc acg ttc ggg ccc cag gac tca ttc tca gag gag aga agt gac Tyr Pro Thr Phe Gly Pro Gln Asp Ser Phe Ser Glu Glu Arg Ser Asp 145 150 155 160 | 480 |
| gtg tgc ctg gtg cag ctg ctg gga acc ggg acg gac agc agc gag ccc Val Cys Leu Val Gln Leu Leu Gly Thr Gly Thr Asp Ser Ser Glu Pro 165 170 175 | 528 |
| tgc ggc ctc tca gac ctc tgc agg agc ctc atg acc aag ccc ggc tgc Cys Gly Leu Ser Asp Leu Cys Arg Ser Leu Met Thr Lys Pro Gly Cys 180 185 190 | 576 |
| tca ggc tac tgc ctg tcc cac caa ctg ctc ttc ttc ctc tgg gcc aga Ser Gly Tyr Cys Leu Ser His Gln Leu Leu Phe Phe Leu Trp Ala Arg 195 200 205 | 624 |
| atg agg gga tgc aca cag gga cca ctc caa cag agc cag gac tat atc Met Arg Gly Cys Thr Gln Gly Pro Leu Gln Gln Ser Gln Asp Tyr Ile 210 215 220 | 672 |

| | |
|---|------|
| aac ctc ttc tgc gcc aac atg atg gac ttg aac cgc aga gct gag gcc | 720 |
| Asn Leu Phe Cys Ala Asn Met Met Asp Leu Asn Arg Arg Ala Glu Ala | |
| 225 230 235 240 | |
| atc gga tac gcc tac cct acc cgg gac atc ttc atg gaa aac atc atg | 768 |
| Ile Gly Tyr Ala Tyr Pro Thr Arg Asp Ile Phe Met Glu Asn Ile Met | |
| 245 250 255 | |
| ttc tgt gga atg ggc ggc ttc tcc gac ttc tac aag ctc cgg tgg ctg | 816 |
| Phe Cys Gly Met Gly Gly Phe Ser Asp Phe Tyr Lys Leu Arg Trp Leu | |
| 260 265 270 | |
| gag gcc att ctc agc tgg cag aaa cag cag gaa gga tgc ttc ggg gag | 864 |
| Glu Ala Ile Leu Ser Trp Gln Lys Gln Gln Glu Gly Cys Phe Gly Glu | |
| 275 280 285 | |
| cct gat gct gaa gat gaa gaa tca tct aaa gct att caa tat cag cag | 912 |
| Pro Asp Ala Glu Asp Glu Glu Ser Ser Lys Ala Ile Gln Tyr Gln Gln | |
| 290 295 300 | |
| cat ttt tcg agg aga gtg aag agg cga gaa aaa caa ttt cca gat ggc | 960 |
| His Phe Ser Arg Arg Val Lys Arg Arg Glu Lys Gln Phe Pro Asp Gly | |
| 305 310 315 320 | |
| tgc tcc tcc cac aac aca gcc aca gca gtg gca gcc ctg ggt ggc ttc | 1008 |
| Cys Ser Ser His Asn Thr Ala Thr Ala Val Ala Ala Leu Gly Gly Phe | |
| 325 330 335 | |
| cta tac atc ctg gca gaa tac ccc cca gca aac aga gag cca cac cca | 1056 |
| Leu Tyr Ile Leu Ala Glu Tyr Pro Pro Ala Asn Arg Glu Pro His Pro | |
| 340 345 350 | |
| tcc aca ccg cca cca cca agc agc cgc tga | 1086 |
| Ser Thr Pro Pro Pro Pro Ser Ser Arg * | |
| 355 360 | |

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<210> 316
<211> 361
<212> PRT
<213> Homo sapiens
<400> 316
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462

Met Ala Ser Leu Gly Leu Leu Leu Leu Leu Leu Thr Ala Leu Pro
 1 5 10 15
 Pro Leu Trp Ser Ser Ser Leu Pro Gly Leu Asp Thr Ala Glu Ser Lys
 20 25 30
 Ala Thr Ile Ala Asp Leu Ile Leu Ser Ala Leu Glu Arg Ala Thr Val
 35 40 45
 Phe Leu Glu Gln Arg Leu Pro Glu Ile Asn Leu Asp Gly Met Val Gly
 50 55 60
 Val Arg Val Leu Glu Glu Gln Leu Lys Ser Val Arg Glu Lys Trp Ala
 65 70 75 80
 Gln Glu Pro Leu Leu Gln Pro Leu Ser Leu Arg Val Gly Met Leu Gly
 85 90 95
 Glu Lys Leu Glu Ala Ala Ile Gln Arg Ser Leu His Tyr Leu Lys Leu
 100 105 110
 Ser Asp Pro Lys Tyr Leu Arg Glu Phe Gln Leu Thr Leu Gln Pro Gly
 115 120 125
 Phe Trp Lys Leu Pro His Ala Trp Ile His Thr Asp Ala Ser Leu Val
 130 135 140
 Tyr Pro Thr Phe Gly Pro Gln Asp Ser Phe Ser Glu Glu Arg Ser Asp
 145 150 155 160
 Val Cys Leu Val Gln Leu Leu Gly Thr Gly Thr Asp Ser Ser Glu Pro
 165 170 175
 Cys Gly Leu Ser Asp Leu Cys Arg Ser Leu Met Thr Lys Pro Gly Cys
 180 185 190
 Ser Gly Tyr Cys Leu Ser His Gln Leu Leu Phe Phe Leu Trp Ala Arg
 195 200 205
 Met Arg Gly Cys Thr Gln Gly Pro Leu Gln Gln Ser Gln Asp Tyr Ile
 210 215 220
 Asn Leu Phe Cys Ala Asn Met Met Asp Leu Asn Arg Arg Ala Glu Ala
 225 230 235 240
 Ile Gly Tyr Ala Tyr Pro Thr Arg Asp Ile Phe Met Glu Asn Ile Met
 245 250 255
 Phe Cys Gly Met Gly Gly Phe Ser Asp Phe Tyr Lys Leu Arg Trp Leu
 260 265 270
 Glu Ala Ile Leu Ser Trp Gln Lys Gln Gln Glu Gly Cys Phe Gly Glu
 275 280 285
 Pro Asp Ala Glu Asp Glu Glu Ser Ser Lys Ala Ile Gln Tyr Gln Gln
 290 295 300
 His Phe Ser Arg Arg Val Lys Arg Arg Glu Lys Gln Phe Pro Asp Gly
 305 310 315 320
 Cys Ser Ser His Asn Thr Ala Thr Ala Val Ala Ala Leu Gly Gly Phe
 325 330 335
 Leu Tyr Ile Leu Ala Glu Tyr Pro Pro Ala Asn Arg Glu Pro His Pro
 340 345 350

463

Ser Thr Pro Pro Pro Pro Ser Ser Arg
 355 360

<210> 317
 <211> 1440
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1440)
 <221> misc_feature
 <222> (1)...(1440)
 <223> n = A,T,C or G

<400> 317
 atg gcg gtc ctc gga gta cag ctg gtg gtg acc ctg ctc act gcc acc 48
 Met Ala Val Leu Gly Val Gln Leu Val Val Thr Leu Leu Thr Ala Thr
 1 5 10 15
 ctc atg cac agg ctg gcg cca cac tgc tcc ttc gcg cgc tgg ctg ctc 96
 Leu Met His Arg Leu Ala Pro His Cys Ser Phe Ala Arg Trp Leu Leu
 20 25 30
 tgt aac ggc agt ttg ttc cga tac aag cac ccg tct gag gag gag ctt 144
 Cys Asn Gly Ser Leu Phe Arg Tyr Lys His Pro Ser Glu Glu Glu Leu
 35 40 45
 cgg gcc ctg gcg ggg aag ccg agg ccc aga ggc agg aaa gag cgg tgg 192
 Arg Ala Leu Ala Gly Lys Pro Arg Pro Arg Gly Arg Lys Glu Arg Trp
 50 55 60
 gcc aat ggc ctt agt gag gag aag cca ctg tct gtg ccc cga gat gcc 240
 Ala Asn Gly Leu Ser Glu Glu Lys Pro Leu Ser Val Pro Arg Asp Ala
 65 70 75 80
 ccg ttc cag ctg gag acc tgc ccc ctc acg acc gtg gat gcc ctg gtc 288
 Pro Phe Gln Leu Glu Thr Cys Pro Leu Thr Thr Val Asp Ala Leu Val
 85 90 95
 ctg cgc ttc ttc ctg gag tac cag tgg ttt gtg gac ttt gct gtg tac 336
 Leu Arg Phe Phe Leu Glu Tyr Gln Trp Phe Val Asp Phe Ala Val Tyr
 100 105 110

464

| | |
|---|-----|
| tcg ggc ggc gtg tac ctc ttc aca gag gcc tac tac tac atg ctg gga Ser Gly Gly Val Tyr Leu Phe Thr Glu Ala Tyr Tyr Tyr Met Leu Gly 115 120 125 | 384 |
| cca gcc aag gag act aac att gct gtg ttc tgg tgc ctg ctc acg gtg Pro Ala Lys Glu Thr Asn Ile Ala Val Phe Trp Cys Leu Leu Thr Val 130 135 140 | 432 |
| acc ttc tcc atc aag atg ttc ctg aca gtg aca cgg ctg tac ttc agc Thr Phe Ser Ile Lys Met Phe Leu Thr Val Thr Arg Leu Tyr Phe Ser 145 150 155 160 | 480 |
| gcc gag gag ggg ggt gag cgc tct gtc tgc ctc acc ttt gcc ttc ctc Ala Glu Glu Gly Gly Glu Arg Ser Val Cys Leu Thr Phe Ala Phe Leu 165 170 175 | 528 |
| ttc ctg ctg ctg gcc atg ctg gtg caa gtg gtg cgg gag gag acc ctc Phe Leu Leu Leu Ala Met Leu Val Gln Val Val Arg Glu Glu Thr Leu 180 185 190 | 576 |
| gag ctg ggc ctg gag cct ggt ctg gcc agc atg acc cag aac tta gag Glu Leu Gly Leu Glu Pro Gly Leu Ala Ser Met Thr Gln Asn Leu Glu 195 200 205 | 624 |
| cca ctt ctg aag aag cag ggc tgg gac tgg gcg ctt cct gtg gcc aag Pro Leu Leu Lys Lys Gln Gly Trp Asp Trp Ala Leu Pro Val Ala Lys 210 215 220 | 672 |
| ctg gct atc cgc gtg gga ctg gca gtg gtg ggc tct gtg ctg ggt gcc Leu Ala Ile Arg Val Gly Leu Ala Val Val Gly Ser Val Leu Gly Ala 225 230 235 240 | 720 |
| ttc ctc acc ttc cca ggc ctg cgg ctg gcc cag acc cac cgg gac gca Phe Leu Thr Phe Pro Gly Leu Arg Leu Ala Gln Thr His Arg Asp Ala 245 250 255 | 768 |
| ctg acc atg tcg gag gac aga ccc atg ctg cag ttc ctc ctg cac acc Leu Thr Met Ser Glu Asp Arg Pro Met Leu Gln Phe Leu Leu His Thr 260 265 270 | 816 |
| agc ttc ctg tct ccc ctg ttc atc ctg tgg ctc tgg aca aag ccc att Ser Phe Leu Ser Pro Leu Phe Ile Leu Trp Leu Trp Thr Lys Pro Ile 275 280 285 | 864 |

465

| | |
|---|------|
| gca cgg gac ttc ctg cac cag ccg ccg ttt ggg gag acg cgt ttc tcc Ala Arg Asp Phe Leu His Gln Pro Pro Phe Gly Glu Thr Arg Phe Ser 290 295 300 | 912 |
| ctg ctg tcc gat tct gcc ttc gac tct ggg cgc ctc tgg ttg ctg gtg Leu Leu Ser Asp Ser Ala Phe Asp Ser Gly Arg Leu Trp Leu Leu Val 305 310 315 320 | 960 |
| gtg ctg tgc ctg ctg cgg ctg gcg gtg acc cgg ccc cac ctg cag gcc Val Leu Cys Leu Leu Arg Leu Ala Val Thr Arg Pro His Leu Gln Ala 325 330 335 | 1008 |
| tac ctg tgc ctg gcc aag gcc cgg gtg gag cag ctg cga agg gag gct Tyr Leu Cys Leu Ala Lys Ala Arg Val Glu Gln Leu Arg Arg Glu Ala 340 345 350 | 1056 |
| ggc cgc atc gaa gcc cgt gaa atc cag cag agg gtg gtc cga gtc tac Gly Arg Ile Glu Ala Arg Glu Ile Gln Gln Arg Val Val Arg Val Tyr 355 360 365 | 1104 |
| tgc tat gtg acc gtg gtg agc ttg cag tac ctg acg ccg ctc atc ctc Cys Tyr Val Thr Val Val Ser Leu Gln Tyr Leu Thr Pro Leu Ile Leu 370 375 380 | 1152 |
| acc ctc aac tgc aca ctt ctg ctc aag acg ctg gga ggc tat tcc tgg Thr Leu Asn Cys Thr Leu Leu Lys Thr Leu Gly Gly Tyr Ser Trp 385 390 395 400 | 1200 |
| ggc ctg ggc cca gct cct cta cta tcc ccc gac cca tcc tca gcc agc Gly Leu Gly Pro Ala Pro Leu Leu Ser Pro Asp Pro Ser Ser Ala Ser 405 410 415 | 1248 |
| gct gcc ccc atc ggc tct ggg gag gac gaa gtc nag cag act gca gcg Ala Ala Pro Ile Gly Ser Gly Glu Asp Glu Val Xaa Gln Thr Ala Ala 420 425 430 | 1296 |
| cgg att gcc ggg gcc ctg ggt ggc ctg ctt act ccc ctc ttc ctc cgt Arg Ile Ala Gly Ala Leu Gly Gly Leu Leu Thr Pro Leu Phe Leu Arg 435 440 445 | 1344 |
| ggc gtc ctg gcc tac ctc atc tgg tgg acg gct gcc tgc cag ctg ctc Gly Val Leu Ala Tyr Leu Ile Trp Trp Thr Ala Ala Cys Gln Leu Leu 450 455 460 | 1392 |

466

gcc agc ctt ttc ggc ctc tac ttc cac cag cac ttg gca ggc tcc tag 1440
 Ala Ser Leu Phe Gly Leu Tyr Phe His Gln His Leu Ala Gly Ser *
 465 470 475

<210> 318
 <211> 479
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(479)
 <223> Xaa = Any Amino Acid

<400> 318
 Met Ala Val Leu Gly Val Gln Leu Val Val Thr Leu Leu Thr Ala Thr
 1 5 10 15
 Leu Met His Arg Leu Ala Pro His Cys Ser Phe Ala Arg Trp Leu Leu
 20 25 30
 Cys Asn Gly Ser Leu Phe Arg Tyr Lys His Pro Ser Glu Glu Glu Leu
 35 40 45
 Arg Ala Leu Ala Gly Lys Pro Arg Pro Arg Gly Arg Lys Glu Arg Trp
 50 55 60
 Ala Asn Gly Leu Ser Glu Glu Lys Pro Leu Ser Val Pro Arg Asp Ala
 65 70 75 80
 Pro Phe Gln Leu Glu Thr Cys Pro Leu Thr Thr Val Asp Ala Leu Val
 85 90 95
 Leu Arg Phe Phe Leu Glu Tyr Gln Trp Phe Val Asp Phe Ala Val Tyr
 100 105 110
 Ser Gly Gly Val Tyr Leu Phe Thr Glu Ala Tyr Tyr Tyr Met Leu Gly
 115 120 125
 Pro Ala Lys Glu Thr Asn Ile Ala Val Phe Trp Cys Leu Leu Thr Val
 130 135 140
 Thr Phe Ser Ile Lys Met Phe Leu Thr Val Thr Arg Leu Tyr Phe Ser
 145 150 155 160
 Ala Glu Glu Gly Gly Glu Arg Ser Val Cys Leu Thr Phe Ala Phe Leu
 165 170 175
 Phe Leu Leu Leu Ala Met Leu Val Gln Val Val Arg Glu Glu Thr Leu
 180 185 190
 Glu Leu Gly Leu Glu Pro Gly Leu Ala Ser Met Thr Gln Asn Leu Glu
 195 200 205
 Pro Leu Leu Lys Lys Gln Gly Trp Asp Trp Ala Leu Pro Val Ala Lys

467

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      210              215              220
Leu Ala Ile Arg Val Gly Leu Ala Val Val Gly Ser Val Leu Gly Ala
225              230              235              240
Phe Leu Thr Phe Pro Gly Leu Arg Leu Ala Gln Thr His Arg Asp Ala
      245              250              255
Leu Thr Met Ser Glu Asp Arg Pro Met Leu Gln Phe Leu Leu His Thr
      260              265              270
Ser Phe Leu Ser Pro Leu Phe Ile Leu Trp Leu Trp Thr Lys Pro Ile
      275              280              285
Ala Arg Asp Phe Leu His Gln Pro Pro Phe Gly Glu Thr Arg Phe Ser
      290              295              300
Leu Leu Ser Asp Ser Ala Phe Asp Ser Gly Arg Leu Trp Leu Leu Val
305              310              315              320
Val Leu Cys Leu Leu Arg Leu Ala Val Thr Arg Pro His Leu Gln Ala
      325              330              335
Tyr Leu Cys Leu Ala Lys Ala Arg Val Glu Gln Leu Arg Arg Glu Ala
      340              345              350
Gly Arg Ile Glu Ala Arg Glu Ile Gln Gln Arg Val Val Arg Val Tyr
      355              360              365
Cys Tyr Val Thr Val Val Ser Leu Gln Tyr Leu Thr Pro Leu Ile Leu
      370              375              380
Thr Leu Asn Cys Thr Leu Leu Leu Lys Thr Leu Gly Gly Tyr Ser Trp
385              390              395              400
Gly Leu Gly Pro Ala Pro Leu Leu Ser Pro Asp Pro Ser Ser Ala Ser
      405              410              415
Ala Ala Pro Ile Gly Ser Gly Glu Asp Glu Val Xaa Gln Thr Ala Ala
      420              425              430
Arg Ile Ala Gly Ala Leu Gly Gly Leu Leu Thr Pro Leu Phe Leu Arg
      435              440              445
Gly Val Leu Ala Tyr Leu Ile Trp Trp Thr Ala Ala Cys Gln Leu Leu
      450              455              460
Ala Ser Leu Phe Gly Leu Tyr Phe His Gln His Leu Ala Gly Ser
465              470              475

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<210> 319

<211> 333

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(333)

<400> 319

468

| | |
|---|-----|
| atg gct gct tca tca tca tcc tcc tca gct ggt ggg gtc agt gga agt | 48 |
| Met Ala Ala Ser Ser Ser Ser Ser Ala Gly Gly Val Ser Gly Ser | |
| 1 5 10 15 | |
| tct gtc act gga tct ggt ttc agt gtc tca gac ctt gcc cca cca cgg | 96 |
| Ser Val Thr Gly Ser Gly Phe Ser Val Ser Asp Leu Ala Pro Pro Arg | |
| 20 25 30 | |
| aaa gcc ctt ttc acc tac ccc aaa gga gct gga gag atg tta gaa gat | 144 |
| Lys Ala Leu Phe Thr Tyr Pro Lys Gly Ala Gly Glu Met Leu Glu Asp | |
| 35 40 45 | |
| ggc tct gag aga ttc ctc tgc gaa tct gtt ttt agc tat caa gtg gca | 192 |
| Gly Ser Glu Arg Phe Leu Cys Glu Ser Val Phe Ser Tyr Gln Val Ala | |
| 50 55 60 | |
| tcc acg ctt aaa cag gtg aaa cat gat cag caa gtt gct cgg atg gaa | 240 |
| Ser Thr Leu Lys Gln Val Lys His Asp Gln Gln Val Ala Arg Met Glu | |
| 65 70 75 80 | |
| aaa cta gct ggt ttg gta gaa gag ctg gag gct gac gag tgg cgg ttt | 288 |
| Lys Leu Ala Gly Leu Val Glu Glu Leu Glu Ala Asp Glu Trp Arg Phe | |
| 85 90 95 | |
| aag ccc atc gag cag ctg ctg gga ttc acc ccc tct tca ggt tga | 336 |
| Lys Pro Ile Glu Gln Leu Leu Gly Phe Thr Pro Ser Ser Gly * | |
| 100 105 110 | |

<210> 320

<211> 110

<212> PRT

<213> Homo sapiens

<400> 320

| |
|---|
| Met Ala Ala Ser Ser Ser Ser Ser Ser Ala Gly Gly Val Ser Gly Ser |
| 1 5 10 15 |
| Ser Val Thr Gly Ser Gly Phe Ser Val Ser Asp Leu Ala Pro Pro Arg |
| 20 25 30 |
| Lys Ala Leu Phe Thr Tyr Pro Lys Gly Ala Gly Glu Met Leu Glu Asp |
| 35 40 45 |
| Gly Ser Glu Arg Phe Leu Cys Glu Ser Val Phe Ser Tyr Gln Val Ala |
| 50 55 60 |
| Ser Thr Leu Lys Gln Val Lys His Asp Gln Gln Val Ala Arg Met Glu |

469

65 70 75 80
 Lys Leu Ala Gly Leu Val Glu Glu Leu Glu Ala Asp Glu Trp Arg Phe
 85 90 95
 Lys Pro Ile Glu Gln Leu Leu Gly Phe Thr Pro Ser Ser Gly
 100 105 110

<210> 321

<211> 1383

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1383)

<221> misc_feature

<222> (1)...(1383)

<223> n = A,T,C or G

<400> 321

atg ctt tgt ctg gca gct ctt cat ggc atg gng gcc ttg gta ggc tct 48
 Met Leu Cys Leu Ala Ala Leu His Gly Met Xaa Ala Leu Val Gly Ser
 1 5 10 15

gaa ggg gat gta atg cag ctg aaa tca gaa gcc atc cag acc tct cat 96
 Glu Gly Asp Val Met Gln Leu Lys Ser Glu Ala Ile Gln Thr Ser His
 20 25 30

ttt caa ggc aga ctt aat gaa gtc att aga acc tta act cag gtc att 144
 Phe Gln Gly Arg Leu Asn Glu Val Ile Arg Thr Leu Thr Gln Val Ile
 35 40 45

agt gtc tct ggg gtg att ggt ctc cag tca aat gca gtc tgg ctt ctt 192
 Ser Val Ser Gly Val Ile Gly Leu Gln Ser Asn Ala Val Trp Leu Leu
 50 55 60

gga cat ctt cat cta tct act cta tcc tca agt caa agt aga gcc tct 240
 Gly His Leu His Leu Ser Thr Leu Ser Ser Ser Gln Ser Arg Ala Ser
 65 70 75 80

gtt cct act gac tat agc tac ttg cct gaa agc agt ttt att gga gca 288
 Val Pro Thr Asp Tyr Ser Tyr Leu Pro Glu Ser Ser Phe Ile Gly Ala
 85 90 95

470

| | |
|---|-----|
| gct att ggc ttc ttc att aca gga gga aaa aaa ggt cct gaa tct gtg Ala Ile Gly Phe Phe Ile Thr Gly Gly Lys Lys Gly Pro Glu Ser Val 100 105 110 | 336 |
| cct cct tcc ctt ctt aaa gta gtg atg aaa ccc ata gca act gtt gga Pro Pro Ser Leu Leu Lys Val Val Met Lys Pro Ile Ala Thr Val Gly 115 120 125 | 384 |
| gaa agc tac caa tat cct cct gtg aac tgg gct gca ctt ctc tct cca Glu Ser Tyr Gln Tyr Pro Pro Val Asn Trp Ala Ala Leu Leu Ser Pro 130 135 140 | 432 |
| ctt atg agg cta aat ttt ggt gaa gag atc cag caa ctg tgc ctt gaa Leu Met Arg Leu Asn Phe Gly Glu Glu Ile Gln Gln Leu Cys Leu Glu 145 150 155 160 | 480 |
| att atg gtg acc cag gca cag tca tcc cag aat gca gct gca cta ttg Ile Met Val Thr Gln Ala Gln Ser Ser Gln Asn Ala Ala Ala Leu Leu 165 170 175 | 528 |
| ggc ttg tgg gtg aca cca cca ctg atc cac agt ctg agt ctg aat acc Gly Leu Trp Val Thr Pro Pro Leu Ile His Ser Leu Ser Leu Asn Thr 180 185 190 | 576 |
| aag aga tat ctc ctg ata tct gca cct ctg tgg ata aaa cac atc tct Lys Arg Tyr Leu Leu Ile Ser Ala Pro Leu Trp Ile Lys His Ile Ser 195 200 205 | 624 |
| gat gaa cag atc ctg ggt ttt gtt gaa aat tta atg gtg gca gtt ttt Asp Glu Gln Ile Leu Gly Phe Val Glu Asn Leu Met Val Ala Val Phe 210 215 220 | 672 |
| aaa gca gct tcc cca ctt gga agt cct gag cta tgc cca agt gct tta Lys Ala Ala Ser Pro Leu Gly Ser Pro Glu Leu Cys Pro Ser Ala Leu 225 230 235 240 | 720 |
| cac ggt ctg agc cag gcc atg aaa ctg ccc agc cct gcc cac cac ctc His Gly Leu Ser Gln Ala Met Lys Leu Pro Ser Pro Ala His His Leu 245 250 255 | 768 |
| tgg agt ctg ctc tct gaa gct act ggg aaa att ttt gac ctc ctg cca Trp Ser Leu Leu Ser Glu Ala Thr Gly Lys Ile Phe Asp Leu Leu Pro 260 265 270 | 816 |

471

| | |
|---|------|
| aat aag att cgg aga aag gat cta gag ctg tat atc agc ata gca aaa Asn Lys Ile Arg Arg Lys Asp Leu Glu Leu Tyr Ile Ser Ile Ala Lys 275 280 285 | 864 |
| tgc ctc tta gaa atg aca gat gat gat gcc aat cgg atc gcc cag gtt Cys Leu Leu Glu Met Thr Asp Asp Asp Ala Asn Arg Ile Ala Gln Val 290 295 300 | 912 |
| act aag agc aac ata gaa aaa gct gcc ttt gtc aaa ctg tac tta gtc Thr Lys Ser Asn Ile Glu Lys Ala Ala Phe Val Lys Leu Tyr Leu Val 305 310 315 320 | 960 |
| tct caa gga cga ttc ccc ttg gtg aac ctg acc gat atg ctg aga ttt Ser Gln Gly Arg Phe Pro Leu Val Asn Leu Thr Asp Met Leu Arg Phe 325 330 335 | 1008 |
| gca acc gca gtg gtt gca tgg gct gac cac act gcc cct ctc ctc ctc Ala Thr Ala Val Val Ala Trp Ala Asp His Thr Ala Pro Leu Leu Leu 340 345 350 | 1056 |
| ggc ctc agt gcc agt tgg ttg cca tgg cat cag gag aat ggc ccg gct Gly Leu Ser Ala Ser Trp Leu Pro Trp His Gln Glu Asn Gly Pro Ala 355 360 365 | 1104 |
| ggg cca gta cca agc ttc ctt ggc agg agt cca atg cac agg gtc act Gly Pro Val Pro Ser Phe Leu Gly Arg Ser Pro Met His Arg Val Thr 370 375 380 | 1152 |
| ctg cag gag gtt ctc act ctc ctt ccc aat agc atg gct ctg ctg ctg Leu Gln Glu Val Leu Thr Leu Leu Pro Asn Ser Met Ala Leu Leu Leu 385 390 395 400 | 1200 |
| cag aaa gag cca tgg aag gaa cag acc cag aag ttc att gac tgg cta Gln Lys Glu Pro Trp Lys Glu Gln Thr Gln Lys Phe Ile Asp Trp Leu 405 410 415 | 1248 |
| ttc agc atc atg gaa agc cct aaa gaa gcc ctc tca gca cag tcc agg Phe Ser Ile Met Glu Ser Pro Lys Glu Ala Leu Ser Ala Gln Ser Arg 420 425 430 | 1296 |
| gat ctt ttg aaa gcc acc ctg ctg tcc ttg aga gtt ctc cca gag ttt Asp Leu Leu Lys Ala Thr Leu Leu Ser Leu Arg Val Leu Pro Glu Phe 435 440 445 | 1344 |

472

aag aag aaa gct gta tgg acc aga gca tat ggt tgg tga
 Lys Lys Lys Ala Val Trp Thr Arg Ala Tyr Gly Trp *
 450 455 460

1383

<210> 322
 <211> 460
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(460)
 <223> Xaa = Any Amino Acid

<400> 322
 Met Leu Cys Leu Ala Ala Leu His Gly Met Xaa Ala Leu Val Gly Ser
 1 5 10 15
 Glu Gly Asp Val Met Gln Leu Lys Ser Glu Ala Ile Gln Thr Ser His
 20 25 30
 Phe Gln Gly Arg Leu Asn Glu Val Ile Arg Thr Leu Thr Gln Val Ile
 35 40 45
 Ser Val Ser Gly Val Ile Gly Leu Gln Ser Asn Ala Val Trp Leu Leu
 50 55 60
 Gly His Leu His Leu Ser Thr Leu Ser Ser Ser Gln Ser Arg Ala Ser
 65 70 75 80
 Val Pro Thr Asp Tyr Ser Tyr Leu Pro Glu Ser Ser Phe Ile Gly Ala
 85 90 95
 Ala Ile Gly Phe Phe Ile Thr Gly Gly Lys Lys Gly Pro Glu Ser Val
 100 105 110
 Pro Pro Ser Leu Leu Lys Val Val Met Lys Pro Ile Ala Thr Val Gly
 115 120 125
 Glu Ser Tyr Gln Tyr Pro Pro Val Asn Trp Ala Ala Leu Leu Ser Pro
 130 135 140
 Leu Met Arg Leu Asn Phe Gly Glu Glu Ile Gln Gln Leu Cys Leu Glu
 145 150 155 160
 Ile Met Val Thr Gln Ala Gln Ser Ser Gln Asn Ala Ala Ala Leu Leu
 165 170 175
 Gly Leu Trp Val Thr Pro Pro Leu Ile His Ser Leu Ser Leu Asn Thr
 180 185 190
 Lys Arg Tyr Leu Leu Ile Ser Ala Pro Leu Trp Ile Lys His Ile Ser
 195 200 205
 Asp Glu Gln Ile Leu Gly Phe Val Glu Asn Leu Met Val Ala Val Phe
 210 215 220

473

Lys Ala Ala Ser Pro Leu Gly Ser Pro Glu Leu Cys Pro Ser Ala Leu
 225 230 235 240
 His Gly Leu Ser Gln Ala Met Lys Leu Pro Ser Pro Ala His His Leu
 245 250 255
 Trp Ser Leu Leu Ser Glu Ala Thr Gly Lys Ile Phe Asp Leu Leu Pro
 260 265 270
 Asn Lys Ile Arg Arg Lys Asp Leu Glu Leu Tyr Ile Ser Ile Ala Lys
 275 280 285
 Cys Leu Leu Glu Met Thr Asp Asp Asp Ala Asn Arg Ile Ala Gln Val
 290 295 300
 Thr Lys Ser Asn Ile Glu Lys Ala Ala Phe Val Lys Leu Tyr Leu Val
 305 310 315 320
 Ser Gln Gly Arg Phe Pro Leu Val Asn Leu Thr Asp Met Leu Arg Phe
 325 330 335
 Ala Thr Ala Val Val Ala Trp Ala Asp His Thr Ala Pro Leu Leu Leu
 340 345 350
 Gly Leu Ser Ala Ser Trp Leu Pro Trp His Gln Glu Asn Gly Pro Ala
 355 360 365
 Gly Pro Val Pro Ser Phe Leu Gly Arg Ser Pro Met His Arg Val Thr
 370 375 380
 Leu Gln Glu Val Leu Thr Leu Leu Pro Asn Ser Met Ala Leu Leu Leu
 385 390 395 400
 Gln Lys Glu Pro Trp Lys Glu Gln Thr Gln Lys Phe Ile Asp Trp Leu
 405 410 415
 Phe Ser Ile Met Glu Ser Pro Lys Glu Ala Leu Ser Ala Gln Ser Arg
 420 425 430
 Asp Leu Leu Lys Ala Thr Leu Leu Ser Leu Arg Val Leu Pro Glu Phe
 435 440 445
 Lys Lys Lys Ala Val Trp Thr Arg Ala Tyr Gly Trp
 450 455 460

<210> 323

<211> 1596

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1596)

<221> misc_feature

<222> (1)...(1596)

<223> n = A,T,C or G

474

<400> 323

| | |
|---|-----|
| atg ctt tgt ctg gca gct ctt cat ggc atg gng gcc ttg gta ggc tct | 48 |
| Met Leu Cys Leu Ala Ala Leu His Gly Met Xaa Ala Leu Val Gly Ser | |
| 1 5 10 15 | |
| gaa ggg gat gta atg cag ctg aaa tca gaa gcc atc cag acc tct cat | 96 |
| Glu Gly Asp Val Met Gln Leu Lys Ser Glu Ala Ile Gln Thr Ser His | |
| 20 25 30 | |
| ttt caa ggc aga ctt aat gaa gtc att aga acc tta act cag gtc att | 144 |
| Phe Gln Gly Arg Leu Asn Glu Val Ile Arg Thr Leu Thr Gln Val Ile | |
| 35 40 45 | |
| agt gtc tct ggg gtg att ggt ctc cag tca aat gca gtc tgg ctt ctt | 192 |
| Ser Val Ser Gly Val Ile Gly Leu Gln Ser Asn Ala Val Trp Leu Leu | |
| 50 55 60 | |
| gga cat ctt cat cta tct act cta tcc tca agt caa agt aga gcc tct | 240 |
| Gly His Leu His Leu Ser Thr Leu Ser Ser Ser Gln Ser Arg Ala Ser | |
| 65 70 75 80 | |
| gtt cct act gac tat agc tac ttg cct gaa agc agt ttt att gga gca | 288 |
| Val Pro Thr Asp Tyr Ser Tyr Leu Pro Glu Ser Ser Phe Ile Gly Ala | |
| 85 90 95 | |
| gct att ggc ttc ttc att aca gga gga aaa aaa ggt cct gaa tct gtg | 336 |
| Ala Ile Gly Phe Phe Ile Thr Gly Gly Lys Lys Gly Pro Glu Ser Val | |
| 100 105 110 | |
| cct cct tcc ctt ctt aaa gta gtg atg aaa ccc ata gca act gtt gga | 384 |
| Pro Pro Ser Leu Leu Lys Val Val Met Lys Pro Ile Ala Thr Val Gly | |
| 115 120 125 | |
| gaa agc tac caa tat cct cct gtg aac tgg gct gca ctt ctc tct cca | 432 |
| Glu Ser Tyr Gln Tyr Pro Pro Val Asn Trp Ala Ala Leu Leu Ser Pro | |
| 130 135 140 | |
| ctt atg agg cta aat ttt ggt gaa gag atc cag caa ctg tgc ctt gaa | 480 |
| Leu Met Arg Leu Asn Phe Gly Glu Glu Ile Gln Gln Leu Cys Leu Glu | |
| 145 150 155 160 | |
| att atg gtg acc cag gca cag tca tcc cag aat gca gct gca cta ttg | 528 |
| Ile Met Val Thr Gln Ala Gln Ser Ser Gln Asn Ala Ala Ala Leu Leu | |
| 165 170 175 | |

475

| | |
|---|------|
| ggc ttg tgg gtg aca cca cca ctg atc cac agt ctg agt ctg aat acc Gly Leu Trp Val Thr Pro Pro Leu Ile His Ser Leu Ser Leu Asn Thr 180 185 190 | 576 |
| aag aga tat ctc ctg ata tct gca cct ctg tgg ata aaa cac atc tct Lys Arg Tyr Leu Leu Ile Ser Ala Pro Leu Trp Ile Lys His Ile Ser 195 200 205 | 624 |
| gat gaa cag atc ctg ggt ttt gtt gaa aat tta atg gtg gca gtt ttt Asp Glu Gln Ile Leu Gly Phe Val Glu Asn Leu Met Val Ala Val Phe 210 215 220 | 672 |
| aaa gca gct tcc cca ctt gga agt cct gag cta tgc cca agt gct tta Lys Ala Ala Ser Pro Leu Gly Ser Pro Glu Leu Cys Pro Ser Ala Leu 225 230 235 240 | 720 |
| cac ggt ctg agc cag gcc atg aaa ctg ccc agc cct gcc cac cac ctc His Gly Leu Ser Gln Ala Met Lys Leu Pro Ser Pro Ala His His Leu 245 250 255 | 768 |
| tgg agt ctg ctc tct gaa gct act ggg aaa att ttt gac ctc ctg cca Trp Ser Leu Leu Ser Glu Ala Thr Gly Lys Ile Phe Asp Leu Leu Pro 260 265 270 | 816 |
| aat aag att cgg aga aag gat cta gag ctg tat atc agc ata gca aaa Asn Lys Ile Arg Arg Lys Asp Leu Glu Leu Tyr Ile Ser Ile Ala Lys 275 280 285 | 864 |
| tgc ctc tta gaa atg aca gat gat gat gcc aat cgg atc gcc cag gtt Cys Leu Leu Glu Met Thr Asp Asp Asp Ala Asn Arg Ile Ala Gln Val 290 295 300 | 912 |
| act aag agc aac ata gaa aaa gct gcc ttt gtc aaa ctg tac tta gtc Thr Lys Ser Asn Ile Glu Lys Ala Ala Phe Val Lys Leu Tyr Leu Val 305 310 315 320 | 960 |
| tct caa gga cga ttc ccc ttg gtg aac ctg acc gat atg ctg agc gtt Ser Gln Gly Arg Phe Pro Leu Val Asn Leu Thr Asp Met Leu Ser Val 325 330 335 | 1008 |
| gct gtg cag cac cgt gag aaa gag gtg ttg gcc tgg atg att ctg cac Ala Val Gln His Arg Glu Lys Glu Val Leu Ala Trp Met Ile Leu His 340 345 350 | 1056 |

476

| | |
|---|------|
| agc tta tac cag gca cgg att gtg agc cat gcc aat acg ggc gtt ttg | 1104 |
| Ser Leu Tyr Gln Ala Arg Ile Val Ser His Ala Asn Thr Gly Val Leu | |
| 355 360 365 | |
| aag aga atg gag tgg ctc ttg gaa ctg atg ggt tat att aga aat gtt | 1152 |
| Lys Arg Met Glu Trp Leu Leu Glu Leu Met Gly Tyr Ile Arg Asn Val | |
| 370 375 380 | |
| gct tac cag tca aca tcc ttt cac aat acg gct ctt gac gag gct ttg | 1200 |
| Ala Tyr Gln Ser Thr Ser Phe His Asn Thr Ala Leu Asp Glu Ala Leu | |
| 385 390 395 400 | |
| gac ttc ttc ttg ctg ata ttt gca acc gca gtg gtt gca tgg gct gac | 1248 |
| Asp Phe Phe Leu Leu Ile Phe Ala Thr Ala Val Val Ala Trp Ala Asp | |
| 405 410 415 | |
| cac act gcc cct ctc ctc ctc ggc ctc agt gcc agt tgg ttg cca tgg | 1296 |
| His Thr Ala Pro Leu Leu Leu Gly Leu Ser Ala Ser Trp Leu Pro Trp | |
| 420 425 430 | |
| cat cag gag aat ggc ccg gct ggg cca gta cca agc ttc ctt ggc agg | 1344 |
| His Gln Glu Asn Gly Pro Ala Gly Pro Val Pro Ser Phe Leu Gly Arg | |
| 435 440 445 | |
| agt cca atg cac agg gtc act ctg cag gag gtt ctc act ctc ctt ccc | 1392 |
| Ser Pro Met His Arg Val Thr Leu Gln Glu Val Leu Thr Leu Leu Pro | |
| 450 455 460 | |
| aat agc atg gct ctg ctg ctg cag aaa gag cca tgg aag gaa cag acc | 1440 |
| Asn Ser Met Ala Leu Leu Leu Gln Lys Glu Pro Trp Lys Glu Gln Thr | |
| 465 470 475 480 | |
| cag aag ttc att gac tgg cta ttc agc atc atg gaa agc cct aaa gaa | 1488 |
| Gln Lys Phe Ile Asp Trp Leu Phe Ser Ile Met Glu Ser Pro Lys Glu | |
| 485 490 495 | |
| gcc ctc tca gca cag tcc agg gat ctt ttg aaa gcc acc ctg ctg tcc | 1536 |
| Ala Leu Ser Ala Gln Ser Arg Asp Leu Leu Lys Ala Thr Leu Leu Ser | |
| 500 505 510 | |
| ttg aga gtt ctc cca gag ttt aag aag aaa gct gta tgg acc aga gca | 1584 |
| Leu Arg Val Leu Pro Glu Phe Lys Lys Lys Ala Val Trp Thr Arg Ala | |
| 515 520 525 | |

477

tat ggt tgg tga
 Tyr Gly Trp *
 530

1596

<210> 324
 <211> 531
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(531)
 <223> Xaa = Any Amino Acid

<400> 324
 Met Leu Cys Leu Ala Ala Leu His Gly Met Xaa Ala Leu Val Gly Ser
 1 5 10 15
 Glu Gly Asp Val Met Gln Leu Lys Ser Glu Ala Ile Gln Thr Ser His
 20 25 30
 Phe Gln Gly Arg Leu Asn Glu Val Ile Arg Thr Leu Thr Gln Val Ile
 35 40 45
 Ser Val Ser Gly Val Ile Gly Leu Gln Ser Asn Ala Val Trp Leu Leu
 50 55 60
 Gly His Leu His Leu Ser Thr Leu Ser Ser Ser Gln Ser Arg Ala Ser
 65 70 75 80
 Val Pro Thr Asp Tyr Ser Tyr Leu Pro Glu Ser Ser Phe Ile Gly Ala
 85 90 95
 Ala Ile Gly Phe Phe Ile Thr Gly Gly Lys Lys Gly Pro Glu Ser Val
 100 105 110
 Pro Pro Ser Leu Leu Lys Val Val Met Lys Pro Ile Ala Thr Val Gly
 115 120 125
 Glu Ser Tyr Gln Tyr Pro Pro Val Asn Trp Ala Ala Leu Leu Ser Pro
 130 135 140
 Leu Met Arg Leu Asn Phe Gly Glu Glu Ile Gln Gln Leu Cys Leu Glu
 145 150 155 160
 Ile Met Val Thr Gln Ala Gln Ser Ser Gln Asn Ala Ala Ala Leu Leu
 165 170 175
 Gly Leu Trp Val Thr Pro Pro Leu Ile His Ser Leu Ser Leu Asn Thr
 180 185 190
 Lys Arg Tyr Leu Leu Ile Ser Ala Pro Leu Trp Ile Lys His Ile Ser
 195 200 205
 Asp Glu Gln Ile Leu Gly Phe Val Glu Asn Leu Met Val Ala Val Phe

478

| | | |
|---|-----|-----|
| 210 | 215 | 220 |
| Lys Ala Ala Ser Pro Leu Gly Ser Pro Glu Leu Cys Pro Ser Ala Leu | | |
| 225 | 230 | 235 |
| His Gly Leu Ser Gln Ala Met Lys Leu Pro Ser Pro Ala His His Leu | | |
| | 245 | 250 |
| Trp Ser Leu Leu Ser Glu Ala Thr Gly Lys Ile Phe Asp Leu Leu Pro | | |
| | 260 | 265 |
| Asn Lys Ile Arg Arg Lys Asp Leu Glu Leu Tyr Ile Ser Ile Ala Lys | | |
| | 275 | 280 |
| Cys Leu Leu Glu Met Thr Asp Asp Asp Ala Asn Arg Ile Ala Gln Val | | |
| | 290 | 295 |
| Thr Lys Ser Asn Ile Glu Lys Ala Ala Phe Val Lys Leu Tyr Leu Val | | |
| 305 | 310 | 315 |
| Ser Gln Gly Arg Phe Pro Leu Val Asn Leu Thr Asp Met Leu Ser Val | | |
| | 325 | 330 |
| Ala Val Gln His Arg Glu Lys Glu Val Leu Ala Trp Met Ile Leu His | | |
| | 340 | 345 |
| Ser Leu Tyr Gln Ala Arg Ile Val Ser His Ala Asn Thr Gly Val Leu | | |
| | 355 | 360 |
| Lys Arg Met Glu Trp Leu Leu Glu Leu Met Gly Tyr Ile Arg Asn Val | | |
| | 370 | 375 |
| Ala Tyr Gln Ser Thr Ser Phe His Asn Thr Ala Leu Asp Glu Ala Leu | | |
| 385 | 390 | 395 |
| Asp Phe Phe Leu Leu Ile Phe Ala Thr Ala Val Val Ala Trp Ala Asp | | |
| | 405 | 410 |
| His Thr Ala Pro Leu Leu Leu Gly Leu Ser Ala Ser Trp Leu Pro Trp | | |
| | 420 | 425 |
| His Gln Glu Asn Gly Pro Ala Gly Pro Val Pro Ser Phe Leu Gly Arg | | |
| | 435 | 440 |
| Ser Pro Met His Arg Val Thr Leu Gln Glu Val Leu Thr Leu Leu Pro | | |
| | 450 | 455 |
| Asn Ser Met Ala Leu Leu Leu Gln Lys Glu Pro Trp Lys Glu Gln Thr | | |
| 465 | 470 | 475 |
| Gln Lys Phe Ile Asp Trp Leu Phe Ser Ile Met Glu Ser Pro Lys Glu | | |
| | 485 | 490 |
| Ala Leu Ser Ala Gln Ser Arg Asp Leu Leu Lys Ala Thr Leu Leu Ser | | |
| | 500 | 505 |
| Leu Arg Val Leu Pro Glu Phe Lys Lys Lys Ala Val Trp Thr Arg Ala | | |
| | 515 | 520 |
| Tyr Gly Trp | | |
| 530 | | |

<210> 325

<211> 666

479

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(666)

<400> 325

| | |
|---|-----|
| atg gcc ggg act ggg ctg ctg gcg ctg cgg acg ctg cca ggg ccc agc | 48 |
| Met Ala Gly Thr Gly Leu Leu Ala Leu Arg Thr Leu Pro Gly Pro Ser | |
| 1 5 10 15 | |
| tgg gtg cga ggc tcg ggc cct tcc gtg ctg agc cgc ctg cag gac gcg | 96 |
| Trp Val Arg Gly Ser Gly Pro Ser Val Leu Ser Arg Leu Gln Asp Ala | |
| 20 25 30 | |
| gcc gtg gtg cgg cct ggc ttc ctg agc acg gca gag gag gag acg ctg | 144 |
| Ala Val Val Arg Pro Gly Phe Leu Ser Thr Ala Glu Glu Glu Thr Leu | |
| 35 40 45 | |
| agc cga gaa ctg gag ccc gag ctg cgc cgc cgc cgc tac gaa tac gat | 192 |
| Ser Arg Glu Leu Glu Pro Glu Leu Arg Arg Arg Arg Tyr Glu Tyr Asp | |
| 50 55 60 | |
| cac tgg gac gcg gcc atc cac ggc ttc cga gag aca gag aag tcg cgc | 240 |
| His Trp Asp Ala Ala Ile His Gly Phe Arg Glu Thr Glu Lys Ser Arg | |
| 65 70 75 80 | |
| tgg tca gaa gcc agc cgg gcc atc ctg cag cgc gtg cag gcg gcc gcc | 288 |
| Trp Ser Glu Ala Ser Arg Ala Ile Leu Gln Arg Val Gln Ala Ala Ala | |
| 85 90 95 | |
| ttt ggc ccc ggc cag acc ctg ctc tcc tcc gtg cac gtg ctg gac ctg | 336 |
| Phe Gly Pro Gly Gln Thr Leu Leu Ser Ser Val His Val Leu Asp Leu | |
| 100 105 110 | |
| gaa gcc cgc ggc tac atc aag ccc cac gtg gac agc atc aag ttc tgc | 384 |
| Glu Ala Arg Gly Tyr Ile Lys Pro His Val Asp Ser Ile Lys Phe Cys | |
| 115 120 125 | |
| ggg gcc acc atc gcc ggc ctg tct ctc ctg tct ccc agc gtt atg cgg | 432 |
| Gly Ala Thr Ile Ala Gly Leu Ser Leu Leu Ser Pro Ser Val Met Arg | |
| 130 135 140 | |

480

ctg gtg cac acc cag gag ccg ggg gag tgg ctg gaa ctc ttg ctg gag 480
 Leu Val His Thr Gln Glu Pro Gly Glu Trp Leu Glu Leu Leu Leu Glu
 145 150 155 160
 ccg ggc tcc ctc tac atc ctt agg ggc tca gcc cgt tat gac ttc tcc 528
 Pro Gly Ser Leu Tyr Ile Leu Arg Gly Ser Ala Arg Tyr Asp Phe Ser
 165 170 175
 cat gag atc ctt cgg gat gaa gag tcc ttc ttt ggg gaa cgc cgg att 576
 His Glu Ile Leu Arg Asp Glu Glu Ser Phe Phe Gly Glu Arg Arg Ile
 180 185 190
 ccc cgg ggc cgg cgc atc tcc gtg atc tgc cgc tcc ctc cct gag ggc 624
 Pro Arg Gly Arg Arg Ile Ser Val Ile Cys Arg Ser Leu Pro Glu Gly
 195 200 205
 atg ggg cca ggg gag tct gga cag ccg ccc cca gcc tgc tga 666
 Met Gly Pro Gly Glu Ser Gly Gln Pro Pro Pro Ala Cys *
 210 215 220

<210> 326

<211> 221

<212> PRT

<213> Homo sapiens

<400> 326

Met Ala Gly Thr Gly Leu Leu Ala Leu Arg Thr Leu Pro Gly Pro Ser
 1 5 10 15
 Trp Val Arg Gly Ser Gly Pro Ser Val Leu Ser Arg Leu Gln Asp Ala
 20 25 30
 Ala Val Val Arg Pro Gly Phe Leu Ser Thr Ala Glu Glu Thr Leu
 35 40 45
 Ser Arg Glu Leu Glu Pro Glu Leu Arg Arg Arg Arg Tyr Glu Tyr Asp
 50 55 60
 His Trp Asp Ala Ala Ile His Gly Phe Arg Glu Thr Glu Lys Ser Arg
 65 70 75 80
 Trp Ser Glu Ala Ser Arg Ala Ile Leu Gln Arg Val Gln Ala Ala Ala
 85 90 95
 Phe Gly Pro Gly Gln Thr Leu Leu Ser Ser Val His Val Leu Asp Leu
 100 105 110
 Glu Ala Arg Gly Tyr Ile Lys Pro His Val Asp Ser Ile Lys Phe Cys
 115 120 125
 Gly Ala Thr Ile Ala Gly Leu Ser Leu Leu Ser Pro Ser Val Met Arg

481

130 135 140
 Leu Val His Thr Gln Glu Pro Gly Glu Trp Leu Glu Leu Leu Leu Glu
 145 150 155 160
 Pro Gly Ser Leu Tyr Ile Leu Arg Gly Ser Ala Arg Tyr Asp Phe Ser
 165 170 175
 His Glu Ile Leu Arg Asp Glu Glu Ser Phe Phe Gly Glu Arg Arg Ile
 180 185 190
 Pro Arg Gly Arg Arg Ile Ser Val Ile Cys Arg Ser Leu Pro Glu Gly
 195 200 205
 Met Gly Pro Gly Glu Ser Gly Gln Pro Pro Pro Ala Cys
 210 215 220

<210> 327
 <211> 294
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(294)

<400> 327
 atg gct gaa aat agt gta tta aca tcc act act ggg agg act agc ttg 48
 Met Ala Glu Asn Ser Val Leu Thr Ser Thr Thr Gly Arg Thr Ser Leu
 1 5 10 15

 gca gac tct tcc att ttt gat tct aaa gtt act gag att tcc aag gaa 96
 Ala Asp Ser Ser Ile Phe Asp Ser Lys Val Thr Glu Ile Ser Lys Glu
 20 25 30

 aac tta ctt att gga tct act tca tat gta gaa gaa gag atg cct cag 144
 Asn Leu Leu Ile Gly Ser Thr Ser Tyr Val Glu Glu Glu Met Pro Gln
 35 40 45

 att gaa aca aga gtg ata ttg gtt caa gaa gct gga aaa caa gaa gaa 192
 Ile Glu Thr Arg Val Ile Leu Val Gln Glu Ala Gly Lys Gln Glu Glu
 50 55 60

 ctt ata aaa gcc tta aag gac att aaa gtg ggc ttt gta aag atg gag 240
 Leu Ile Lys Ala Leu Lys Asp Ile Lys Val Gly Phe Val Lys Met Glu
 65 70 75 80

 tca gtg gaa gaa ttt gaa ggt ttg gat tct ccg gaa ttt gaa atg tat 288
 Ser Val Glu Glu Phe Glu Gly Leu Asp Ser Pro Glu Phe Glu Met Tyr

482

85

90

95

ttg tag

294

Leu *

<210> 328

<211> 97

<212> PRT

<213> Homo sapiens

<400> 328

```

Met Ala Glu Asn Ser Val Leu Thr Ser Thr Thr Gly Arg Thr Ser Leu
 1              5              10              15
Ala Asp Ser Ser Ile Phe Asp Ser Lys Val Thr Glu Ile Ser Lys Glu
      20              25              30
Asn Leu Leu Ile Gly Ser Thr Ser Tyr Val Glu Glu Glu Met Pro Gln
      35              40              45
Ile Glu Thr Arg Val Ile Leu Val Gln Glu Ala Gly Lys Gln Glu Glu
      50              55              60
Leu Ile Lys Ala Leu Lys Asp Ile Lys Val Gly Phe Val Lys Met Glu
65              70              75              80
Ser Val Glu Glu Phe Glu Gly Leu Asp Ser Pro Glu Phe Glu Met Tyr
      85              90              95
Leu

```

<210> 329

<211> 270

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(270)

<400> 329

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atg gtg tca gct agc gtg ttt gtg ggc ctg gtg atc ttc tac atc gcc
Met Val Ser Ala Ser Val Phe Val Gly Leu Val Ile Phe Tyr Ile Ala
 1              5              10              15

```

48

```

ttc tgc ctc ctg tgg ccc ctc gtg gtg aag ggc tgc acg atg atc cgg
Phe Cys Leu Leu Trp Pro Leu Val Val Lys Gly Cys Thr Met Ile Arg

```

96

483

| | 20 | 25 | 30 | |
|---|----|----|----|-----|
| tgg aag ata aac aac ctc att gcc tca gaa tcc tac tac acc tac gcc | | | | 144 |
| Trp Lys Ile Asn Asn Leu Ile Ala Ser Glu Ser Tyr Tyr Thr Tyr Ala | | | | |
| | 35 | 40 | 45 | |
| tcc att tcc gga atc tcg agc atg cca tct ctg aga cat tcc agg atg | | | | 192 |
| Ser Ile Ser Gly Ile Ser Ser Met Pro Ser Leu Arg His Ser Arg Met | | | | |
| | 50 | 55 | 60 | |
| ggc tcc atg ttc agc tcc agg atg aca gag gac agg gct gaa ccc aag | | | | 240 |
| Gly Ser Met Phe Ser Ser Arg Met Thr Glu Asp Arg Ala Glu Pro Lys | | | | |
| | 65 | 70 | 75 | 80 |
| gaa gcc gtg gag aga cag ttg atg acc tga | | | | 270 |
| Glu Ala Val Glu Arg Gln Leu Met Thr * | | | | |
| | 85 | | | |

<210> 330
 <211> 89
 <212> PRT
 <213> Homo sapiens

<400> 330
 Met Val Ser Ala Ser Val Phe Val Gly Leu Val Ile Phe Tyr Ile Ala
 1 5 10 15
 Phe Cys Leu Leu Trp Pro Leu Val Val Lys Gly Cys Thr Met Ile Arg
 20 25 30
 Trp Lys Ile Asn Asn Leu Ile Ala Ser Glu Ser Tyr Tyr Thr Tyr Ala
 35 40 45
 Ser Ile Ser Gly Ile Ser Ser Met Pro Ser Leu Arg His Ser Arg Met
 50 55 60
 Gly Ser Met Phe Ser Ser Arg Met Thr Glu Asp Arg Ala Glu Pro Lys
 65 70 75 80
 Glu Ala Val Glu Arg Gln Leu Met Thr
 85

<210> 331
 <211> 255
 <212> DNA
 <213> Homo sapiens

<220>

<210> 332
<211> 84
<212> PRT
<213> Homo sapiens

| | | | | | | | | | | | | | | | | |
|------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| <400> 332 | | | | | | | | | | | | | | | | |
| Met | Leu | Gly | Leu | Leu | Gln | Phe | Asp | Ser | Gly | Phe | Ile | Cys | Leu | Cys | Ala | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| Arg | Val | Tyr | Pro | Ser | Cys | Leu | Glu | Pro | Gly | Gln | Ser | Phe | Ile | Thr | Glu | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Glu | Asp | Asp | Ala | Arg | Ser | Glu | Ser | Ser | Thr | Glu | Trp | Asp | Leu | Asp | Gly | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| Phe | Ser | Glu | Leu | Asp | Ser | Glu | Ser | Gly | Ser | Ser | Ser | Ser | Phe | Ser | Asp | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| Asp | Glu | Val | Trp | Val | Gln | Val | Ala | Pro | Gln | Arg | Asn | Ala | Gln | Asp | Gln | |

485

65
Gln Gly Ser Leu

70

75

80

<210> 333
<211> 243
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(243)

<400> 333

atg gag att ctc tgg ctg atg gtc aag tcc tgg aat acc gga gta ctt 48
Met Glu Ile Leu Trp Leu Met Val Lys Ser Trp Asn Thr Gly Val Leu
1 5 10 15

atg ttt agc agg agc aag tat gca tct gct gaa aag tgg tgt ggc ctg 96
Met Phe Ser Arg Ser Lys Tyr Ala Ser Ala Glu Lys Trp Cys Gly Leu
20 25 30

gcc ttg cgt ttc ctt aac cac ctt acc tcc ttc aag gaa agc tat gaa 144
Ala Leu Arg Phe Leu Asn His Leu Thr Ser Phe Lys Glu Ser Tyr Glu
35 40 45

act cag atg aat atg ctg tat agt cag ctt gtg gaa gca ttg agt aac 192
Thr Gln Met Asn Met Leu Tyr Ser Gln Leu Val Glu Ala Leu Ser Asn
50 55 60

aac aag ggc cca gtt ttt cat gaa cat ggc tac tgg agc aag tca gat 240
Asn Lys Gly Pro Val Phe His Glu His Gly Tyr Trp Ser Lys Ser Asp
65 70 75 80

tag 243
*

<210> 334
<211> 80
<212> PRT
<213> Homo sapiens

486

<400> 334

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Ile | Leu | Trp | Leu | Met | Val | Lys | Ser | Trp | Asn | Thr | Gly | Val | Leu |
| 1 | | | 5 | | | | | 10 | | | | | 15 | | |
| Met | Phe | Ser | Arg | Ser | Lys | Tyr | Ala | Ser | Ala | Glu | Lys | Trp | Cys | Gly | Leu |
| | | | 20 | | | | 25 | | | | | | 30 | | |
| Ala | Leu | Arg | Phe | Leu | Asn | His | Leu | Thr | Ser | Phe | Lys | Glu | Ser | Tyr | Glu |
| | | 35 | | | | 40 | | | | | 45 | | | | |
| Thr | Gln | Met | Asn | Met | Leu | Tyr | Ser | Gln | Leu | Val | Glu | Ala | Leu | Ser | Asn |
| | 50 | | | | 55 | | | | 60 | | | | | | |
| Asn | Lys | Gly | Pro | Val | Phe | His | Glu | His | Gly | Tyr | Trp | Ser | Lys | Ser | Asp |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | |

<210> 335

<211> 237

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(237)

<400> 335

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| atg | cct | gtg | gtc | ctg | tcg | caa | gag | gtg | gag | tcc | gtt | ctt | gtg | ggg | gct | 48 |
| Met | Pro | Val | Val | Leu | Ser | Gln | Glu | Val | Glu | Ser | Val | Leu | Val | Gly | Ala | |
| 1 | | | 5 | | | | | 10 | | | | | 15 | | | |
| gct | gtt | ctg | ggg | gcc | tgt | gcc | tca | ggg | gat | ttc | gct | tct | gta | cag | gaa | 96 |
| Ala | Val | Leu | Gly | Ala | Cys | Ala | Ser | Gly | Asp | Phe | Ala | Ser | Val | Gln | Glu | |
| | | 20 | | | | 25 | | | | | 30 | | | | | |
| gca | atg | gca | aaa | atg | agc | aaa | gtt | ggg | aaa | gtt | gtg | ttc | ccg | aga | cta | 144 |
| Ala | Met | Ala | Lys | Met | Ser | Lys | Val | Gly | Lys | Val | Val | Phe | Pro | Arg | Leu | |
| | | 35 | | | | 40 | | | | | 45 | | | | | |
| cag | gat | aaa | aaa | tac | tat | gat | aag | aaa | tac | caa | gta | ttc | ctg | aag | ctg | 192 |
| Gln | Asp | Lys | Lys | Tyr | Tyr | Asp | Lys | Lys | Tyr | Gln | Val | Phe | Leu | Lys | Leu | |
| | 50 | | | | 55 | | | | 60 | | | | | | | |
| gtt | gaa | cac | cag | aag | gag | tat | ttg | gcg | atc | atg | aat | gat | gac | tga | | 237 |
| Val | Glu | His | Gln | Lys | Glu | Tyr | Leu | Ala | Ile | Met | Asn | Asp | Asp | * | | |
| | 65 | | | | 70 | | | | 75 | | | | | | | |

<210> 336

487

<211> 78
 <212> PRT
 <213> Homo sapiens

<400> 336
 Met Pro Val Val Leu Ser Gln Glu Val Glu Ser Val Leu Val Gly Ala
 1 5 10 15
 Ala Val Leu Gly Ala Cys Ala Ser Gly Asp Phe Ala Ser Val Gln Glu
 20 25 30
 Ala Met Ala Lys Met Ser Lys Val Gly Lys Val Val Phe Pro Arg Leu
 35 40 45
 Gln Asp Lys Lys Tyr Tyr Asp Lys Lys Tyr Gln Val Phe Leu Lys Leu
 50 55 60
 Val Glu His Gln Lys Glu Tyr Leu Ala Ile Met Asn Asp Asp
 65 70 75

<210> 337
 <211> 567
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(567)

<400> 337
 atg cac tct att ctg gat att att gct gga ttc cta tat acc att tta 48
 Met His Ser Ile Leu Asp Ile Ile Ala Gly Phe Leu Tyr Thr Ile Leu
 1 5 10 15
 atc tta gct gtc ttc tat cca ttt gtg gac ctg att gac aac ttc aac 96
 Ile Leu Ala Val Phe Tyr Pro Phe Val Asp Leu Ile Asp Asn Phe Asn
 20 25 30
 caa act cac aaa tat gct cca ttc atc atc atc ggg ctt cat tta gct 144
 Gln Thr His Lys Tyr Ala Pro Phe Ile Ile Ile Gly Leu His Leu Ala
 35 40 45
 ttg ggg atc ttt tct ttc act ctt gac acc tgg agc aca tcc cga gga 192
 Leu Gly Ile Phe Ser Phe Thr Leu Asp Thr Trp Ser Thr Ser Arg Gly
 50 55 60
 gac aca gcc gag ata cta gga agt ggt gct gga att gca tgt gga tct 240
 Asp Thr Ala Glu Ile Leu Gly Ser Gly Ala Gly Ile Ala Cys Gly Ser

488

| | | | | |
|---|-----|-----|-----|--|
| 65 | 70 | 75 | 80 | |
| cat gtt act tat aac atg ggt cta gta tta gat cct tct cta gat aca | 288 | | | |
| His Val Thr Tyr Asn Met Gly Leu Val Leu Asp Pro Ser Leu Asp Thr | | | | |
| 85 | 90 | 95 | | |
| tta cct tta gct ggg ccc ccc att act gtg act ctg ttt gga aaa gcc | 336 | | | |
| Leu Pro Leu Ala Gly Pro Pro Ile Thr Val Thr Leu Phe Gly Lys Ala | | | | |
| 100 | 105 | 110 | | |
| ata ttg cgg atc ctc ata ggg atg gta ttt gta cta ata atc aga gat | 384 | | | |
| Ile Leu Arg Ile Leu Ile Gly Met Val Phe Val Leu Ile Ile Arg Asp | | | | |
| 115 | 120 | 125 | | |
| gta atg aaa aag atc acc att cct tta gcc tgc aaa atc ttc aat ata | 432 | | | |
| Val Met Lys Lys Ile Thr Ile Pro Leu Ala Cys Lys Ile Phe Asn Ile | | | | |
| 130 | 135 | 140 | | |
| ccg tgt gat gat att cga aaa gca aga cag cac atg gaa gtt gaa ctt | 480 | | | |
| Pro Cys Asp Asp Ile Arg Lys Ala Arg Gln His Met Glu Val Glu Leu | | | | |
| 145 | 150 | 155 | 160 | |
| cct tat cgg tat att acc tat gga atg gtt ggt ttc tcc atc aca ttt | 528 | | | |
| Pro Tyr Arg Tyr Ile Thr Tyr Gly Met Val Gly Phe Ser Ile Thr Phe | | | | |
| 165 | 170 | 175 | | |
| ttt gtt cct tac ata ttt ttc ttt att ggt atc tct tga | 567 | | | |
| Phe Val Pro Tyr Ile Phe Phe Phe Ile Gly Ile Ser * | | | | |
| 180 | 185 | | | |

<210> 338

<211> 188

<212> PRT

<213> Homo sapiens

<400> 338

| | |
|---|----|
| Met His Ser Ile Leu Asp Ile Ile Ala Gly Phe Leu Tyr Thr Ile Leu | |
| 1 | 15 |
| Ile Leu Ala Val Phe Tyr Pro Phe Val Asp Leu Ile Asp Asn Phe Asn | |
| 20 | 30 |
| Gln Thr His Lys Tyr Ala Pro Phe Ile Ile Ile Gly Leu His Leu Ala | |
| 35 | 45 |
| Leu Gly Ile Phe Ser Phe Thr Leu Asp Thr Trp Ser Thr Ser Arg Gly | |

489

50 55 60
 Asp Thr Ala Glu Ile Leu Gly Ser Gly Ala Gly Ile Ala Cys Gly Ser
 65 70 75 80
 His Val Thr Tyr Asn Met Gly Leu Val Leu Asp Pro Ser Leu Asp Thr
 85 90 95
 Leu Pro Leu Ala Gly Pro Pro Ile Thr Val Thr Leu Phe Gly Lys Ala
 100 105 110
 Ile Leu Arg Ile Leu Ile Gly Met Val Phe Val Leu Ile Ile Arg Asp
 115 120 125
 Val Met Lys Lys Ile Thr Ile Pro Leu Ala Cys Lys Ile Phe Asn Ile
 130 135 140
 Pro Cys Asp Asp Ile Arg Lys Ala Arg Gln His Met Glu Val Glu Leu
 145 150 155 160
 Pro Tyr Arg Tyr Ile Thr Tyr Gly Met Val Gly Phe Ser Ile Thr Phe
 165 170 175
 Phe Val Pro Tyr Ile Phe Phe Phe Ile Gly Ile Ser
 180 185

<210> 339
 <211> 210
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(210)

<400> 339
 atg gtt tcc cat ttc atg ggg tct ctc agt gtc ctg tgt ttc ctt ctg 48
 Met Val Ser His Phe Met Gly Ser Leu Ser Val Leu Cys Phe Leu Leu
 1 5 10 15

 ctg ctt gga ttc cag ttc gtc tgc cca cag ccc tcc act caa cac agg 96
 Leu Leu Gly Phe Gln Phe Val Cys Pro Gln Pro Ser Thr Gln His Arg
 20 25 30

 aag gtc ccg cag cgg atg gcg gcg gag ggc gcc ccc gag gac gac ggc 144
 Lys Val Pro Gln Arg Met Ala Ala Glu Gly Ala Pro Glu Asp Asp Gly
 35 40 45

 ggc ggc ggc gcc ccg gga gtg tgg ggc gct ggg gcc cct gct gaa ggt 192
 Gly Gly Gly Ala Pro Gly Val Trp Gly Ala Gly Ala Pro Ala Glu Gly
 50 55 60

490

tac cta acc att ctt taa
 Tyr Leu Thr Ile Leu *
 65

210

<210> 340
 <211> 69
 <212> PRT
 <213> Homo sapiens

<400> 340
 Met Val Ser His Phe Met Gly Ser Leu Ser Val Leu Cys Phe Leu Leu
 1 5 10 15
 Leu Leu Gly Phe Gln Phe Val Cys Pro Gln Pro Ser Thr Gln His Arg
 20 25 30
 Lys Val Pro Gln Arg Met Ala Ala Glu Gly Ala Pro Glu Asp Asp Gly
 35 40 45
 Gly Gly Gly Ala Pro Gly Val Trp Gly Ala Gly Ala Pro Ala Glu Gly
 50 55 60
 Tyr Leu Thr Ile Leu
 65

<210> 341
 <211> 225
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(225)

<400> 341
 atg ccg gct aag gac aca agt tca gtg ttt gcc ctg gct tgt agc cca 48
 Met Pro Ala Lys Asp Thr Ser Ser Val Phe Ala Leu Ala Cys Ser Pro
 1 5 10 15
 gcg ggg gct ccg tca tcc cct ggg gaa tgc ctc ggc ctg caa gac cgc 96
 Ala Gly Ala Pro Ser Ser Pro Gly Glu Cys Leu Gly Leu Gln Asp Arg
 20 25 30
 ata ccg cat tgg aac agg gaa acc acc tac ttc agc acc tcc ctc agc 144
 Ile Pro His Trp Asn Arg Glu Thr Thr Tyr Phe Ser Thr Ser Leu Ser
 35 40 45

aag gtg gca ggt ccc aac aag cct tgc acc acg agg aag tgg cag tgg 192
Lys Val Ala Gly Pro Asn Lys Pro Cys Thr Thr Arg Lys Trp Gln Trp
50 55 60

cat tcg gga tat ggc tcc ctg gcc agc ttg tga 225
His Ser Gly Tyr Gly Ser Leu Ala Ser Leu *
65 70

```
<210> 342
<211> 74
<212> PRT
<213> Homo sapiens
```

[illegible]

```
<210> 343
<211> 240
<212> DNA
<213> Homo sapiens
```

<220>
<221> CDS
<222> (1)...(240)

| | | | | | | | | | | | | | | | | |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| <400> 343 | | | | | | | | | | | | | | | | |
| atg | tgc | atc | acg | cac | ctg | gac | cac | aaa | gac | tac | atc | ttc | ctg | ctg | ctc | 48 |
| Met | Cys | Ile | Thr | His | Leu | Asp | His | Lys | Asp | Tyr | Ile | Phe | Leu | Leu | Leu | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| | | | | | | | | | | | | | | | | |
| atc | ggc | ttc | tgc | atc | ttc | gcc | gcg | gga | act | gtg | gct | gcc | tgg | ctc | aca | 96 |
| Ile | Gly | Phe | Cys | Ile | Phe | Ala | Ala | Gly | Thr | Val | Ala | Ala | Trp | Leu | Thr | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |

492

ggt gtg tgt gct gtg ctc tac cag aac acc cgc cac aag tcg agt gaa 144
 Gly Val Cys Ala Val Leu Tyr Gln Asn Thr Arg His Lys Ser Ser Glu
 35 40 45
 gaa gat gag gac gag gcc ggg act agg gtg gaa gtc agc cgg cgg att 192
 Glu Asp Glu Asp Glu Ala Gly Thr Arg Val Glu Val Ser Arg Arg Ile
 50 55 60
 ttt caa acc cag acg agc tcg gtc cag gag ttc cct cag ctt att tag 240
 Phe Gln Thr Gln Thr Ser Ser Val Gln Glu Phe Pro Gln Leu Ile *
 65 70 75

<210> 344
 <211> 79
 <212> PRT
 <213> Homo sapiens

<400> 344
 Met Cys Ile Thr His Leu Asp His Lys Asp Tyr Ile Phe Leu Leu Leu
 1 5 10 15
 Ile Gly Phe Cys Ile Phe Ala Ala Gly Thr Val Ala Ala Trp Leu Thr
 20 25 30
 Gly Val Cys Ala Val Leu Tyr Gln Asn Thr Arg His Lys Ser Ser Glu
 35 40 45
 Glu Asp Glu Asp Glu Ala Gly Thr Arg Val Glu Val Ser Arg Arg Ile
 50 55 60
 Phe Gln Thr Gln Thr Ser Ser Val Gln Glu Phe Pro Gln Leu Ile
 65 70 75

<210> 345
 <211> 285
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(285)

<400> 345
 atg act gcc aag gac tgc tcc atc atg att gca ctg tct ccc tgt ctg 48
 Met Thr Ala Lys Asp Cys Ser Ile Met Ile Ala Leu Ser Pro Cys Leu
 1 5 10 15

493

| | |
|---|-----|
| cag gat gcc agc tct gat caa agg cct gtc gtc cct tca tcg agg tcc | 96 |
| Gln Asp Ala Ser Ser Asp Gln Arg Pro Val Val Pro Ser Ser Arg Ser | |
| 20 25 30 | |
| agg ttt gcc ttt tcc gtg tct gtg ctg gac ctt gac ctc aag ccc tac | 144 |
| Arg Phe Ala Phe Ser Val Ser Val Leu Asp Leu Asp Leu Lys Pro Tyr | |
| 35 40 45 | |
| gag agc att ccc cat cag tat aaa ctg gac ggc aag atc gtc aac tat | 192 |
| Glu Ser Ile Pro His Gln Tyr Lys Leu Asp Gly Lys Ile Val Asn Tyr | |
| 50 55 60 | |
| tat tca aag act gta cgt gcc aaa gac aac gcc gtg atg tcg act cgg | 240 |
| Tyr Ser Lys Thr Val Arg Ala Lys Asp Asn Ala Val Met Ser Thr Arg | |
| 65 70 75 80 | |
| ttc aag gaa agc gaa gat tgc aca tta gtt ctc cac aag gtc taa | 285 |
| Phe Lys Glu Ser Glu Asp Cys Thr Leu Val Leu His Lys Val * | |
| 85 90 | |

<210> 346

<211> 94

<212> PRT

<213> Homo sapiens

<400> 346

| | |
|---|--|
| Met Thr Ala Lys Asp Cys Ser Ile Met Ile Ala Leu Ser Pro Cys Leu | |
| 1 5 10 15 | |
| Gln Asp Ala Ser Ser Asp Gln Arg Pro Val Val Pro Ser Ser Arg Ser | |
| 20 25 30 | |
| Arg Phe Ala Phe Ser Val Ser Val Leu Asp Leu Asp Leu Lys Pro Tyr | |
| 35 40 45 | |
| Glu Ser Ile Pro His Gln Tyr Lys Leu Asp Gly Lys Ile Val Asn Tyr | |
| 50 55 60 | |
| Tyr Ser Lys Thr Val Arg Ala Lys Asp Asn Ala Val Met Ser Thr Arg | |
| 65 70 75 80 | |
| Phe Lys Glu Ser Glu Asp Cys Thr Leu Val Leu His Lys Val | |
| 85 90 | |

<210> 347

<211> 474

<212> DNA

<213> Homo sapiens

494

<220>

<221> CDS

<222> (1)...(474)

<400> 347

| | |
|--|-----|
| atg gag gcc ctg agg agg gcc cac gag gtc gcg ctc cgc ctg ctg ctg | 48 |
| Met Glu Ala Leu Arg Arg Ala His Glu Val Ala Leu Arg Leu Leu Leu | |
| 1 5 10 15 | |
| tgt agg ccg tgg gcc tcg cgc gcc gcc gcc cgc ccc aag ccc agc gcc | 96 |
| Cys Arg Pro Trp Ala Ser Arg Ala Ala Ala Arg Pro Lys Pro Ser Ala | |
| 20 25 30 | |
| tcg gag gtg ctg acg cgg cat ctg ctg cag cgg cgc ctg ccg cac tgg | 144 |
| Ser Glu Val Leu Thr Arg His Leu Leu Gln Arg Arg Leu Pro His Trp | |
| 35 40 45 | |
| acc tcc ttc tgc gtg ccc tac agc gcc gtc cgc aac gac cag ttc ggc | 192 |
| Thr Ser Phe Cys Val Pro Tyr Ser Ala Val Arg Asn Asp Gln Phe Gly | |
| 50 55 60 | |
| ctc tcg cac ttc aac tgg ccg gtg cag gcc gcc aac tac cac gtc ctg | 240 |
| Leu Ser His Phe Asn Trp Pro Val Gln Gly Ala Asn Tyr His Val Leu | |
| 65 70 75 80 | |
| cgc acc gcc tgc ttc ccc ttc atc aag tac cac tgc tcc aag gct ccc | 288 |
| Arg Thr Gly Cys Phe Pro Phe Ile Lys Tyr His Cys Ser Lys Ala Pro | |
| 85 90 95 | |
| tgg cag gac ctg gcc cgg cag aac cgc ttc ttc acg gcg ctc aag gtc | 336 |
| Trp Gln Asp Leu Ala Arg Gln Asn Arg Phe Phe Thr Ala Leu Lys Val | |
| 100 105 110 | |
| gtc aac ctc ggt att cca act tta tta tat gga ctt ggc tcc tgg tta | 384 |
| Val Asn Leu Gly Ile Pro Thr Leu Leu Tyr Gly Leu Gly Ser Trp Leu | |
| 115 120 125 | |
| ttt gcc aga gtc aca gag act gtg cat acc agt tat gga ccc ata aca | 432 |
| Phe Ala Arg Val Thr Glu Thr Val His Thr Ser Tyr Gly Pro Ile Thr | |
| 130 135 140 | |
| gtt tat ttt ctc aat aaa gaa gat gaa ggt gcc atg tat tga | 474 |
| Val Tyr Phe Leu Asn Lys Glu Asp Glu Gly Ala Met Tyr * | |

495

145

150

155

<210> 348
 <211> 157
 <212> PRT
 <213> Homo sapiens

<400> 348
 Met Glu Ala Leu Arg Arg Ala His Glu Val Ala Leu Arg Leu Leu Leu
 1 5 10 15
 Cys Arg Pro Trp Ala Ser Arg Ala Ala Arg Pro Lys Pro Ser Ala
 20 25 30
 Ser Glu Val Leu Thr Arg His Leu Leu Gln Arg Arg Leu Pro His Trp
 35 40 45
 Thr Ser Phe Cys Val Pro Tyr Ser Ala Val Arg Asn Asp Gln Phe Gly
 50 55 60
 Leu Ser His Phe Asn Trp Pro Val Gln Gly Ala Asn Tyr His Val Leu
 65 70 75 80
 Arg Thr Gly Cys Phe Pro Phe Ile Lys Tyr His Cys Ser Lys Ala Pro
 85 90 95
 Trp Gln Asp Leu Ala Arg Gln Asn Arg Phe Phe Thr Ala Leu Lys Val
 100 105 110
 Val Asn Leu Gly Ile Pro Thr Leu Leu Tyr Gly Leu Gly Ser Trp Leu
 115 120 125
 Phe Ala Arg Val Thr Glu Thr Val His Thr Ser Tyr Gly Pro Ile Thr
 130 135 140
 Val Tyr Phe Leu Asn Lys Glu Asp Glu Gly Ala Met Tyr
 145 150 155

<210> 349
 <211> 288
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(288)

<400> 349
 atg gcg aaa gca ctg att gtc att ttt agc agt cac tta agg cct ata
 Met Ala Lys Ala Leu Ile Val Ile Phe Ser Ser His Leu Arg Pro Ile
 1 5 10 15

48

496

gaa ctt ttt tca agt cgg aag gtc ctg ttc tta cta tct caa aaa tgg 96
 Glu Leu Phe Ser Ser Arg Lys Val Leu Phe Leu Leu Ser Gln Lys Trp
 20 25 30

gca tcg aac aat caa tct agg agc gtg gca gtg ggt aaa atg gtg gac 144
 Ala Ser Asn Asn Gln Ser Arg Ser Val Ala Val Gly Lys Met Val Asp
 35 40 45

agg cac caa agc tat ttt ctc atc tgt cct gtg gat gag tgg aac tgt 192
 Arg His Gln Ser Tyr Phe Leu Ile Cys Pro Val Asp Glu Trp Asn Cys
 50 55 60

gga aca agt gat gtg gaa tta atg ggt gca aca gct gta cag aca atc 240
 Gly Thr Ser Asp Val Glu Leu Met Gly Ala Thr Ala Val Gln Thr Ile
 65 70 75 80

aat aac aca cac agt tct gga aag aac aca tca ctt gtg ctt gtt tga 288
 Asn Asn Thr His Ser Ser Gly Lys Asn Thr Ser Leu Val Leu Val *
 85 90 95

<210> 350

<211> 95

<212> PRT

<213> Homo sapiens

<400> 350

Met Ala Lys Ala Leu Ile Val Ile Phe Ser Ser His Leu Arg Pro Ile
 1 5 10 15

Glu Leu Phe Ser Ser Arg Lys Val Leu Phe Leu Leu Ser Gln Lys Trp
 20 25 30

Ala Ser Asn Asn Gln Ser Arg Ser Val Ala Val Gly Lys Met Val Asp
 35 40 45

Arg His Gln Ser Tyr Phe Leu Ile Cys Pro Val Asp Glu Trp Asn Cys
 50 55 60

Gly Thr Ser Asp Val Glu Leu Met Gly Ala Thr Ala Val Gln Thr Ile
 65 70 75 80

Asn Asn Thr His Ser Ser Gly Lys Asn Thr Ser Leu Val Leu Val
 85 90 95

<210> 351

<211> 165

<212> DNA

<213> Homo sapiens

497

<220>

<221> CDS

<222> (1)...(165)

<400> 351

| | |
|--|----|
| atg tgc tcc atc ccc cgg cat ctg ctg cca ttg gtc ctg cct gtt gcg | 48 |
| Met Cys Ser Ile Pro Arg His Leu Leu Pro Leu Val Leu Pro Val Ala | |
| 1 5 10 15 | |

| | |
|---|----|
| tta ctt ctc tgt gcc ctg gag ccc ctc aag cac aga ggc ctc gaa agg | 96 |
| Leu Leu Leu Cys Ala Leu Glu Pro Leu Lys His Arg Gly Leu Glu Arg | |
| 20 25 30 | |

| | |
|---|-----|
| ttg atc aga cat cct cag cac ctg gag cgg ggc ctg gca cac aag acg | 144 |
| Leu Ile Arg His Pro Gln His Leu Glu Arg Gly Leu Ala His Lys Thr | |
| 35 40 45 | |

| | |
|-----------------------------|-----|
| gca atg aac ggc caa ccc tag | 165 |
| Ala Met Asn Gly Gln Pro * | |
| 50 | |

<210> 352

<211> 54

<212> PRT

<213> Homo sapiens

<400> 352

| |
|--|
| Met Cys Ser Ile Pro Arg His Leu Leu Pro Leu Val Leu Pro Val Ala |
| 1 5 10 15 |

| |
|---|
| Leu Leu Leu Cys Ala Leu Glu Pro Leu Lys His Arg Gly Leu Glu Arg |
| 20 25 30 |

| |
|---|
| Leu Ile Arg His Pro Gln His Leu Glu Arg Gly Leu Ala His Lys Thr |
| 35 40 45 |

| |
|-------------------------|
| Ala Met Asn Gly Gln Pro |
| 50 |

<210> 353

<211> 159

<212> DNA

<213> Homo sapiens

<220>

498

<222> (1)...(159)

atg tgc ttg agg gtt ttc acc ctg gcc ctc agt tgc ctg ctg tgc ggg 48
Met Cys Leu Arg Val Phe Thr Leu Ala Leu Ser Cys Leu Leu Cys Gly
1 5 10 15

tcc ctg ggg cag ctg cag ggg ctc acg gac cca tca ggg tct cca cag 96
Ser Leu Gly Gln Leu Gln Gly Leu Thr Asp Pro Ser Gly Ser Pro Gln
20 25 30

ctc ccc tgc agt gtg tgc acc cca caa tgt ctg cgg ctc ttc ttc cgg 144
Leu Pro Cys Ser Val Cys Thr Pro Gln Cys Leu Arg Leu Phe Phe Arg
35 40 45

cgt gtc ggg ctt tga
Arg Val Gly Leu *
50

<213> Homo sapiens

Met Cys Leu Arg Val Phe Thr Leu Ala Leu Ser Cys Leu Leu Cys Gly
1 5 10 15
Ser Leu Gly Gln Leu Gln Gly Leu Thr Asp Pro Ser Gly Ser Pro Gln
20 25 30
Leu Pro Cys Ser Val Cys Thr Pro Gln Cys Leu Arg Leu Phe Phe Arg
35 40 45
Arg Val Gly Leu
50

<213> Homo sapiens

$\langle 222 \rangle$ (1)...(210)

499

<400> 355
 atg ggt gcc atg aac cat gat acc aac tac agc ttt cag gtt caa tgt 48
 Met Gly Ala Met Asn His Asp Thr Asn Tyr Ser Phe Gln Val Gln Cys
 1 5 10 15
 ggc tta att gtg gtg gcc tac aaa gat gga tca cct gcc cac cca cat 96
 Gly Leu Ile Val Val Ala Tyr Lys Asp Gly Ser Pro Ala His Pro His
 20 25 30
 ttc atg gat gca gag ctc tgt tcc cag tac tgg acc aag tgg ctt ctt 144
 Phe Met Asp Ala Glu Leu Cys Ser Gln Tyr Trp Thr Lys Trp Leu Leu
 35 40 45
 cga cta gaa gaa tat acg gaa aag aaa aag aac cag aat att cag aaa 192
 Arg Leu Glu Glu Tyr Thr Glu Lys Lys Lys Asn Gln Asn Ile Gln Lys
 50 55 60
 cca gaa tat tca gaa tag 210
 Pro Glu Tyr Ser Glu *
 65

<210> 356
 <211> 69
 <212> PRT
 <213> Homo sapiens

<400> 356
 Met Gly Ala Met Asn His Asp Thr Asn Tyr Ser Phe Gln Val Gln Cys
 1 5 10 15
 Gly Leu Ile Val Val Ala Tyr Lys Asp Gly Ser Pro Ala His Pro His
 20 25 30
 Phe Met Asp Ala Glu Leu Cys Ser Gln Tyr Trp Thr Lys Trp Leu Leu
 35 40 45
 Arg Leu Glu Glu Tyr Thr Glu Lys Lys Lys Asn Gln Asn Ile Gln Lys
 50 55 60
 Pro Glu Tyr Ser Glu
 65

<210> 357
 <211> 243
 <212> DNA
 <213> Homo sapiens

500

<220>

<221> CDS

<222> (1)...(243)

<221> misc_feature

<222> (1)...(243)

<223> n = A,T,C or G

<400> 357

| | |
|---|-----|
| atg gtc ctg ccg gtg gca gcc tat ggn ctg atc ctg atg gcc atg ctg | 48 |
| Met Val Leu Pro Val Ala Ala Tyr Xaa Leu Ile Leu Met Ala Met Leu | |
| 1 5 10 15 | |
| tgg cgc ggc ctg gcc cag ggc ggg agt gcc ggc tgg ggc gcg ctg ctc | 96 |
| Trp Arg Gly Leu Ala Gln Gly Gly Ser Ala Gly Trp Gly Ala Leu Leu | |
| 20 25 30 | |
| ttc acg ctc tct gat ggc gtg ctg gcc tgg gac acc ttc gcc cag ccc | 144 |
| Phe Thr Leu Ser Asp Gly Val Leu Ala Trp Asp Thr Phe Ala Gln Pro | |
| 35 40 45 | |
| ctg ccc cat gcc cgc ctg gtg atc atg acc acc tac tat gct gcc cag | 192 |
| Leu Pro His Ala Arg Leu Val Ile Met Thr Thr Tyr Tyr Ala Ala Gln | |
| 50 55 60 | |
| ctc ctc atc aca ctg tca gcc ctc agg agc ccg gtg ccc aag act gac | 240 |
| Leu Leu Ile Thr Leu Ser Ala Leu Arg Ser Pro Val Pro Lys Thr Asp | |
| 65 70 75 80 | |
| tga | 243 |
| * | |

<210> 358

<211> 80

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(80)

<223> Xaa = Any Amino Acid

501

<400> 358

```

Met Val Leu Pro Val Ala Ala Tyr Xaa Leu Ile Leu Met Ala Met Leu
 1           5           10           15
Trp Arg Gly Leu Ala Gln Gly Gly Ser Ala Gly Trp Gly Ala Leu Leu
          20           25           30
Phe Thr Leu Ser Asp Gly Val Leu Ala Trp Asp Thr Phe Ala Gln Pro
        35           40           45
Leu Pro His Ala Arg Leu Val Ile Met Thr Thr Tyr Tyr Ala Ala Gln
      50           55           60
Leu Leu Ile Thr Leu Ser Ala Leu Arg Ser Pro Val Pro Lys Thr Asp
65           70           75           80

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<210> 359

<211> 324

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(324)

<400> 359

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atg aag agc acc tgt ggt tcc ctt gtg gcc atg agt gtt gtg gtg gga      48
Met Lys Ser Thr Cys Gly Ser Leu Val Ala Met Ser Val Val Val Gly
 1           5           10           15

cca gca tca agc gca aga gat ctg ccg agt cca cgt gga tac act atg      96
Pro Ala Ser Ser Ala Arg Asp Leu Pro Ser Pro Arg Gly Tyr Thr Met
          20           25           30

acc ccg cag acc atg aag gta gat gag gag gta atg gca ttc cgt ggt      144
Thr Pro Gln Thr Met Lys Val Asp Glu Glu Val Met Ala Phe Arg Gly
        35           40           45

gcc cga tgt gat ggc atc agg gtt ctt cct agc agc gtg gaa gac act      192
Ala Arg Cys Asp Gly Ile Arg Val Leu Pro Ser Ser Val Glu Asp Thr
      50           55           60

cct gcc ctc aag agg gct aag tcc agt aaa acc caa cca aca gga gac      240
Pro Ala Leu Lys Arg Ala Lys Ser Ser Lys Thr Gln Pro Thr Gly Asp
65           70           75           80

agt tgg gca gga aga ctc att ctg agt gta gat ggc tct ggg ttt tgt      288

```

502

Ser Trp Ala Gly Arg Leu Ile Leu Ser Val Asp Gly Ser Gly Phe Cys
 85 90 95

gag agg gtg aaa tct ttg gtc gtt aaa caa ttc tag 324
 Glu Arg Val Lys Ser Leu Val Val Lys Gln Phe *
 100 105

<210> 360
 <211> 107
 <212> PRT
 <213> Homo sapiens

<400> 360
 Met Lys Ser Thr Cys Gly Ser Leu Val Ala Met Ser Val Val Val Gly
 1 5 10 15
 Pro Ala Ser Ser Ala Arg Asp Leu Pro Ser Pro Arg Gly Tyr Thr Met
 20 25 30
 Thr Pro Gln Thr Met Lys Val Asp Glu Glu Val Met Ala Phe Arg Gly
 35 40 45
 Ala Arg Cys Asp Gly Ile Arg Val Leu Pro Ser Ser Val Glu Asp Thr
 50 55 60
 Pro Ala Leu Lys Arg Ala Lys Ser Ser Lys Thr Gln Pro Thr Gly Asp
 65 70 75 80
 Ser Trp Ala Gly Arg Leu Ile Leu Ser Val Asp Gly Ser Gly Phe Cys
 85 90 95
 Glu Arg Val Lys Ser Leu Val Val Lys Gln Phe
 100 105

<210> 361
 <211> 252
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(252)

<400> 361
 atg gag gaa gga ggc ggc ggc gta cgg agt ctg gtc ccg ggc ggc ccg 48
 Met Glu Glu Gly Gly Gly Gly Val Arg Ser Leu Val Pro Gly Gly Pro
 1 5 10 15
 gtg tta ctg gtc ctc tgc ggc ctc ctg gag gcg tcc ggc ggc ggc cga 96

503

Val Leu Leu Val Leu Cys Gly Leu Leu Glu Ala Ser Gly Gly Gly Arg
 20 25 30

gcc ctt cct caa ctc agc gat gac atc cct ttc cga gtc aac tgg ccc 144
 Ala Leu Pro Gln Leu Ser Asp Asp Ile Pro Phe Arg Val Asn Trp Pro
 35 40 45

ggc acc gag ttc tct ctg ccc aca act gga gtt tta tat aaa gaa gat 192
 Gly Thr Glu Phe Ser Leu Pro Thr Thr Gly Val Leu Tyr Lys Glu Asp
 50 55 60

aat tat gtc atc atg aca act gca cat aaa gaa aaa tat aaa aaa aaa 240
 Asn Tyr Val Ile Met Thr Thr Ala His Lys Glu Lys Tyr Lys Lys Lys
 65 70 75 80

aaa aaa aac taa 252
 Lys Lys Asn *

<210> 362
 <211> 83
 <212> PRT
 <213> Homo sapiens

<400> 362

Met Glu Glu Gly Gly Gly Val Arg Ser Leu Val Pro Gly Gly Pro
 1 5 10 15

Val Leu Leu Val Leu Cys Gly Leu Leu Glu Ala Ser Gly Gly Arg
 20 25 30

Ala Leu Pro Gln Leu Ser Asp Asp Ile Pro Phe Arg Val Asn Trp Pro
 35 40 45

Gly Thr Glu Phe Ser Leu Pro Thr Thr Gly Val Leu Tyr Lys Glu Asp
 50 55 60

Asn Tyr Val Ile Met Thr Thr Ala His Lys Glu Lys Tyr Lys Lys Lys
 65 70 75 80

Lys Lys Asn

<210> 363
 <211> 459
 <212> DNA
 <213> Homo sapiens

| | | | | | | | | | | | | | | | | | | |
|---|-----|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|
| <400> 363 | | | | | | | | | | | | | | | | | | |
| atg gat gga aca caa cag cag att ttt aaa atg tta gca gag gta cta | 48 | | | | | | | | | | | | | | | | | |
| Met Asp Gly Thr Gln Gln Gln Ile Phe Lys Met Leu Ala Glu Val Leu | | | | | | | | | | | | | | | | | | |
| 1 5 10 15 | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | |
| gga gga atc aat tgt gta aaa gcc tcg gtt ctt acg cct tat tac cac | 96 | | | | | | | | | | | | | | | | | |
| Gly Gly Ile Asn Cys Val Lys Ala Ser Val Leu Thr Pro Tyr Tyr His | | | | | | | | | | | | | | | | | | |
| 20 25 30 | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | |
| aaa gta gat ttt gag tgt atc ttg gat aaa aga aaa aaa cct ctt ccg | 144 | | | | | | | | | | | | | | | | | |
| Lys Val Asp Phe Glu Cys Ile Leu Asp Lys Arg Lys Lys Pro Leu Pro | | | | | | | | | | | | | | | | | | |
| 35 40 45 | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | |
| tat gga agc cat aat ata gca ttg gga caa cta cca gaa atg ccc tgg | 192 | | | | | | | | | | | | | | | | | |
| Tyr Gly Ser His Asn Ile Ala Leu Gly Gln Leu Pro Glu Met Pro Trp | | | | | | | | | | | | | | | | | | |
| 50 55 60 | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | |
| gaa tca aat atc gaa ata gtt gga tca agg ctg cca cca ggg gct gaa | 240 | | | | | | | | | | | | | | | | | |
| Glu Ser Asn Ile Glu Ile Val Gly Ser Arg Leu Pro Pro Gly Ala Glu | | | | | | | | | | | | | | | | | | |
| 65 70 75 80 | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | |
| agg att gct ttg gaa ttt ttg gat tca aaa gca ctt tgt aga aat atc | 288 | | | | | | | | | | | | | | | | | |
| Arg Ile Ala Leu Glu Phe Leu Asp Ser Lys Ala Leu Cys Arg Asn Ile | | | | | | | | | | | | | | | | | | |
| 85 90 95 | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | |
| cct cac atg aaa gga aaa tct gct atg aaa aaa cga cat ttg gaa att | 336 | | | | | | | | | | | | | | | | | |
| Pro His Met Lys Gly Lys Ser Ala Met Lys Lys Arg His Leu Glu Ile | | | | | | | | | | | | | | | | | | |
| 100 105 110 | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | |
| ctg ggg tat cgt gta att cag att tcc cag ttt gaa tgg aac tct atg | 384 | | | | | | | | | | | | | | | | | |
| Leu Gly Tyr Arg Val Ile Gln Ile Ser Gln Phe Glu Trp Asn Ser Met | | | | | | | | | | | | | | | | | | |
| 115 120 125 | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | |
| gca ctg tca aca aag gat gct cgg atg gac tac ctg aga gaa tgt ata | 432 | | | | | | | | | | | | | | | | | |
| Ala Leu Ser Thr Lys Asp Ala Arg Met Asp Tyr Leu Arg Glu Cys Ile | | | | | | | | | | | | | | | | | | |
| 130 135 140 | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | |
| ttt gga gaa gtc aag tca tgt ttg tag | 459 | | | | | | | | | | | | | | | | | |
| Phe Gly Glu Val Lys Ser Cys Leu * | | | | | | | | | | | | | | | | | | |
| 145 150 | | | | | | | | | | | | | | | | | | |

505

<210> 364
 <211> 152
 <212> PRT
 <213> Homo sapiens

<400> 364
 Met Asp Gly Thr Gln Gln Gln Ile Phe Lys Met Leu Ala Glu Val Leu
 1 5 10 15
 Gly Gly Ile Asn Cys Val Lys Ala Ser Val Leu Thr Pro Tyr Tyr His
 20 25 30
 Lys Val Asp Phe Glu Cys Ile Leu Asp Lys Arg Lys Lys Pro Leu Pro
 35 40 45
 Tyr Gly Ser His Asn Ile Ala Leu Gly Gln Leu Pro Glu Met Pro Trp
 50 55 60
 Glu Ser Asn Ile Glu Ile Val Gly Ser Arg Leu Pro Pro Gly Ala Glu
 65 70 75 80
 Arg Ile Ala Leu Glu Phe Leu Asp Ser Lys Ala Leu Cys Arg Asn Ile
 85 90 95
 Pro His Met Lys Gly Lys Ser Ala Met Lys Lys Arg His Leu Glu Ile
 100 105 110
 Leu Gly Tyr Arg Val Ile Gln Ile Ser Gln Phe Glu Trp Asn Ser Met
 115 120 125
 Ala Leu Ser Thr Lys Asp Ala Arg Met Asp Tyr Leu Arg Glu Cys Ile
 130 135 140
 Phe Gly Glu Val Lys Ser Cys Leu
 145 150

<210> 365
 <211> 600
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(600)

<400> 365
 atg gtg tgg cgc cgg ctt ctg cgg aag agg tgg gtg ctc gcc ctg gtc 48
 Met Val Trp Arg Arg Leu Leu Arg Lys Arg Trp Val Leu Ala Leu Val
 1 5 10 15
 ttc ggg ctg tcg ctc gtc tac ttc ctc agc agc acc ttc aag cag gag 96

506

| | |
|---|-----|
| Phe Gly Leu Ser Leu Val Tyr Phe Leu Ser Ser Thr Phe Lys Gln Glu | |
| 20 25 30 | |
| gag agg gca gtg aga gat agg aat ctc ctc cag gtt cat gac cat aat | 144 |
| Glu Arg Ala Val Arg Asp Arg Asn Leu Leu Gln Val His Asp His Asn | |
| 35 40 45 | |
| cag ccc atc ccg tgg aaa gtg cag ttt aac ttg ggc aat agc agt cgt | 192 |
| Gln Pro Ile Pro Trp Lys Val Gln Phe Asn Leu Gly Asn Ser Ser Arg | |
| 50 55 60 | |
| ccg agc aat cag tgc cgc aac tcc att caa ggg aag cac ctc atc acg | 240 |
| Pro Ser Asn Gln Cys Arg Asn Ser Ile Gln Gly Lys His Leu Ile Thr | |
| 65 70 75 80 | |
| gat gaa ctc ggc tac gtt tgc gag agg aag gat ttg ctg gta aat ggc | 288 |
| Asp Glu Leu Gly Tyr Val Cys Glu Arg Lys Asp Leu Leu Val Asn Gly | |
| 85 90 95 | |
| tgc tgt aat gtc aac gtc cct agc acg aag cag tac tgc tgt gat ggc | 336 |
| Cys Cys Asn Val Asn Val Pro Ser Thr Lys Gln Tyr Cys Cys Asp Gly | |
| 100 105 110 | |
| tgc tgg ccc aac ggc tgc tgc agc gcc tat gag tac tgt gtc tcc tgc | 384 |
| Cys Trp Pro Asn Gly Cys Cys Ser Ala Tyr Glu Tyr Cys Val Ser Cys | |
| 115 120 125 | |
| tgc ctg cag ccc aac aag caa ctt ctc ctg gag cgc ttc ctc aac cgg | 432 |
| Cys Leu Gln Pro Asn Lys Gln Leu Leu Leu Glu Arg Phe Leu Asn Arg | |
| 130 135 140 | |
| gca gcc gtg gca ttc cag aac ctc ttc atg gca gtc gaa gat cac ttt | 480 |
| Ala Ala Val Ala Phe Gln Asn Leu Phe Met Ala Val Glu Asp His Phe | |
| 145 150 155 160 | |
| gag ttg tgc ctg gcc aaa tgc agg acc tca tct cag agc gtg cag cat | 528 |
| Glu Leu Cys Leu Ala Lys Cys Arg Thr Ser Ser Gln Ser Val Gln His | |
| 165 170 175 | |
| gag aac acc tac cgg gac ccc ata gca aag tat tgc tat gga gaa agc | 576 |
| Glu Asn Thr Tyr Arg Asp Pro Ile Ala Lys Tyr Cys Tyr Gly Glu Ser | |
| 180 185 190 | |
| ccg ccc gag ctc ttc ccc gct tga | 600 |

507

Pro Pro Glu Leu Phe Pro Ala *

195

<210> 366

<211> 199

<212> PRT

<213> Homo sapiens

<400> 366

Met Val Trp Arg Arg Leu Leu Arg Lys Arg Trp Val Leu Ala Leu Val
 1 5 10 15
 Phe Gly Leu Ser Leu Val Tyr Phe Leu Ser Ser Thr Phe Lys Gln Glu
 20 25 30
 Glu Arg Ala Val Arg Asp Arg Asn Leu Leu Gln Val His Asp His Asn
 35 40 45
 Gln Pro Ile Pro Trp Lys Val Gln Phe Asn Leu Gly Asn Ser Ser Arg
 50 55 60
 Pro Ser Asn Gln Cys Arg Asn Ser Ile Gln Gly Lys His Leu Ile Thr
 65 70 75 80
 Asp Glu Leu Gly Tyr Val Cys Glu Arg Lys Asp Leu Leu Val Asn Gly
 85 90 95
 Cys Cys Asn Val Asn Val Pro Ser Thr Lys Gln Tyr Cys Cys Asp Gly
 100 105 110
 Cys Trp Pro Asn Gly Cys Cys Ser Ala Tyr Glu Tyr Cys Val Ser Cys
 115 120 125
 Cys Leu Gln Pro Asn Lys Gln Leu Leu Leu Glu Arg Phe Leu Asn Arg
 130 135 140
 Ala Ala Val Ala Phe Gln Asn Leu Phe Met Ala Val Glu Asp His Phe
 145 150 155 160
 Glu Leu Cys Leu Ala Lys Cys Arg Thr Ser Ser Gln Ser Val Gln His
 165 170 175
 Glu Asn Thr Tyr Arg Asp Pro Ile Ala Lys Tyr Cys Tyr Gly Glu Ser
 180 185 190
 Pro Pro Glu Leu Phe Pro Ala
 195

<210> 367

<211> 249

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(249)

| | |
|---|-----|
| atg agc aaa tac aag cac aag agc agc cct tta ttg cct ctt ctt atc | 48 |
| Met Ser Lys Tyr Lys His Lys Ser Ser Pro Leu Leu Pro Leu Leu Ile | |
| 1 5 10 15 | |
| ttt cat aat gtt tgc ttc agt cct gca aat aaa ccc aag atc ctg gct | 96 |
| Phe His Asn Val Cys Phe Ser Pro Ala Asn Lys Pro Lys Ile Leu Ala | |
| 20 25 30 | |
| aat gaa aaa gtc att act gtg ctt gct gcc tgt ctg gaa agt gag aat | 144 |
| Asn Glu Lys Val Ile Thr Val Leu Ala Ala Cys Leu Glu Ser Glu Asn | |
| 35 40 45 | |
| caa aat gct cag agg att gga gca gct gcc ctt ggc tct gat tta caa | 192 |
| Gln Asn Ala Gln Arg Ile Gly Ala Ala Ala Leu Gly Ser Asp Leu Gln | |
| 50 55 60 | |
| tta tca gaa ggc aaa aac agc ttt gaa aag ccc atc agt aaa aag aag | 240 |
| Leu Ser Glu Gly Lys Asn Ser Phe Glu Lys Pro Ile Ser Lys Lys Lys | |
| 65 70 75 80 | |
| agt gga tga | 249 |
| Ser Gly * | |

<213> Homo sapiens

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Lys | Tyr | Lys | His | Lys | Ser | Ser | Pro | Leu | Leu | Pro | Leu | Ile |
| 1 | | | | 5 | | | | | 10 | | | | 15 | |
| Phe | His | Asn | Val | Cys | Phe | Ser | Pro | Ala | Asn | Lys | Pro | Lys | Ile | Leu |
| | | | 20 | | | | | 25 | | | | | 30 | Ala |
| Asn | Glu | Lys | Val | Ile | Thr | Val | Leu | Ala | Ala | Cys | Leu | Glu | Ser | Glu |
| | | 35 | | | | | 40 | | | | | 45 | | Asn |
| Gln | Asn | Ala | Gln | Arg | Ile | Gly | Ala | Ala | Ala | Leu | Gly | Ser | Asp | Leu |
| | 50 | | | | | 55 | | | | | 60 | | | Gln |
| Leu | Ser | Glu | Gly | Lys | Asn | Ser | Phe | Glu | Lys | Pro | Ile | Ser | Lys | Lys |
| 65 | | | | | 70 | | | | | 75 | | | | 80 |

509

Ser Gly

<210> 369
 <211> 285
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(285)

<400> 369
 atg gac ggc cgc ggg gct ttc tgg aca gtg gcc att ccc aga gcc agg 48
 Met Asp Gly Arg Gly Ala Phe Trp Thr Val Ala Ile Pro Arg Ala Arg
 1 5 10 15
 cag gaa ggc ctc ggg agg ctg ggg ctc ccg ttc ccg gtg aag cgg acg 96
 Gln Glu Gly Leu Gly Arg Leu Gly Leu Pro Phe Pro Val Lys Arg Thr
 20 25 30
 ccg cca gcg ccc cag aac cca gga gga agc aca cag gcc cca cag aga 144
 Pro Pro Ala Pro Gln Asn Pro Gly Gly Ser Thr Gln Ala Pro Gln Arg
 35 40 45
 gtg gtt ggc aag agt cac tcg ggg att agg atg ccg gcc aaa tcg cgg 192
 Val Val Gly Lys Ser His Ser Gly Ile Arg Met Pro Ala Lys Ser Arg
 50 55 60
 aat ttg agg ctg gaa tcc aag ctc aac agg act gct gtg tgt gaa gca 240
 Asn Leu Arg Leu Glu Ser Lys Leu Asn Arg Thr Ala Val Cys Glu Ala
 65 70 75 80
 ctc aag agg gcc cct aca acc aac ctg cca gga gtc ggc tcc tga 285
 Leu Lys Arg Ala Pro Thr Thr Asn Leu Pro Gly Val Gly Ser *
 85 90

<210> 370
 <211> 94
 <212> PRT
 <213> Homo sapiens

<400> 370

510

Met Asp Gly Arg Gly Ala Phe Trp Thr Val Ala Ile Pro Arg Ala Arg
 1 5 10 15
 Gln Glu Gly Leu Gly Arg Leu Gly Leu Pro Phe Pro Val Lys Arg Thr
 20 25 30
 Pro Pro Ala Pro Gln Asn Pro Gly Gly Ser Thr Gln Ala Pro Gln Arg
 35 40 45
 Val Val Gly Lys Ser His Ser Gly Ile Arg Met Pro Ala Lys Ser Arg
 50 55 60
 Asn Leu Arg Leu Glu Ser Lys Leu Asn Arg Thr Ala Val Cys Glu Ala
 65 70 75 80
 Leu Lys Arg Ala Pro Thr Thr Asn Leu Pro Gly Val Gly Ser
 85 90

<210> 371
 <211> 249
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(249)

<400> 371
 atg cgc gac tgc gac atc aac gac gac gaa ttc ctg cac ctg ccg gcg 48
 Met Arg Asp Cys Asp Ile Asn Asp Asp Glu Phe Leu His Leu Pro Ala
 1 5 10 15
 cat ttg cgg gtg gtc ggg ccc cag cag ctg cat tcc gag acc aac gag 96
 His Leu Arg Val Val Gly Pro Gln Gln Leu His Ser Glu Thr Asn Glu
 20 25 30
 cgg ctc ttc gat gag aag tac aag cct gtc gtg ctc acc gac gat cag 144
 Arg Leu Phe Asp Glu Lys Tyr Lys Pro Val Val Leu Thr Asp Asp Gln
 35 40 45
 gtg gac cag gcg ctg tgg gag gag cag gtc ttg cag aag gag aag aag 192
 Val Asp Gln Ala Leu Trp Glu Glu Gln Val Leu Gln Lys Glu Lys Lys
 50 55 60
 gac agg ctc gcc ctg agc cag gcc cac tcg ctg gtg cag gcg gag gcc 240
 Asp Arg Leu Ala Leu Ser Gln Ala His Ser Leu Val Gln Ala Glu Ala
 65 70 75 80
 ccg aga tga 249

511

Pro Arg *

<210> 372
 <211> 82
 <212> PRT
 <213> Homo sapiens

<400> 372
 Met Arg Asp Cys Asp Ile Asn Asp Asp Glu Phe Leu His Leu Pro Ala
 1 5 10 15
 His Leu Arg Val Val Gly Pro Gln Gln Leu His Ser Glu Thr Asn Glu
 20 25 30
 Arg Leu Phe Asp Glu Lys Tyr Lys Pro Val Val Leu Thr Asp Asp Gln
 35 40 45
 Val Asp Gln Ala Leu Trp Glu Glu Gln Val Leu Gln Lys Glu Lys Lys
 50 55 60
 Asp Arg Leu Ala Leu Ser Gln Ala His Ser Leu Val Gln Ala Glu Ala
 65 70 75 80
 Pro Arg

<210> 373
 <211> 219
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(219)
 <221> misc_feature
 <222> (1)...(219)
 <223> n = A,T,C or G

<400> 373
 atg ggc cga gcg ctg ccc ccc ggg ggt cct cgg cgc cgg gcg can tta 48
 Met Gly Arg Ala Leu Pro Pro Gly Gly Pro Arg Arg Arg Ala Xaa Leu
 1 5 10 15
 nga gcg can gca gca ggc tcc att ccc ggc cgc cgc tca gcc cat 96
 Xaa Ala Xaa Ala Ala Gly Ser Ile Pro Gly Arg Arg Arg Ser Ala His
 20 25 30

512

tac gca aac ctg gcg ggt cca acc aac ccc gct ctg ccg ccg ctg ctg 144
 Tyr Ala Asn Leu Ala Gly Pro Thr Asn Pro Ala Leu Pro Pro Leu Leu
 35 40 45

 gaa ccc agg agg cgt gct tgc agg ctt cgg gca cta cgc ggg gct gga 192
 Glu Pro Arg Arg Arg Ala Cys Arg Leu Arg Ala Leu Arg Gly Ala Gly
 50 55 60

 aat acc acg cac tgc ccc ttc gcc tag 219
 Asn Thr Thr His Cys Pro Phe Ala *
 65 70

<210> 374
 <211> 72
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(72)
 <223> Xaa = Any Amino Acid

<400> 374
 Met Gly Arg Ala Leu Pro Pro Gly Gly Pro Arg Arg Arg Ala Xaa Leu
 1 5 10 15
 Xaa Ala Xaa Ala Ala Gly Ser Ile Pro Gly Arg Arg Arg Ser Ala His
 20 25 30
 Tyr Ala Asn Leu Ala Gly Pro Thr Asn Pro Ala Leu Pro Pro Leu Leu
 35 40 45
 Glu Pro Arg Arg Arg Ala Cys Arg Leu Arg Ala Leu Arg Gly Ala Gly
 50 55 60
 Asn Thr Thr His Cys Pro Phe Ala
 65 70

<210> 375
 <211> 579
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(579)

513

<400> 375

| | |
|---|-----|
| atg gcc ccc aag ccg ggg gcc gag tgg agc aca gcc ctg tcc cat ctg | 48 |
| Met Ala Pro Lys Pro Gly Ala Glu Trp Ser Thr Ala Leu Ser His Leu | |
| 1 5 10 15 | |
| gtg ctg gga gtg gtg tct ctg cac gca gcc gtg agc aca gcc gag gca | 96 |
| Val Leu Gly Val Val Ser Leu His Ala Ala Val Ser Thr Ala Glu Ala | |
| 20 25 30 | |
| agt cga ggg gct gct gct ggc ttc ctg ctc cag gtc ttg gct gcc acc | 144 |
| Ser Arg Gly Ala Ala Ala Gly Phe Leu Leu Gln Val Leu Ala Ala Thr | |
| 35 40 45 | |
| acc acg ctg gcc cca ggg ctg agc aca cat gaa gac tgc ctt gct gga | 192 |
| Thr Thr Leu Ala Pro Gly Leu Ser Thr His Glu Asp Cys Leu Ala Gly | |
| 50 55 60 | |
| gcc tgg gtg gcc acc gtc atc ggc ctt ccc ctt ctg gcc ttc gat ttc | 240 |
| Ala Trp Val Ala Thr Val Ile Gly Leu Pro Leu Leu Ala Phe Asp Phe | |
| 65 70 75 80 | |
| cac tgg gtg aat ggg gac cgc tcc tct gcc aac ctg ctc ctg gga gga | 288 |
| His Trp Val Asn Gly Asp Arg Ser Ser Ala Asn Leu Leu Leu Gly Gly | |
| 85 90 95 | |
| ggc atg gtg ctg gca gtg gct ggc ggc cac ctc ggc cct gag ggc cgc | 336 |
| Gly Met Val Leu Ala Val Ala Gly Gly His Leu Gly Pro Glu Gly Arg | |
| 100 105 110 | |
| tct gtg gct ggt cag gca atg ctg ttg gtg gtc gca gtg acc atc ctc | 384 |
| Ser Val Ala Gly Gln Ala Met Leu Leu Val Val Ala Val Thr Ile Leu | |
| 115 120 125 | |
| att gta gct gtc ttc acg gcc aac act tat ggg atg tgg ggg ggg gcg | 432 |
| Ile Val Ala Val Phe Thr Ala Asn Thr Tyr Gly Met Trp Gly Gly Ala | |
| 130 135 140 | |
| atg ctg ggt gtg gca ggc ctc ctg agc cgg ctg gag gag gac agg ctg | 480 |
| Met Leu Gly Val Ala Gly Leu Leu Ser Arg Leu Glu Glu Asp Arg Leu | |
| 145 150 155 160 | |
| ctg ctg,cta ccg aag gag gat gtc tgt cgc tgg gcc ttg gct gta ggc | 528 |
| Leu Leu Leu Pro Lys Glu Asp Val Cys Arg Trp Ala Leu Ala Val Gly | |

514

165

170

175

agc tgg gct tac tgc cgg gcc ctg cat aca cag cgc ctc cag tgg gag 576
 Ser Trp Ala Tyr Cys Arg Ala Leu His Thr Gln Arg Leu Gln Trp Glu
 180 185 190

tga 579
 *

<210> 376

<211> 192

<212> PRT

<213> Homo sapiens

<400> 376

Met Ala Pro Lys Pro Gly Ala Glu Trp Ser Thr Ala Leu Ser His Leu
 1 5 10 15
 Val Leu Gly Val Val Ser Leu His Ala Ala Val Ser Thr Ala Glu Ala
 20 25 30
 Ser Arg Gly Ala Ala Ala Gly Phe Leu Leu Gln Val Leu Ala Ala Thr
 35 40 45
 Thr Thr Leu Ala Pro Gly Leu Ser Thr His Glu Asp Cys Leu Ala Gly
 50 55 60
 Ala Trp Val Ala Thr Val Ile Gly Leu Pro Leu Leu Ala Phe Asp Phe
 65 70 75 80
 His Trp Val Asn Gly Asp Arg Ser Ser Ala Asn Leu Leu Leu Gly Gly
 85 90 95
 Gly Met Val Leu Ala Val Ala Gly Gly His Leu Gly Pro Glu Gly Arg
 100 105 110
 Ser Val Ala Gly Gln Ala Met Leu Leu Val Val Ala Val Thr Ile Leu
 115 120 125
 Ile Val Ala Val Phe Thr Ala Asn Thr Tyr Gly Met Trp Gly Gly Ala
 130 135 140
 Met Leu Gly Val Ala Gly Leu Leu Ser Arg Leu Glu Glu Asp Arg Leu
 145 150 155 160
 Leu Leu Leu Pro Lys Glu Asp Val Cys Arg Trp Ala Leu Ala Val Gly
 165 170 175
 Ser Trp Ala Tyr Cys Arg Ala Leu His Thr Gln Arg Leu Gln Trp Glu
 180 185 190

<210> 377

<211> 606

515

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(606)

<400> 377

| | |
|---|-----|
| atg acc gtg cag aga ctc gtg gcc gcg gcc gtg ctg gtg gcc ctg gtc | 48 |
| Met Thr Val Gln Arg Leu Val Ala Ala Ala Val Leu Val Ala Leu Val | |
| 1 5 10 15 | |
| tca ctc atc ctc aac aac gtg gcg gcc ttc acc tcc aac tgg gtg tgc | 96 |
| Ser Leu Ile Leu Asn Asn Val Ala Ala Phe Thr Ser Asn Trp Val Cys | |
| 20 25 30 | |
| cag acg ctg gag gat ggg cgc agg cgc agc gtg ggg ctg tgg agg tcc | 144 |
| Gln Thr Leu Glu Asp Gly Arg Arg Arg Ser Val Gly Leu Trp Arg Ser | |
| 35 40 45 | |
| tgc tgg ctg gtg gac agg acc cgg gga ggg ccg agc cct ggg gcc aga | 192 |
| Cys Trp Leu Val Asp Arg Thr Arg Gly Gly Pro Ser Pro Gly Ala Arg | |
| 50 55 60 | |
| gcc ggc cag gtg gac gca cat gac tgt gag gcg ctg ggc tgg ggc tcc | 240 |
| Ala Gly Gln Val Asp Ala His Asp Cys Glu Ala Leu Gly Trp Gly Ser | |
| 65 70 75 80 | |
| gag gca gcc ggc ttc cag gag tcc cga ggc acc gtc aaa ctg cag ttc | 288 |
| Glu Ala Ala Gly Phe Gln Glu Ser Arg Gly Thr Val Lys Leu Gln Phe | |
| 85 90 95 | |
| gac atg atg cgc gcc tgc aac ctg gtg gcc acg gcc gcg ctc acc gca | 336 |
| Asp Met Met Arg Ala Cys Asn Leu Val Ala Thr Ala Ala Leu Thr Ala | |
| 100 105 110 | |
| ggc cag ctc acc ttc ctc ctg ggg ctg gtg ggc ctg ccc ctg ctg tca | 384 |
| Gly Gln Leu Thr Phe Leu Leu Gly Leu Val Gly Leu Pro Leu Leu Ser | |
| 115 120 125 | |
| ccc gac gcc ccg tgc tgg gag gag gcc atg gcc gct gca ttc caa ctg | 432 |
| Pro Asp Ala Pro Cys Trp Glu Glu Ala Met Ala Ala Ala Phe Gln Leu | |
| 130 135 140 | |

516

gcg agt ttt gtc ctg gtc atc ggg ctc gtg act ttc tac aga att ggc 480
 Ala Ser Phe Val Leu Val Ile Gly Leu Val Thr Phe Tyr Arg Ile Gly
 145 150 155 160

 cca tac acc aac ctg tcc tgg tcc tgc tac ctg aac att ggc gcc tgc 528
 Pro Tyr Thr Asn Leu Ser Trp Ser Cys Tyr Leu Asn Ile Gly Ala Cys
 165 170 175

 ctt ctg gcc acg ctg gcg gca gca tgc tca tct gga aca ttc tcc aca 576
 Leu Leu Ala Thr Leu Ala Ala Ala Cys Ser Ser Gly Thr Phe Ser Thr
 180 185 190

 aga ggg agg act gca tgg ccc ccc ggg tga 606
 Arg Gly Arg Thr Ala Trp Pro Pro Gly *
 195 200

<210> 378
 <211> 201
 <212> PRT
 <213> Homo sapiens

<400> 378
 Met Thr Val Gln Arg Leu Val Ala Ala Ala Val Leu Val Ala Leu Val
 1 5 10 15
 Ser Leu Ile Leu Asn Asn Val Ala Ala Phe Thr Ser Asn Trp Val Cys
 20 25 30
 Gln Thr Leu Glu Asp Gly Arg Arg Arg Ser Val Gly Leu Trp Arg Ser
 35 40 45
 Cys Trp Leu Val Asp Arg Thr Arg Gly Gly Pro Ser Pro Gly Ala Arg
 50 55 60
 Ala Gly Gln Val Asp Ala His Asp Cys Glu Ala Leu Gly Trp Gly Ser
 65 70 75 80
 Glu Ala Ala Gly Phe Gln Glu Ser Arg Gly Thr Val Lys Leu Gln Phe
 85 90 95
 Asp Met Met Arg Ala Cys Asn Leu Val Ala Thr Ala Ala Leu Thr Ala
 100 105 110
 Gly Gln Leu Thr Phe Leu Leu Gly Leu Val Gly Leu Pro Leu Leu Ser
 115 120 125
 Pro Asp Ala Pro Cys Trp Glu Glu Ala Met Ala Ala Ala Phe Gln Leu
 130 135 140
 Ala Ser Phe Val Leu Val Ile Gly Leu Val Thr Phe Tyr Arg Ile Gly
 145 150 155 160
 Pro Tyr Thr Asn Leu Ser Trp Ser Cys Tyr Leu Asn Ile Gly Ala Cys

Leu Leu Ala Thr 165 Leu Ala Ala Ala Cys 170 Ser Ser Gly Thr 175 Phe Ser Thr
180 185 190
Arg Gly Arg Thr Ala Trp Pro Pro Gly
195 200

```
<220>
<221> CDS
<222> (1)...(297)

<221> misc_feature
<222> (1)...(297)
<223> n = A,T,C or G
```

| | | | | | | | | | | | | | | | | |
|---|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> 379 | | | | | | | | | | | | | | | | |
| atg | gnc | ncg | acg | ctg | gtg | gtc | atc | tgc | aca | gca | gtc | atc | gtg | gtg | gtc | 48 |
| Met | Xaa | Xaa | Thr | Leu | Val | Val | Ile | Cys | Thr | Ala | Val | Ile | Val | Val | Val | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| gcg ttg act aga aag aaa gcc ctc aga atc cat tct gtg gaa ggt gac | | | | | | | | | | | | | | | | 96 |
| Ala | Leu | Thr | Arg | Lys | Lys | Ala | Leu | Arg | Ile | His | Ser | Val | Glu | Gly | Asp | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| ctc agg aga aaa tca gct gga cag gag gaa tgg agc ccc agt gct ccc | | | | | | | | | | | | | | | | 144 |
| Leu | Arg | Arg | Lys | Ser | Ala | Gly | Gln | Glu | Glu | Trp | Ser | Pro | Ser | Ala | Pro | |
| | | | 35 | | | | 40 | | | | | 45 | | | | |
| tca ccc cca gga agc tgt gtc cag gca gaa gct gca cct gct ggg ctc | | | | | | | | | | | | | | | | 192 |
| Ser | Pro | Pro | Gly | Ser | Cys | Val | Gln | Ala | Glu | Ala | Ala | Pro | Ala | Gly | Leu | |
| | | | 50 | | | | 55 | | | | | 60 | | | | |
| tgt gga gag cag cgg gga gag gac tgt gcc gag ctg cat gac tac ttc | | | | | | | | | | | | | | | | 240 |
| Cys | Gly | Glu | Gln | Arg | Gly | Glu | Asp | Cys | Ala | Glu | Leu | His | Asp | Tyr | Phe | |
| | | | | | 70 | | | | | 75 | | | | | 80 | |
| 65 | | | | | | | | | | | | | | | | |
| aat gtc ctg agt tac aga agc ctg ggt aac tgc agc ttc ttc aca gag | | | | | | | | | | | | | | | | 288 |
| Asn | Val | Leu | Ser | Tyr | Arg | Ser | Leu | Gly | Asn | Cys | Ser | Phe | Phe | Thr | Glu | |
| | | | | | 85 | | | | 90 | | | | | 95 | | |

518

act ggt tag
 Thr Gly *

297

<210> 380
 <211> 98
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(98)
 <223> Xaa = Any Amino Acid

<400> 380
 Met Xaa Xaa Thr Leu Val Val Ile Cys Thr Ala Val Ile Val Val Val
 1 5 10 15
 Ala Leu Thr Arg Lys Lys Ala Leu Arg Ile His Ser Val Glu Gly Asp
 20 25 30
 Leu Arg Arg Lys Ser Ala Gly Gln Glu Glu Trp Ser Pro Ser Ala Pro
 35 40 45
 Ser Pro Pro Gly Ser Cys Val Gln Ala Glu Ala Ala Pro Ala Gly Leu
 50 55 60
 Cys Gly Glu Gln Arg Gly Glu Asp Cys Ala Glu Leu His Asp Tyr Phe
 65 70 75 80
 Asn Val Leu Ser Tyr Arg Ser Leu Gly Asn Cys Ser Phe Phe Thr Glu
 85 90 95
 Thr Gly

<210> 381
 <211> 264
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(264)

<400> 381
 atg gct gtc tta gta ctt cgc ctg aca gtt gtc ctg gga ctg ctt gtc
 Met Ala Val Leu Val Leu Arg Leu Thr Val Val Leu Gly Leu Leu Val
 1 5 10 15

48

519

tta ttc ctg acc tgc tat gca gac gac aaa cca gac aag cca gac gac 96
 Leu Phe Leu Thr Cys Tyr Ala Asp Asp Lys Pro Asp Lys Pro Asp Asp
 20 25 30

 aag cca gac gac tcg ggc aaa gac cca aag cca gac ttc ccc aaa ttc 144
 Lys Pro Asp Asp Ser Gly Lys Asp Pro Lys Pro Asp Phe Pro Lys Phe
 35 40 45

 cta agc ctc ctg ggc aca gag atc att gag aat gca gtc gag ttc atc 192
 Leu Ser Leu Leu Gly Thr Glu Ile Ile Glu Asn Ala Val Glu Phe Ile
 50 55 60

 ctc cgc tcc atg tcc agg agc aca gga ttt atg gaa ttt gat gat aat 240
 Leu Arg Ser Met Ser Arg Ser Thr Gly Phe Met Glu Phe Asp Asp Asn
 65 70 75 80

 gaa gga aaa cat tca tca aag tga 264
 Glu Gly Lys His Ser Ser Lys *
 85

<210> 382
 <211> 87
 <212> PRT
 <213> Homo sapiens

<400> 382
 Met Ala Val Leu Val Leu Arg Leu Thr Val Val Leu Gly Leu Leu Val
 1 5 10 15
 Leu Phe Leu Thr Cys Tyr Ala Asp Asp Lys Pro Asp Lys Pro Asp Asp
 20 25 30
 Lys Pro Asp Asp Ser Gly Lys Asp Pro Lys Pro Asp Phe Pro Lys Phe
 35 40 45
 Leu Ser Leu Leu Gly Thr Glu Ile Ile Glu Asn Ala Val Glu Phe Ile
 50 55 60
 Leu Arg Ser Met Ser Arg Ser Thr Gly Phe Met Glu Phe Asp Asp Asn
 65 70 75 80
 Glu Gly Lys His Ser Ser Lys
 85

<210> 383
 <211> 225
 <212> DNA

520

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(225)

<400> 383

| | |
|---|-----|
| atg act gcc ctc acc tcc tgg cac ctg gcc tat ctc atc act tgg acc | 48 |
| Met Thr Ala Leu Thr Ser Trp His Leu Ala Tyr Leu Ile Thr Trp Thr | |
| 1 5 10 15 | |
| acc tgc ctg gcc tcc cac ctg ctg cag gct gcc ttt gag cac acg acc | 96 |
| Thr Cys Leu Ala Ser His Leu Leu Gln Ala Ala Phe Glu His Thr Thr | |
| 20 25 30 | |
| cag ctt gcc gag gcc cag gag gtt gaa ccc cag gag gtc tca ggg tct | 144 |
| Gln Leu Ala Glu Ala Gln Glu Val Glu Pro Gln Glu Val Ser Gly Ser | |
| 35 40 45 | |
| tcc ttg ctg ccc tca ctg tct gcg tcc tcg gac tca gag tct gga aca | 192 |
| Ser Leu Leu Pro Ser Leu Ser Ala Ser Ser Asp Ser Glu Ser Gly Thr | |
| 50 55 60 | |
| gtt ttg cca gag caa gaa act ccc aga gaa taa | 225 |
| Val Leu Pro Glu Gln Glu Thr Pro Arg Glu * | |
| 65 70 | |

<210> 384

<211> 74

<212> PRT

<213> Homo sapiens

<400> 384

| | |
|---|--|
| Met Thr Ala Leu Thr Ser Trp His Leu Ala Tyr Leu Ile Thr Trp Thr | |
| 1 5 10 15 | |
| Thr Cys Leu Ala Ser His Leu Leu Gln Ala Ala Phe Glu His Thr Thr | |
| 20 25 30 | |
| Gln Leu Ala Glu Ala Gln Glu Val Glu Pro Gln Glu Val Ser Gly Ser | |
| 35 40 45 | |
| Ser Leu Leu Pro Ser Leu Ser Ala Ser Ser Asp Ser Glu Ser Gly Thr | |
| 50 55 60 | |
| Val Leu Pro Glu Gln Glu Thr Pro Arg Glu | |
| 65 70 | |

521

<210> 385
 <211> 288
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(288)

<221> misc_feature
 <222> (1)...(288)
 <223> n = A,T,C or G

<400> 385
 atg gcc ccc ccg cnc gcg tnc cgg tcc ccg atg tca ccn cng ncg nng 48
 Met Ala Pro Pro Xaa Ala Xaa Arg Ser Pro Met Ser Xaa Xaa Xaa Xaa
 1 5 10 15
 ntg ctg ctg ctg ctg ctg agt ctg gcg ctg ctg ggc gcc cgg gcc 96
 Xaa Leu Leu Leu Leu Leu Ser Leu Ala Leu Leu Gly Ala Arg Ala
 20 25 30
 cgc gcc gag ccc gcc ggg agt gcc gtc ccc gcg cag agc cgc cca tgc 144
 Arg Ala Glu Pro Ala Gly Ser Ala Val Pro Ala Gln Ser Arg Pro Cys
 35 40 45
 gtg gac tgc cac gcc ttc gag ttc atg cag cgc gcc ctg cag gac ctg 192
 Val Asp Cys His Ala Phe Glu Phe Met Gln Arg Ala Leu Gln Asp Leu
 50 55 60
 cgg aag aca gcc tgc agc ctg gac gcg cgg acg gag acc cta ctg ctg 240
 Arg Lys Thr Ala Cys Ser Leu Asp Ala Arg Thr Glu Thr Leu Leu Leu
 65 70 75 80
 cag gca gag cgc cgt gcc ctg tgt gcc tgc tgg cca gcg ggg cac tga 288
 Gln Ala Glu Arg Arg Ala Leu Cys Ala Cys Trp Pro Ala Gly His *
 85 90 95

<210> 386
 <211> 95
 <212> PRT
 <213> Homo sapiens

522

<220>

<221> VARIANT

<222> (1)...(95)

<223> Xaa = Any Amino Acid

<400> 386

```

Met Ala Pro Pro Xaa Ala Xaa Arg Ser Pro Met Ser Xaa Xaa Xaa Xaa
 1             5             10             15
Xaa Leu Leu Leu Leu Leu Ser Leu Ala Leu Leu Gly Ala Arg Ala
      20             25             30
Arg Ala Glu Pro Ala Gly Ser Ala Val Pro Ala Gln Ser Arg Pro Cys
      35             40             45
Val Asp Cys His Ala Phe Glu Phe Met Gln Arg Ala Leu Gln Asp Leu
      50             55             60
Arg Lys Thr Ala Cys Ser Leu Asp Ala Arg Thr Glu Thr Leu Leu Leu
      65             70             75             80
Gln Ala Glu Arg Arg Ala Leu Cys Ala Cys Trp Pro Ala Gly His
      85             90             95

```

<210> 387

<211> 351

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(351)

<400> 387

```

atg aag gga ctc aga agt ctg gca gca aca acc ttg gct ctt ttc ctg      48
Met Lys Gly Leu Arg Ser Leu Ala Ala Thr Thr Leu Ala Leu Phe Leu
 1             5             10             15

gtg ttt gtt ttc ctg gga aac tcc agc tgc gct ccg cag aga ctg ttg      96
Val Phe Val Phe Leu Gly Asn Ser Ser Cys Ala Pro Gln Arg Leu Leu
      20             25             30

gag aga agg aac tgg act cct caa gct atg ctc tac ctg aaa ggg gca      144
Glu Arg Arg Asn Trp Thr Pro Gln Ala Met Leu Tyr Leu Lys Gly Ala
      35             40             45

cag ggt cgc cgc ttc atc tcc gac cag agc cgg aga aag gac ctc tcc      192
Gln Gly Arg Arg Phe Ile Ser Asp Gln Ser Arg Arg Lys Asp Leu Ser

```

523

| | | | |
|---|-----|-----|-----|
| 50 | 55 | 60 | |
| gac cgg cca ctg ccg gaa aga cga agc cca aat ccc caa cta cta act | | | 240 |
| Asp Arg Pro Leu Pro Glu Arg Arg Ser Pro Asn Pro Gln Leu Leu Thr | | | |
| 65 | 70 | 75 | 80 |
| att ccg gag gca gca acc atc tta ctg gcg tcc ctt cag aaa tca cca | | | 288 |
| Ile Pro Glu Ala Ala Thr Ile Leu Leu Ala Ser Leu Gln Lys Ser Pro | | | |
| | 85 | 90 | 95 |
| gaa gat gaa gaa aaa aac ttt gat caa acc aga ttc ctg gaa gac agt | | | 336 |
| Glu Asp Glu Glu Lys Asn Phe Asp Gln Thr Arg Phe Leu Glu Asp Ser | | | |
| | 100 | 105 | 110 |
| ctg ctt aac tgg tga | | | 351 |
| Leu Leu Asn Trp * | | | |
| | 115 | | |

<210> 388
 <211> 116
 <212> PRT
 <213> Homo sapiens

| | | |
|---|-----|-----|
| <400> 388 | | |
| Met Lys Gly Leu Arg Ser Leu Ala Ala Thr Thr Leu Ala Leu Phe Leu | | |
| 1 | 5 | 10 |
| Val Phe Val Phe Leu Gly Asn Ser Ser Cys Ala Pro Gln Arg Leu Leu | | |
| | 20 | 25 |
| Glu Arg Arg Asn Trp Thr Pro Gln Ala Met Leu Tyr Leu Lys Gly Ala | | |
| | 35 | 40 |
| Gln Gly Arg Arg Phe Ile Ser Asp Gln Ser Arg Arg Lys Asp Leu Ser | | |
| | 50 | 55 |
| Asp Arg Pro Leu Pro Glu Arg Arg Ser Pro Asn Pro Gln Leu Leu Thr | | |
| 65 | 70 | 75 |
| Ile Pro Glu Ala Ala Thr Ile Leu Leu Ala Ser Leu Gln Lys Ser Pro | | |
| | 85 | 90 |
| Glu Asp Glu Glu Lys Asn Phe Asp Gln Thr Arg Phe Leu Glu Asp Ser | | |
| | 100 | 105 |
| Leu Leu Asn Trp | | |
| | 115 | |

<210> 389
 <211> 318

524

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(318)

<400> 389

| | |
|---|-----|
| atg aac ttg ggg gtc agc atg ctg agg atc ctc ttc ctc ctg gat gta | 48 |
| Met Asn Leu Gly Val Ser Met Leu Arg Ile Leu Phe Leu Leu Asp Val | |
| 1 5 10 15 | |
| gga gga gct caa gtg ctg gca aca ggc aag acc cct ggg gct gaa att | 96 |
| Gly Gly Ala Gln Val Leu Ala Thr Gly Lys Thr Pro Gly Ala Glu Ile | |
| 20 25 30 | |
| gat ttc aag tac gcc ctc atc ggg act gct gtg ggt gtc gcc ata tct | 144 |
| Asp Phe Lys Tyr Ala Leu Ile Gly Thr Ala Val Gly Val Ala Ile Ser | |
| 35 40 45 | |
| gct ggc ttc ctg gcc ctg aag atc tgc atg atc agg agg cac tta ttt | 192 |
| Ala Gly Phe Leu Ala Leu Lys Ile Cys Met Ile Arg Arg His Leu Phe | |
| 50 55 60 | |
| gac gac gac tct tcc gac ctg aaa agc acg cct ggg ggc ctc agt gac | 240 |
| Asp Asp Asp Ser Ser Asp Leu Lys Ser Thr Pro Gly Gly Leu Ser Asp | |
| 65 70 75 80 | |
| acc atc ccg cta aag aag aga gcc cca agg cga aac cac aat ttc tcc | 288 |
| Thr Ile Pro Leu Lys Lys Arg Ala Pro Arg Arg Asn His Asn Phe Ser | |
| 85 90 95 | |
| aaa aga gat gca cag gtg att gag ctg tag | 318 |
| Lys Arg Asp Ala Gln Val Ile Glu Leu * | |
| 100 105 | |

<210> 390

<211> 105

<212> PRT

<213> Homo sapiens

<400> 390

Met Asn Leu Gly Val Ser Met Leu Arg Ile Leu Phe Leu Leu Asp Val

525

```

      1             5             10             15
Gly Gly Ala Gln Val Leu Ala Thr Gly Lys Thr Pro Gly Ala Glu Ile
      20             25             30
Asp Phe Lys Tyr Ala Leu Ile Gly Thr Ala Val Gly Val Ala Ile Ser
      35             40             45
Ala Gly Phe Leu Ala Leu Lys Ile Cys Met Ile Arg Arg His Leu Phe
      50             55             60
Asp Asp Asp Ser Ser Asp Leu Lys Ser Thr Pro Gly Gly Leu Ser Asp
65             70             75             80
Thr Ile Pro Leu Lys Lys Arg Ala Pro Arg Arg Asn His Asn Phe Ser
      85             90             95
Lys Arg Asp Ala Gln Val Ile Glu Leu
      100             105

```

<210> 391
 <211> 150
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(150)

<221> misc_feature
 <222> (1)...(150)
 <223> n = A,T,C or G

```

      <400> 391
atg gcc atc ctc cag gtc act gcg ggc nac ccc ctg gcc atg gcc cag      48
Met Ala Ile Leu Gln Val Thr Ala Gly Xaa Pro Leu Ala Met Ala Gln
      1             5             10             15

ggc ccc cac ccc ctg gtc cac atc act gag gaa gta gaa gaa aac agg      96
Gly Pro His Pro Leu Val His Ile Thr Glu Glu Val Glu Glu Asn Arg
      20             25             30

aca caa gat ggc aag cct gag aga att gcc cag ctg acc tgg aat gag      144
Thr Gln Asp Gly Lys Pro Glu Arg Ile Ala Gln Leu Thr Trp Asn Glu
      35             40             45

gcc taa      150
Ala *

```

526

<210> 392
 <211> 49
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(49)
 <223> Xaa = Any Amino Acid

<400> 392
 Met Ala Ile Leu Gln Val Thr Ala Gly Xaa Pro Leu Ala Met Ala Gln
 1 5 10 15
 Gly Pro His Pro Leu Val His Ile Thr Glu Glu Val Glu Glu Asn Arg
 20 25 30
 Thr Gln Asp Gly Lys Pro Glu Arg Ile Ala Gln Leu Thr Trp Asn Glu
 35 40 45
 Ala

<210> 393
 <211> 294
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(294)

<400> 393
 atg gat cct gag gtg acc ttg ctg ctg cag tgc cct ggc ggg ggc ctg 48
 Met Asp Pro Glu Val Thr Leu Leu Leu Gln Cys Pro Gly Gly Gly Leu
 1 5 10 15
 ccc cag gag cag ata cag gcc gag ctg agc ccc gcc cat gac cgt cgc 96
 Pro Gln Glu Gln Ile Gln Ala Glu Leu Ser Pro Ala His Asp Arg Arg
 20 25 30
 cca ctg cca ggt ggg gac gag gcc atc act gcc atc tgg gag acc cgg 144
 Pro Leu Pro Gly Gly Asp Glu Ala Ile Thr Ala Ile Trp Glu Thr Arg
 35 40 45
 cta aag gcc caa ccc tgg ctc ttc gac gcc ccc aag ttc cgc ctg cac 192

527

Leu Lys Ala Gln Pro Trp Leu Phe Asp Ala Pro Lys Phe Arg Leu His
 50 55 60

 tca gcc acc ctg gcg cct att ggc tct cgg ggg cca cag ctg ctc ctg 240
 Ser Ala Thr Leu Ala Pro Ile Gly Ser Arg Gly Pro Gln Leu Leu Leu
 65 70 75 80

 cgc ctg ggc ctt act tcc tgc cga gtt cta tgt cca gtg cag cct gac 288
 Arg Leu Gly Leu Thr Ser Cys Arg Val Leu Cys Pro Val Gln Pro Asp
 85 90 95

 ttc tga 294
 Phe *

<210> 394
 <211> 97
 <212> PRT
 <213> Homo sapiens

<400> 394
 Met Asp Pro Glu Val Thr Leu Leu Leu Gln Cys Pro Gly Gly Gly Leu
 1 5 10 15
 Pro Gln Glu Gln Ile Gln Ala Glu Leu Ser Pro Ala His Asp Arg Arg
 20 25 30
 Pro Leu Pro Gly Gly Asp Glu Ala Ile Thr Ala Ile Trp Glu Thr Arg
 35 40 45
 Leu Lys Ala Gln Pro Trp Leu Phe Asp Ala Pro Lys Phe Arg Leu His
 50 55 60
 Ser Ala Thr Leu Ala Pro Ile Gly Ser Arg Gly Pro Gln Leu Leu Leu
 65 70 75 80
 Arg Leu Gly Leu Thr Ser Cys Arg Val Leu Cys Pro Val Gln Pro Asp
 85 90 95

 Phe

<210> 395
 <211> 303
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

528

<222> (1)...(303)

<400> 395

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| atg | cga | caa | gtt | ttt | ggt | gat | gag | aag | aag | tac | tgg | ttg | cta | ccc | att | 48 |
| Met | Arg | Gln | Val | Phe | Gly | Asp | Glu | Lys | Lys | Tyr | Trp | Leu | Leu | Pro | Ile | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| ttt | tca | agt | cta | ggt | gat | ggc | tgc | tcc | ttt | cca | act | tgc | ctt | gtt | aac | 96 |
| Phe | Ser | Ser | Leu | Gly | Asp | Gly | Cys | Ser | Phe | Pro | Thr | Cys | Leu | Val | Asn | |
| | | | 20 | | | | | 25 | | | | | | 30 | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| cag | gat | cct | gaa | caa | gca | tct | act | cct | gca | ggg | ctg | aat | tcc | aca | gct | 144 |
| Gln | Asp | Pro | Glu | Gln | Ala | Ser | Thr | Pro | Ala | Gly | Leu | Asn | Ser | Thr | Ala | |
| | | 35 | | | | | 40 | | | | | | 45 | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| aaa | aat | ctc | gaa | aac | cat | cag | ttt | cct | gca | aag | cca | ttg | aga | gag | tcc | 192 |
| Lys | Asn | Leu | Glu | Asn | His | Gln | Phe | Pro | Ala | Lys | Pro | Leu | Arg | Glu | Ser | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| cag | agc | cac | ctt | ctt | act | gat | tct | cag | tct | tgg | acg | gag | agc | agc | ata | 240 |
| Gln | Ser | His | Leu | Leu | Thr | Asp | Ser | Gln | Ser | Trp | Thr | Glu | Ser | Ser | Ile | |
| | 65 | | | | 70 | | | | | 75 | | | | | 80 | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| aac | cca | gga | aaa | tgc | aaa | gct | ggt | atg | agc | aat | cct | gca | tta | acc | atg | 288 |
| Asn | Pro | Gly | Lys | Cys | Lys | Ala | Gly | Met | Ser | Asn | Pro | Ala | Leu | Thr | Met | |
| | | | 85 | | | | | 90 | | | | | | 95 | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|--|--|--|--|--|--|--|--|--|--|--|-----|
| gaa | aat | gag | act | taa | | | | | | | | | | | | 303 |
| Glu | Asn | Glu | Thr | * | | | | | | | | | | | | |
| | | | 100 | | | | | | | | | | | | | |

<210> 396

<211> 100

<212> PRT

<213> Homo sapiens

<400> 396

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Arg | Gln | Val | Phe | Gly | Asp | Glu | Lys | Lys | Tyr | Trp | Leu | Leu | Pro | Ile | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| Phe | Ser | Ser | Leu | Gly | Asp | Gly | Cys | Ser | Phe | Pro | Thr | Cys | Leu | Val | Asn | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Gln | Asp | Pro | Glu | Gln | Ala | Ser | Thr | Pro | Ala | Gly | Leu | Asn | Ser | Thr | Ala | |
| | | 35 | | | | | 40 | | | | | | 45 | | | |

529

Lys Asn Leu Glu Asn His Gln Phe Pro Ala Lys Pro Leu Arg Glu Ser
 50 55 60
 Gln Ser His Leu Leu Thr Asp Ser Gln Ser Trp Thr Glu Ser Ser Ile
 65 70 75 80
 Asn Pro Gly Lys Cys Lys Ala Gly Met Ser Asn Pro Ala Leu Thr Met
 85 90 95
 Glu Asn Glu Thr
 100

<210> 397
 <211> 141
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(141)

<400> 397
 atg ctc tcc ttc ctg ccc ttc ctg gtg ctg ctg gtt ttc atc agg aac 48
 Met Leu Ser Phe Leu Pro Phe Leu Val Leu Leu Val Phe Ile Arg Asn
 1 5 10 15
 ctc cga gcc ctg tcc atc ttc tcc ctg ttg gcc aac atc acc atg ctg 96
 Leu Arg Ala Leu Ser Ile Phe Ser Leu Leu Ala Asn Ile Thr Met Leu
 20 25 30
 gtc agc ttg gtc atg atc tac cag ttc att gtt cag atc ctg tga 141
 Val Ser Leu Val Met Ile Tyr Gln Phe Ile Val Gln Ile Leu *
 35 40 45

<210> 398
 <211> 46
 <212> PRT
 <213> Homo sapiens

<400> 398
 Met Leu Ser Phe Leu Pro Phe Leu Val Leu Leu Val Phe Ile Arg Asn
 1 5 10 15
 Leu Arg Ala Leu Ser Ile Phe Ser Leu Leu Ala Asn Ile Thr Met Leu
 20 25 30
 Val Ser Leu Val Met Ile Tyr Gln Phe Ile Val Gln Ile Leu
 35 40 45

530

<210> 399
 <211> 360
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(360)

<400> 399
 atg cag agc agc cac gcc tac tgc aca cct ctc aat gca gct tta cag 48
 Met Gln Ser Ser His Ala Tyr Cys Thr Pro Leu Asn Ala Ala Leu Gln
 1 5 10 15
 gct tca atg gct gag aat agt ata cct cta tac act acc gct tcc atg 96
 Ala Ser Met Ala Glu Asn Ser Ile Pro Leu Tyr Thr Thr Ala Ser Met
 20 25 30
 gga aat ccc act ctg ggc aac tta gcc agc gca ata cgg gaa gag ctg 144
 Gly Asn Pro Thr Leu Gly Asn Leu Ala Ser Ala Ile Arg Glu Glu Leu
 35 40 45
 aac ggg gca atg gag cat acc aac agc aac gag agt gac agc agt cca 192
 Asn Gly Ala Met Glu His Thr Asn Ser Asn Glu Ser Asp Ser Ser Pro
 50 55 60
 ggc aga tct cct atg caa gcc gtg cat cct gta cac gtc aaa gaa gag 240
 Gly Arg Ser Pro Met Gln Ala Val His Pro Val His Val Lys Glu Glu
 65 70 75 80
 ccc ctc gat cca gag gaa gct gaa ggg ccc ctg tcc tta gtg aca aca 288
 Pro Leu Asp Pro Glu Glu Ala Glu Gly Pro Leu Ser Leu Val Thr Thr
 85 90 95
 gcc aac cac agt cca gat ttt gac cat gac aga gat tac gaa gat gaa 336
 Ala Asn His Ser Pro Asp Phe Asp His Asp Arg Asp Tyr Glu Asp Glu
 100 105 110
 cca gta aac gag gac atg gag tga 360
 Pro Val Asn Glu Asp Met Glu *
 115

531

<210> 400
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 400
 Met Gln Ser Ser His Ala Tyr Cys Thr Pro Leu Asn Ala Ala Leu Gln
 1 5 10 15
 Ala Ser Met Ala Glu Asn Ser Ile Pro Leu Tyr Thr Thr Ala Ser Met
 20 25 30
 Gly Asn Pro Thr Leu Gly Asn Leu Ala Ser Ala Ile Arg Glu Glu Leu
 35 40 45
 Asn Gly Ala Met Glu His Thr Asn Ser Asn Glu Ser Asp Ser Ser Pro
 50 55 60
 Gly Arg Ser Pro Met Gln Ala Val His Pro Val His Val Lys Glu Glu
 65 70 75 80
 Pro Leu Asp Pro Glu Ala Glu Gly Pro Leu Ser Leu Val Thr Thr
 85 90 95
 Ala Asn His Ser Pro Asp Phe Asp His Asp Arg Asp Tyr Glu Asp Glu
 100 105 110
 Pro Val Asn Glu Asp Met Glu
 115

<210> 401
 <211> 474
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(474)

<400> 401
 atg tcg aaa agc tgt gga aat aat tta gcg gcc att tct gta gga att 48
 Met Ser Lys Ser Cys Gly Asn Asn Leu Ala Ala Ile Ser Val Gly Ile
 1 5 10 15
 tcg ctt ctt tta ctc tta gtg gtt tgt gga att ggg tgt gtt tgg cac 96
 Ser Leu Leu Leu Leu Val Val Cys Gly Ile Gly Cys Val Trp His
 20 25 30
 tgg aaa cac cgt gtt gcc aca cga ttt acc tta ccg agg ttt tta caa 144
 Trp Lys His Arg Val Ala Thr Arg Phe Thr Leu Pro Arg Phe Leu Gln
 35 40 45

532

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agg aga agc agc agg aga aaa gtc tgt act aaa aca ttc ttg ggc ccc      192
Arg Arg Ser Ser Arg Arg Lys Val Cys Thr Lys Thr Phe Leu Gly Pro
      50                      55                      60

cgc atc att ggc tta agg cat gaa atc tca gtt gaa acc caa gac cac      240
Arg Ile Ile Gly Leu Arg His Glu Ile Ser Val Glu Thr Gln Asp His
      65                      70                      75                      80

aaa tct gct gtc agg gga aat aac aca cac gac aac tat gaa aat gtg      288
Lys Ser Ala Val Arg Gly Asn Asn Thr His Asp Asn Tyr Glu Asn Val
                      85                      90                      95

gaa gca ggt cct ccc aaa gct aaa gga aaa acc gat aag gaa cta tat      336
Glu Ala Gly Pro Pro Lys Ala Lys Gly Lys Thr Asp Lys Glu Leu Tyr
                      100                      105                      110

gaa aac aca ggg cag tct aat ttc gag gag cat atc tat gga aat gag      384
Glu Asn Thr Gly Gln Ser Asn Phe Glu Glu His Ile Tyr Gly Asn Glu
                      115                      120                      125

aca tct tct gac tat tat aac ttc cag aag cct cgt cct tct gaa gtt      432
Thr Ser Ser Asp Tyr Tyr Asn Phe Gln Lys Pro Arg Pro Ser Glu Val
                      130                      135                      140

cct caa gat gaa gat ata tac att ctt cca gat tca tat tag      474
Pro Gln Asp Glu Asp Ile Tyr Ile Leu Pro Asp Ser Tyr *
      145                      150                      155

```

<210> 402

<211> 157

<212> PRT

<213> Homo sapiens

<400> 402

```

Met Ser Lys Ser Cys Gly Asn Asn Leu Ala Ala Ile Ser Val Gly Ile
  1                      5                      10                      15
Ser Leu Leu Leu Leu Leu Val Val Cys Gly Ile Gly Cys Val Trp His
      20                      25                      30
Trp Lys His Arg Val Ala Thr Arg Phe Thr Leu Pro Arg Phe Leu Gln
      35                      40                      45
Arg Arg Ser Ser Arg Arg Lys Val Cys Thr Lys Thr Phe Leu Gly Pro
      50                      55                      60

```


533

Arg Ile Ile Gly Leu Arg His Glu Ile Ser Val Glu Thr Gln Asp His
 65 70 75 80
 Lys Ser Ala Val Arg Gly Asn Asn Thr His Asp Asn Tyr Glu Asn Val
 85 90 95
 Glu Ala Gly Pro Pro Lys Ala Lys Gly Lys Thr Asp Lys Glu Leu Tyr
 100 105 110
 Glu Asn Thr Gly Gln Ser Asn Phe Glu Glu His Ile Tyr Gly Asn Glu
 115 120 125
 Thr Ser Ser Asp Tyr Tyr Asn Phe Gln Lys Pro Arg Pro Ser Glu Val
 130 135 140
 Pro Gln Asp Glu Asp Ile Tyr Ile Leu Pro Asp Ser Tyr
 145 150 155

<210> 403
 <211> 279
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(279)

<400> 403
 atg tgg cct gtg ttt tgg acc gtg gtt cgt acc tat gct cct tat gtc 48
 Met Trp Pro Val Phe Trp Thr Val Val Arg Thr Tyr Ala Pro Tyr Val
 1 5 10 15
 aca ttc cct gtt gcc ttc gtg gtc ggg gct gtg ggt tac cac ctg gaa 96
 Thr Phe Pro Val Ala Phe Val Val Gly Ala Val Gly Tyr His Leu Glu
 20 25 30
 tgg ttc atc agg gga aag gac ccc cag ccc gtg gag gag gaa aag agc 144
 Trp Phe Ile Arg Gly Lys Asp Pro Gln Pro Val Glu Glu Glu Lys Ser
 35 40 45
 atc tca gag cgc cgg gag gat cgc aag ctg gat gag ctt cta ggc aag 192
 Ile Ser Glu Arg Arg Glu Asp Arg Lys Leu Asp Glu Leu Leu Gly Lys
 50 55 60
 gac cac acg cag gtg gtg agc ctt aag gac aag cta gaa ttt gcc ccg 240
 Asp His Thr Gln Val Val Ser Leu Lys Asp Lys Leu Glu Phe Ala Pro
 65 70 75 80
 aaa gct gtg ctg aac aga aac cgc cca gag aag aat taa 279

534

Lys Ala Val Leu Asn Arg Asn Arg Pro Glu Lys Asn *
 85 90

<210> 404

<211> 92

<212> PRT

<213> Homo sapiens

<400> 404

Met Trp Pro Val Phe Trp Thr Val Val Arg Thr Tyr Ala Pro Tyr Val
 1 5 10 15
 Thr Phe Pro Val Ala Phe Val Val Gly Ala Val Gly Tyr His Leu Glu
 20 25 30
 Trp Phe Ile Arg Gly Lys Asp Pro Gln Pro Val Glu Glu Glu Lys Ser
 35 40 45
 Ile Ser Glu Arg Arg Glu Asp Arg Lys Leu Asp Glu Leu Leu Gly Lys
 50 55 60
 Asp His Thr Gln Val Val Ser Leu Lys Asp Lys Leu Glu Phe Ala Pro
 65 70 75 80
 Lys Ala Val Leu Asn Arg Asn Arg Pro Glu Lys Asn
 85 90

<210> 405

<211> 255

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(255)

<400> 405

atg agt gaa ttc tgg ttg tgt ttc aac tgc tgt att gca gaa cag cct 48
 Met Ser Glu Phe Trp Leu Cys Phe Asn Cys Cys Ile Ala Glu Gln Pro
 1 5 10 15
 cag cct aaa agg cga cgg cgg att gac aga agt atg att gga gag ccc 96
 Gln Pro Lys Arg Arg Arg Arg Ile Asp Arg Ser Met Ile Gly Glu Pro
 20 25 30
 aca aac ttt gtg cat aca gct cat gtt gga tca gga gac ctg ttc agt 144
 Thr Asn Phe Val His Thr Ala His Val Gly Ser Gly Asp Leu Phe Ser
 35 40 45

535

gga atg aat tca gtt agc tcc att cag aac caa atg cag tcc aag gga 192
 Gly Met Asn Ser Val Ser Ser Ile Gln Asn Gln Met Gln Ser Lys Gly
 50 55 60

ggt tat gga ggt gga atg cct gcc aat gtc cag atg cag ctc gtg gat 240
 Gly Tyr Gly Gly Gly Met Pro Ala Asn Val Gln Met Gln Leu Val Asp
 65 70 75 80

acg aag gcg gga tag 255
 Thr Lys Ala Gly *

<210> 406
 <211> 84
 <212> PRT
 <213> Homo sapiens

<400> 406
 Met Ser Glu Phe Trp Leu Cys Phe Asn Cys Cys Ile Ala Glu Gln Pro
 1 5 10 15
 Gln Pro Lys Arg Arg Arg Arg Ile Asp Arg Ser Met Ile Gly Glu Pro
 20 25 30
 Thr Asn Phe Val His Thr Ala His Val Gly Ser Gly Asp Leu Phe Ser
 35 40 45
 Gly Met Asn Ser Val Ser Ser Ile Gln Asn Gln Met Gln Ser Lys Gly
 50 55 60
 Gly Tyr Gly Gly Gly Met Pro Ala Asn Val Gln Met Gln Leu Val Asp
 65 70 75 80
 Thr Lys Ala Gly

<210> 407
 <211> 249
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(249)

<400> 407
 atg gcg agt agc ggc ggt gct ggg gcg gcg gcg gcc gcg gcg gcg 48

536

Met Ala Ser Ser Gly Gly Ala Gly Ala Ala Ala Ala Ala Ala Ala
 1 5 10 15

aat ctg aat gcg gtg cgg gag acc atg gac gtt ctg ctt gag att tca 96
 Asn Leu Asn Ala Val Arg Glu Thr Met Asp Val Leu Leu Glu Ile Ser
 20 25 30

aga att ttg aat act ggc tta gat atg gaa act ctg tct att tgt gta 144
 Arg Ile Leu Asn Thr Gly Leu Asp Met Glu Thr Leu Ser Ile Cys Val
 35 40 45

cgg ctt tgt gaa caa gga att aac cca gaa gct tta tca tcg gtt att 192
 Arg Leu Cys Glu Gln Gly Ile Asn Pro Glu Ala Leu Ser Ser Val Ile
 50 55 60

aag gag ctt cgc aag gct act gaa gca ctg aag gct gct gaa aat atg 240
 Lys Glu Leu Arg Lys Ala Thr Glu Ala Leu Lys Ala Ala Glu Asn Met
 65 70 75 80

aca agc tga 249
 Thr Ser *

<210> 408

<211> 82

<212> PRT

<213> Homo sapiens

<400> 408

Met Ala Ser Ser Gly Gly Ala Gly Ala Ala Ala Ala Ala Ala Ala
 1 5 10 15

Asn Leu Asn Ala Val Arg Glu Thr Met Asp Val Leu Leu Glu Ile Ser
 20 25 30

Arg Ile Leu Asn Thr Gly Leu Asp Met Glu Thr Leu Ser Ile Cys Val
 35 40 45

Arg Leu Cys Glu Gln Gly Ile Asn Pro Glu Ala Leu Ser Ser Val Ile
 50 55 60

Lys Glu Leu Arg Lys Ala Thr Glu Ala Leu Lys Ala Ala Glu Asn Met
 65 70 75 80

Thr Ser

<210> 409

537

<211> 156
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(156)

<400> 409
 atg cag.tgc tgc ctg ctg ctg cgc tgg ctg gca tct gcc ctc ctc cgt 48
 Met Gln Cys Cys Leu Leu Leu Arg Trp Leu Ala Ser Ala Leu Leu Arg
 1 5 10 15
 ctc ctg ggt gct gcc aca gag aag aga gag aga gtg aag cgg gca gag 96
 Leu Leu Gly Ala Ala Thr Glu Lys Arg Glu Arg Val Lys Arg Ala Glu
 20 25 30
 act ggc tgt tgc cat cac aca act gag ggc gga cct gga gct cac cgg 144
 Thr Gly Cys Cys His His Thr Thr Glu Gly Gly Pro Gly Ala His Arg
 35 40 45
 ctg agg gtt tga 156
 Leu Arg Val *
 50

<210> 410
 <211> 51
 <212> PRT
 <213> Homo sapiens

<400> 410
 Met Gln Cys Cys Leu Leu Leu Arg Trp Leu Ala Ser Ala Leu Leu Arg
 1 5 10 15
 Leu Leu Gly Ala Ala Thr Glu Lys Arg Glu Arg Val Lys Arg Ala Glu
 20 25 30
 Thr Gly Cys Cys His His Thr Thr Glu Gly Gly Pro Gly Ala His Arg
 35 40 45
 Leu Arg Val
 50

<210> 411
 <211> 420
 <212> DNA

538

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(420)

<221> misc_feature

<222> (1)...(420)

<223> n = A,T,C or G

<400> 411

| | |
|---|-----|
| atg cac gtc act gag gct ctg cac cag aac atg cag gct ctg ttt agc | 48 |
| Met His Val Thr Glu Ala Leu His Gln Asn Met Gln Ala Leu Phe Ser | |
| 1 5 10 15 | |
| acc ctg gct cag gcg gag gag cag cag ccc tac ctg gag ggc tcc acc | 96 |
| Thr Leu Ala Gln Ala Glu Glu Gln Gln Pro Tyr Leu Glu Gly Ser Thr | |
| 20 25 30 | |
| gtt atg cgc ggg act cgc tgt ctg gca gag tac cac ctg ggg gat tat | 144 |
| Val Met Arg Gly Thr Arg Cys Leu Ala Glu Tyr His Leu Gly Asp Tyr | |
| 35 40 45 | |
| gga cac gcc tgg aac agg tgt tgg gtg ctg gac agg gtg gac acc tgg | 192 |
| Gly His Ala Trp Asn Arg Cys Trp Val Leu Asp Arg Val Asp Thr Trp | |
| 50 55 60 | |
| gct gtg gtc atg ttc att gat ttt gga cag ttg gcc acc atc cct gtg | 240 |
| Ala Val Val Met Phe Ile Asp Phe Gly Gln Leu Ala Thr Ile Pro Val | |
| 65 70 75 80 | |
| cag tct ctg cgc anc tna gac agc gac gac ttc tgg acc atc cca ccc | 288 |
| Gln Ser Leu Arg Xaa Xaa Asp Ser Asp Asp Phe Trp Thr Ile Pro Pro | |
| 85 90 95 | |
| ctg act cag cca ttc atg ctg gag aaa gac att ttg agt tcg tat gag | 336 |
| Leu Thr Gln Pro Phe Met Leu Glu Lys Asp Ile Leu Ser Ser Tyr Glu | |
| 100 105 110 | |
| gtt gtc cat cga atc ctc aaa ggg aaa atc act ggt gct ttg aac tcg | 384 |
| Val Val His Arg Ile Leu Lys Gly Lys Ile Thr Gly Ala Leu Asn Ser | |
| 115 120 125 | |
| gcg ttg cac atc cta aag ttt gaa gag tct aaa taa | 420 |

539

Ala Leu His Ile Leu Lys Phe Glu Glu Ser Lys *
 130 135

<210> 412

<211> 139

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(139)

<223> Xaa = Any Amino Acid

<400> 412

Met His Val Thr Glu Ala Leu His Gln Asn Met Gln Ala Leu Phe Ser
 1 5 10 15
 Thr Leu Ala Gln Ala Glu Glu Gln Gln Pro Tyr Leu Glu Gly Ser Thr
 20 25 30
 Val Met Arg Gly Thr Arg Cys Leu Ala Glu Tyr His Leu Gly Asp Tyr
 35 40 45
 Gly His Ala Trp Asn Arg Cys Trp Val Leu Asp Arg Val Asp Thr Trp
 50 55 60
 Ala Val Val Met Phe Ile Asp Phe Gly Gln Leu Ala Thr Ile Pro Val
 65 70 75 80
 Gln Ser Leu Arg Xaa Xaa Asp Ser Asp Asp Phe Trp Thr Ile Pro Pro
 85 90 95
 Leu Thr Gln Pro Phe Met Leu Glu Lys Asp Ile Leu Ser Ser Tyr Glu
 100 105 110
 Val Val His Arg Ile Leu Lys Gly Lys Ile Thr Gly Ala Leu Asn Ser
 115 120 125
 Ala Leu His Ile Leu Lys Phe Glu Glu Ser Lys
 130 135

<210> 413

<211> 795

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(795)

<400> 413

540

| | |
|---|-----|
| atg ttc gtt ccc tgc ggg gag tcg gcc ccc gac ctt gcc ggc ttc acc | 48 |
| Met Phe Val Pro Cys Gly Glu Ser Ala Pro Asp Leu Ala Gly Phe Thr | |
| 1 5 10 15 | |
| ctc cta atg cca gca gta tct gtt gga aat gtt ggc cag ctt gca atg | 96 |
| Leu Leu Met Pro Ala Val Ser Val Gly Asn Val Gly Gln Leu Ala Met | |
| 20 25 30 | |
| gat ctg att att tct aca ctg aat atg tct aag att ggt tac ttc tat | 144 |
| Asp Leu Ile Ile Ser Thr Leu Asn Met Ser Lys Ile Gly Tyr Phe Tyr | |
| 35 40 45 | |
| acc gat tgt ctt gtg cca atg gtt gga aac aat cca tat gcg acc aca | 192 |
| Thr Asp Cys Leu Val Pro Met Val Gly Asn Asn Pro Tyr Ala Thr Thr | |
| 50 55 60 | |
| gaa gga aat tca aca gaa ctt agc ata aat gct gaa gtg tat tca ttg | 240 |
| Glu Gly Asn Ser Thr Glu Leu Ser Ile Asn Ala Glu Val Tyr Ser Leu | |
| 65 70 75 80 | |
| cct tca aga aag ctg gtg gct cta cag tta aga tcc att ttt att aag | 288 |
| Pro Ser Arg Lys Leu Val Ala Leu Gln Leu Arg Ser Ile Phe Ile Lys | |
| 85 90 95 | |
| tat aaa tca aag cca ttc tgt gaa aaa ctg ctt tcc tgg gtg aaa agc | 336 |
| Tyr Lys Ser Lys Pro Phe Cys Glu Lys Leu Leu Ser Trp Val Lys Ser | |
| 100 105 110 | |
| agt ggc tgt gcc aga gtc att gtt ctt tca agc agt cat tca tat cag | 384 |
| Ser Gly Cys Ala Arg Val Ile Val Leu Ser Ser Ser His Ser Tyr Gln | |
| 115 120 125 | |
| cgt aat gat ctg cag ctt cgt agt act ccc ttc cgg tac cta ctt aca | 432 |
| Arg Asn Asp Leu Gln Leu Arg Ser Thr Pro Phe Arg Tyr Leu Leu Thr | |
| 130 135 140 | |
| cct tcc atg caa aaa agt gtt caa aat aaa ata aag agc ctt aac tgg | 480 |
| Pro Ser Met Gln Lys Ser Val Gln Asn Lys Ile Lys Ser Leu Asn Trp | |
| 145 150 155 160 | |
| gaa gaa atg gaa aaa agc cgg tgc att cct gaa ata gat gat tcc gag | 528 |
| Glu Glu Met Glu Lys Ser Arg Cys Ile Pro Glu Ile Asp Asp Ser Glu | |
| 165 170 175 | |

541

ttt tgt atc cgc att ccg gga gga ggt atc aca aaa aca ctc tat gat 576
 Phe Cys Ile Arg Ile Pro Gly Gly Gly Ile Thr Lys Thr Leu Tyr Asp
 180 185 190

 gaa agc tgt tct aaa gaa atc caa atg gca gtt ctg ctg aaa ttt gtt 624
 Glu Ser Cys Ser Lys Glu Ile Gln Met Ala Val Leu Leu Lys Phe Val
 195 200 205

 tca gaa ggg gac aac atc cca gat gca tta ggt ctt gtt gag tat ctt 672
 Ser Glu Gly Asp Asn Ile Pro Asp Ala Leu Gly Leu Val Glu Tyr Leu
 210 215 220

 aat gag tgg ctt cag ata ctc aaa cca ctt agc gat gac ccc aca gta 720
 Asn Glu Trp Leu Gln Ile Leu Lys Pro Leu Ser Asp Asp Pro Thr Val
 225 230 235 240

 tct gcc tca cgg tgg aaa ata cca agt tct tgg aga tta ctc ttt ggc 768
 Ser Ala Ser Arg Trp Lys Ile Pro Ser Ser Trp Arg Leu Leu Phe Gly
 245 250 255

 agt ggt ctt ccc cct gca ctt ttc tga 795
 Ser Gly Leu Pro Pro Ala Leu Phe *
 260

<210> 414
 <211> 264
 <212> PRT
 <213> Homo sapiens

<400> 414
 Met Phe Val Pro Cys Gly Glu Ser Ala Pro Asp Leu Ala Gly Phe Thr
 1 5 10 15
 Leu Leu Met Pro Ala Val Ser Val Gly Asn Val Gly Gln Leu Ala Met
 20 25 30
 Asp Leu Ile Ile Ser Thr Leu Asn Met Ser Lys Ile Gly Tyr Phe Tyr
 35 40 45
 Thr Asp Cys Leu Val Pro Met Val Gly Asn Asn Pro Tyr Ala Thr Thr
 50 55 60
 Glu Gly Asn Ser Thr Glu Leu Ser Ile Asn Ala Glu Val Tyr Ser Leu
 65 70 75 80
 Pro Ser Arg Lys Leu Val Ala Leu Gln Leu Arg Ser Ile Phe Ile Lys
 85 90 95
 Tyr Lys Ser Lys Pro Phe Cys Glu Lys Leu Leu Ser Trp Val Lys Ser

542

100 105 110
 Ser Gly Cys Ala Arg Val Ile Val Leu Ser Ser Ser His Ser Tyr Gln
 115 120 125
 Arg Asn Asp Leu Gln Leu Arg Ser Thr Pro Phe Arg Tyr Leu Leu Thr
 130 135 140
 Pro Ser Met Gln Lys Ser Val Gln Asn Lys Ile Lys Ser Leu Asn Trp
 145 150 155 160
 Glu Glu Met Glu Lys Ser Arg Cys Ile Pro Glu Ile Asp Asp Ser Glu
 165 170 175
 Phe Cys Ile Arg Ile Pro Gly Gly Gly Ile Thr Lys Thr Leu Tyr Asp
 180 185 190
 Glu Ser Cys Ser Lys Glu Ile Gln Met Ala Val Leu Leu Lys Phe Val
 195 200 205
 Ser Glu Gly Asp Asn Ile Pro Asp Ala Leu Gly Leu Val Glu Tyr Leu
 210 215 220
 Asn Glu Trp Leu Gln Ile Leu Lys Pro Leu Ser Asp Asp Pro Thr Val
 225 230 235 240
 Ser Ala Ser Arg Trp Lys Ile Pro Ser Ser Trp Arg Leu Leu Phe Gly
 245 250 255
 Ser Gly Leu Pro Pro Ala Leu Phe
 260

<210> 415
 <211> 225
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(225)

<400> 415
 atg ggg aaa tta ttc tgg att ata cag atg gac tgt gtt cag tca cag 48
 Met Gly Lys Leu Phe Trp Ile Ile Gln Met Asp Cys Val Gln Ser Gln
 1 5 10 15
 gag ctc tta aaa gca gag acg ctt tcc cag ctt ggg tca gag aga ttc 96
 Glu Leu Leu Lys Ala Glu Thr Leu Ser Gln Leu Gly Ser Glu Arg Phe
 20 25 30
 atc atg aga aga tct cca cta gct gtt gct gga ttt cag gat gga gga 144
 Ile Met Arg Arg Ser Pro Leu Ala Val Ala Gly Phe Gln Asp Gly Gly
 35 40 45

544

aaa gag ttg aat gag aaa caa cca tct tta tct ttt ggt ctt gct ata 144
 Lys Glu Leu Asn Glu Lys Gln Pro Ser Leu Ser Phe Gly Leu Ala Ile
 35 40 45

ctt cat ctg ttc tct gca gac atg aaa aaa gtt ggc att aag cta ctt 192
 Leu His Leu Phe Ser Ala Asp Met Lys Lys Val Gly Ile Lys Leu Leu
 50 55 60

caa gaa atc aat aaa ggt ggg ata gat gca gta gaa agt ctt atg ata 240
 Gln Glu Ile Asn Lys Gly Gly Ile Asp Ala Val Glu Ser Leu Met Ile
 65 70 75 80

aat gat tcc ttt tgc tcc ata gaa aag tgg caa gaa gtg gca aat ata 288
 Asn Asp Ser Phe Cys Ser Ile Glu Lys Trp Gln Glu Val Ala Asn Ile
 85 90 95

tgt tca cag aat ggc ttt gac aaa tta tct aat gac atc acg tct att 336
 Cys Ser Gln Asn Gly Phe Asp Lys Leu Ser Asn Asp Ile Thr Ser Ile
 100 105 110

ctt cga tct cag gct gca gtt aca gaa att tct gaa gag gat gac gca 384
 Leu Arg Ser Gln Ala Ala Val Thr Glu Ile Ser Glu Glu Asp Asp Ala
 115 120 125

gtc aac cta atg gaa cat gtg ttt tgg tag 414
 Val Asn Leu Met Glu His Val Phe Trp *
 130 135

<210> 418

<211> 137

<212> PRT

<213> Homo sapiens

<400> 418

Met Glu Tyr Ile Gln Gln Leu Lys Asp Phe Thr Thr Asp Asp Leu Leu
 1 5 10 15

Gln Leu Leu Met Ser Cys Pro Gln Val Glu Leu Ile Gln Cys Leu Thr
 20 25 30

Lys Glu Leu Asn Glu Lys Gln Pro Ser Leu Ser Phe Gly Leu Ala Ile
 35 40 45

Leu His Leu Phe Ser Ala Asp Met Lys Lys Val Gly Ile Lys Leu Leu
 50 55 60

Gln Glu Ile Asn Lys Gly Gly Ile Asp Ala Val Glu Ser Leu Met Ile

65 70 75 80
Asn Asp Ser Phe Cys Ser Ile Glu Lys Trp Gln Glu Val Ala Asn Ile
 85 90 95
Cys Ser Gln Asn Gly Phe Asp Lys Leu Ser Asn Asp Ile Thr Ser Ile
 100 105 110
Leu Arg Ser Gln Ala Ala Val Thr Glu Ile Ser Glu Glu Asp Asp Ala
 115 120 125
Val Asn Leu Met Glu His Val Phe Trp
 130 135

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<210> 419
<211> 285
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (1)...(285)

| | | | | | | | | | | | | | | | | |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> 419 | | | | | | | | | | | | | | | | |
| atg | act | aca | gtt | ccc | acg | tgc | gca | act | ctg | ccc | ttg | gct | caa | gga | ttc | 48 |
| Met | Thr | Thr | Val | Pro | Thr | Cys | Ala | Thr | Leu | Pro | Leu | Ala | Gln | Gly | Phe | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| | | | | | | | | | | | | | | | | |
| cgt | gat | gtt | cat | ttt | ggg | ttt | cta | agc | gag | agg | ctc | cga | gcc | ttc | caa | 96 |
| Arg | Asp | Val | His | Phe | Gly | Phe | Leu | Ser | Glu | Arg | Leu | Arg | Ala | Phe | Gln | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| | | | | | | | | | | | | | | | | |
| cct | ctg | act | ggc | tgg | tcc | tgt | gag | acc | cct | cga | tca | ggg | atg | ctg | ctg | 144 |
| Pro | Leu | Thr | Gly | Trp | Ser | Cys | Glu | Thr | Pro | Arg | Ser | Gly | Met | Leu | Leu | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| | | | | | | | | | | | | | | | | |
| caa | gtg | gtc | atg | gca | gtt | gct | gac | acc | tct | gcg | aag | gcc | gtg | gag | acc | 192 |
| Gln | Val | Val | Met | Ala | Val | Ala | Asp | Thr | Ser | Ala | Lys | Ala | Val | Glu | Thr | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| | | | | | | | | | | | | | | | | |
| gtg | aag | aag | cag | caa | ggc | gag | cag | atc | tgc | tgg | ggg | ggc | agc | agc | tcc | 240 |
| Val | Lys | Lys | Gln | Gln | Gly | Glu | Gln | Ile | Cys | Trp | Gly | Gly | Ser | Ser | Ser | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| | | | | | | | | | | | | | | | | |
| gtc | atg | agt | cta | gct | acc | aag | atg | aat | gaa | cta | atg | gag | aaa | tag | | 285 |
| Val | Met | Ser | Leu | Ala | Thr | Lys | Met | Asn | Glu | Leu | Met | Glu | Lys | * | | |
| | | | | 85 | | | | | 90 | | | | | | | |

546

<210> 420
 <211> 94
 <212> PRT
 <213> Homo sapiens

<400> 420
 Met Thr Thr Val Pro Thr Cys Ala Thr Leu Pro Leu Ala Gln Gly Phe
 1 5 10 15
 Arg Asp Val His Phe Gly Phe Leu Ser Glu Arg Leu Arg Ala Phe Gln
 20 25 30
 Pro Leu Thr Gly Trp Ser Cys Glu Thr Pro Arg Ser Gly Met Leu Leu
 35 40 45
 Gln Val Val Met Ala Val Ala Asp Thr Ser Ala Lys Ala Val Glu Thr
 50 55 60
 Val Lys Lys Gln Gln Gly Glu Gln Ile Cys Trp Gly Gly Ser Ser Ser
 65 70 75 80
 Val Met Ser Leu Ala Thr Lys Met Asn Glu Leu Met Glu Lys
 85 90

<210> 421
 <211> 240
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(240)

<400> 421
 atg cag ggc cgg ctg gag ctc gtg ggc agg ggc tgc cga cct ctg agc 48
 Met Gln Gly Arg Leu Glu Leu Val Gly Arg Gly Cys Arg Pro Leu Ser
 1 5 10 15
 tgg gtg tgc tgg gag cca ggg atc act ggg tgc cgg cca cag agg aag 96
 Trp Val Cys Trp Glu Pro Gly Ile Thr Gly Cys Arg Pro Gln Arg Lys
 20 25 30
 gtc cct gag gac aca gta ccg aag tct gat ccc aga gga gga agg aag 144
 Val Pro Glu Asp Thr Val Pro Lys Ser Asp Pro Arg Gly Gly Arg Lys
 35 40 45
 gtg ggc cgg gga gaa ggt ctg agt gca ggg atg gtc cag gag gag gac 192
 Val Gly Arg Gly Glu Gly Leu Ser Ala Gly Met Val Gln Glu Glu Asp

547

50

55

60

tgg aag ctg cag gat ggc tgc agg ggg ccg tgg acc ctc ctg gcc tga 240
 Trp Lys Leu Gln Asp Gly Cys Arg Gly Pro Trp Thr Leu Leu Ala *
 65 70 75

<210> 422

<211> 79

<212> PRT

<213> Homo sapiens

<400> 422

Met Gln Gly Arg Leu Glu Leu Val Gly Arg Gly Cys Arg Pro Leu Ser
 1 5 10 15
 Trp Val Cys Trp Glu Pro Gly Ile Thr Gly Cys Arg Pro Gln Arg Lys
 20 25 30
 Val Pro Glu Asp Thr Val Pro Lys Ser Asp Pro Arg Gly Gly Arg Lys
 35 40 45
 Val Gly Arg Gly Glu Gly Leu Ser Ala Gly Met Val Gln Glu Glu Asp
 50 55 60
 Trp Lys Leu Gln Asp Gly Cys Arg Gly Pro Trp Thr Leu Leu Ala
 65 70 75

<210> 423

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> peptide tag

<400> 423

Glu Tyr Met Pro Met Glu
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